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(54) Title: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

(57) Abstract: The present invention is directed to novel polypeptides and to nucleic acid molecules encoding those polypeptides. Also provided herein are vectors and host cells comprising those nucleic acid sequences, chimeric polypeptide molecules comprising the polypeptides of the present invention fused to heterologous polypeptide sequences, antibodies which bind to the polypeptides of the present invention and to methods for producing the polypeptides of the present invention.

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SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

FIELD OF THE INVENTION

5 The present invention relates generally to the identification and isolation of novel DNA and to the recombinant production of novel polypeptides.

BACKGROUND OF THE INVENTION

10 Extracellular proteins play important roles in, among other things, the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells, e.g., proliferation, migration, differentiation, or interaction with other cells, is typically governed by information received from other cells and/or the immediate environment. This information is often transmitted by secreted polypeptides (for instance, mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides, and hormones) which are, in turn, received and interpreted by diverse cell receptors or membrane-bound proteins. These secreted polypeptides or signaling molecules normally pass through the cellular secretory pathway to reach their site of
15 action in the extracellular environment.

Secreted proteins have various industrial applications, including as pharmaceuticals, diagnostics, biosensors and bioreactors. Most protein drugs available at present, such as thrombolytic agents, interferons, interleukins, erythropoietins, colony stimulating factors, and various other cytokines, are secretory proteins. Their receptors, which are membrane proteins, also have potential as therapeutic or diagnostic agents. Efforts
20 are being undertaken by both industry and academia to identify new, native secreted proteins. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel secreted proteins. Examples of screening methods and techniques are described in the literature [see, for example, Klein et al., *Proc. Natl. Acad. Sci.* 93:7108-7113 (1996); U.S. Patent No. 5,536,637].

Membrane-bound proteins and receptors can play important roles in, among other things, the formation,
25 differentiation and maintenance of multicellular organisms. The fate of many individual cells, e.g., proliferation, migration, differentiation, or interaction with other cells, is typically governed by information received from other cells and/or the immediate environment. This information is often transmitted by secreted polypeptides (for instance, mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides, and hormones) which are, in turn, received and interpreted by diverse cell receptors or membrane-bound proteins.
30 Such membrane-bound proteins and cell receptors include, but are not limited to, cytokine receptors, receptor kinases, receptor phosphatases, receptors involved in cell-cell interactions, and cellular adhesion molecules like selectins and integrins. For instance, transduction of signals that regulate cell growth and differentiation is regulated in part by phosphorylation of various cellular proteins. Protein tyrosine kinases, enzymes that catalyze that process, can also act as growth factor receptors. Examples include fibroblast growth factor receptor and

nerve growth factor receptor.

Membrane-bound proteins and receptor molecules have various industrial applications, including as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be employed as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction.

5 Efforts are being undertaken by both industry and academia to identify new, native receptor or membrane-bound proteins. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel receptor or membrane-bound proteins.

SUMMARY OF THE INVENTION

10 In one embodiment, the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence that encodes a PRO polypeptide.

15 In one aspect, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule encoding a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

25 In other aspects, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94%
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nucleic acid sequence identity, alternatively at least about 95 % nucleic acid sequence identity, alternatively at least about 96 % nucleic acid sequence identity, alternatively at least about 97 % nucleic acid sequence identity, alternatively at least about 98 % nucleic acid sequence identity and alternatively at least about 99 % nucleic acid sequence identity to (a) a DNA molecule comprising the coding sequence of a full-length PRO polypeptide cDNA as disclosed herein, the coding sequence of a PRO polypeptide lacking the signal peptide as disclosed herein, the coding sequence of an extracellular domain of a transmembrane PRO polypeptide, with or without the signal peptide, as disclosed herein or the coding sequence of any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

In a further aspect, the invention concerns an isolated nucleic acid molecule comprising a nucleotide sequence having at least about 80 % nucleic acid sequence identity, alternatively at least about 81 % nucleic acid sequence identity, alternatively at least about 82 % nucleic acid sequence identity, alternatively at least about 83 % nucleic acid sequence identity, alternatively at least about 84 % nucleic acid sequence identity, alternatively at least about 85 % nucleic acid sequence identity, alternatively at least about 86 % nucleic acid sequence identity, alternatively at least about 87 % nucleic acid sequence identity, alternatively at least about 88 % nucleic acid sequence identity, alternatively at least about 89 % nucleic acid sequence identity, alternatively at least about 90 % nucleic acid sequence identity, alternatively at least about 91 % nucleic acid sequence identity, alternatively at least about 92 % nucleic acid sequence identity, alternatively at least about 93 % nucleic acid sequence identity, alternatively at least about 94 % nucleic acid sequence identity, alternatively at least about 95 % nucleic acid sequence identity, alternatively at least about 96 % nucleic acid sequence identity, alternatively at least about 97 % nucleic acid sequence identity, alternatively at least about 98 % nucleic acid sequence identity and alternatively at least about 99 % nucleic acid sequence identity to (a) a DNA molecule that encodes the same mature polypeptide encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein, or (b) the complement of the DNA molecule of (a).

Another aspect the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence encoding a PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated, or is complementary to such encoding nucleotide sequence, wherein the transmembrane domain(s) of such polypeptide are disclosed herein. Therefore, soluble extracellular domains of the herein described PRO polypeptides are contemplated.

Another embodiment is directed to fragments of a PRO polypeptide coding sequence, or the complement thereof, that may find use as, for example, hybridization probes, for encoding fragments of a PRO polypeptide that may optionally encode a polypeptide comprising a binding site for an anti-PRO antibody or as antisense oligonucleotide probes. Such nucleic acid fragments are usually at least about 10 nucleotides in length, alternatively at least about 15 nucleotides in length, alternatively at least about 20 nucleotides in length, alternatively at least about 30 nucleotides in length, alternatively at least about 40 nucleotides in length, alternatively at least about 50 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 70 nucleotides in length, alternatively at least about 80 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 100 nucleotides in length, alternatively at least about 110 nucleotides in length, alternatively at least about 120 nucleotides in length,

alternatively at least about 130 nucleotides in length, alternatively at least about 140 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 160 nucleotides in length, alternatively at least about 170 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 190 nucleotides in length, alternatively at least about 200 nucleotides in length, alternatively at least about 250 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 350 nucleotides in length, alternatively at least about 400 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 500 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 700 nucleotides in length, alternatively at least about 800 nucleotides in length, alternatively at least about 900 nucleotides in length and alternatively at least about 1000 nucleotides in length, wherein in this context the term "about" means the referenced nucleotide sequence length plus or minus 10% of that referenced length. It is noted that novel fragments of a PRO polypeptide-encoding nucleotide sequence may be determined in a routine manner by aligning the PRO polypeptide-encoding nucleotide sequence with other known nucleotide sequences using any of a number of well known sequence alignment programs and determining which PRO polypeptide-encoding nucleotide sequence fragment(s) are novel. All of such PRO polypeptide-encoding nucleotide sequences are contemplated herein. Also contemplated are the PRO polypeptide fragments encoded by these nucleotide molecule fragments, preferably those PRO polypeptide fragments that comprise a binding site for an anti-PRO antibody.

In another embodiment, the invention provides isolated PRO polypeptide encoded by any of the isolated nucleic acid sequences hereinabove identified.

In a certain aspect, the invention concerns an isolated PRO polypeptide, comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein.

In a further aspect, the invention concerns an isolated PRO polypeptide comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83%

amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to an amino acid sequence encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein.

In a specific aspect, the invention provides an isolated PRO polypeptide without the N-terminal signal sequence and/or the initiating methionine and is encoded by a nucleotide sequence that encodes such an amino acid sequence as hereinbefore described. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

Another aspect the invention provides an isolated PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

In yet another embodiment, the invention concerns agonists and antagonists of a native PRO polypeptide as defined herein. In a particular embodiment, the agonist or antagonist is an anti-PRO antibody or a small molecule.

In a further embodiment, the invention concerns a method of identifying agonists or antagonists to a PRO polypeptide which comprise contacting the PRO polypeptide with a candidate molecule and monitoring a biological activity mediated by said PRO polypeptide. Preferably, the PRO polypeptide is a native PRO polypeptide.

In a still further embodiment, the invention concerns a composition of matter comprising a PRO polypeptide, or an agonist or antagonist of a PRO polypeptide as herein described, or an anti-PRO antibody, in combination with a carrier. Optionally, the carrier is a pharmaceutically acceptable carrier.

Another embodiment of the present invention is directed to the use of a PRO polypeptide, or an agonist or antagonist thereof as hereinbefore described, or an anti-PRO antibody, for the preparation of a medicament useful in the treatment of a condition which is responsive to the PRO polypeptide, an agonist or antagonist thereof or an anti-PRO antibody.

In other embodiments of the present invention, the invention provides vectors comprising DNA encoding any of the herein described polypeptides. Host cell comprising any such vector are also provided. By way of example, the host cells may be CHO cells, *E. coli*, or yeast. A process for producing any of the herein described

polypeptides is further provided and comprises culturing host cells under conditions suitable for expression of the desired polypeptide and recovering the desired polypeptide from the cell culture.

In other embodiments, the invention provides chimeric molecules comprising any of the herein described polypeptides fused to a heterologous polypeptide or amino acid sequence. Example of such chimeric molecules comprise any of the herein described polypeptides fused to an epitope tag sequence or a Fc region of an immunoglobulin.

In another embodiment, the invention provides an antibody which binds, preferably specifically, to any of the above or below described polypeptides. Optionally, the antibody is a monoclonal antibody, humanized antibody, antibody fragment or single-chain antibody.

In yet other embodiments, the invention provides oligonucleotide probes which may be useful for isolating genomic and cDNA nucleotide sequences, measuring or detecting expression of an associated gene or as antisense probes, wherein those probes may be derived from any of the above or below described nucleotide sequences. Preferred probe lengths are described above.

In yet other embodiments, the present invention is directed to methods of using the PRO polypeptides of the present invention for a variety of uses based upon the functional biological assay data presented in the Examples below.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows a nucleotide sequence (SEQ ID NO:1) of a native sequence PRO276 cDNA, wherein SEQ ID NO:1 is a clone designated herein as "DNA16435-1208".

Figure 2 shows the amino acid sequence (SEQ ID NO:2) derived from the coding sequence of SEQ ID NO:1 shown in Figure 1.

Figure 3 shows a nucleotide sequence (SEQ ID NO:3) of a native sequence PRO284 cDNA, wherein SEQ ID NO:3 is a clone designated herein as "DNA23318-1211".

Figure 4 shows the amino acid sequence (SEQ ID NO:4) derived from the coding sequence of SEQ ID NO:3 shown in Figure 3.

Figure 5 shows a nucleotide sequence (SEQ ID NO:5) of a native sequence PRO193 cDNA, wherein SEQ ID NO:5 is a clone designated herein as "DNA23322-1393".

Figure 6 shows the amino acid sequence (SEQ ID NO:6) derived from the coding sequence of SEQ ID NO:5 shown in Figure 5.

Figure 7 shows a nucleotide sequence (SEQ ID NO:7) of a native sequence PRO190 cDNA, wherein SEQ ID NO:7 is a clone designated herein as "DNA23334-1392".

Figure 8 shows the amino acid sequence (SEQ ID NO:8) derived from the coding sequence of SEQ ID NO:7 shown in Figure 7.

Figure 9 shows a nucleotide sequence (SEQ ID NO:9) of a native sequence PRO180 cDNA, wherein SEQ ID NO:9 is a clone designated herein as "DNA26843-1389".

Figure 10 shows the amino acid sequence (SEQ ID NO:10) derived from the coding sequence of SEQ ID NO:9 shown in Figure 9.

Figure 11 shows a nucleotide sequence (SEQ ID NO:11) of a native sequence PRO194 cDNA, wherein SEQ ID NO:11 is a clone designated herein as "DNA26844-1394".

Figure 12 shows the amino acid sequence (SEQ ID NO:12) derived from the coding sequence of SEQ ID NO:11 shown in Figure 11.

5 Figure 13 shows a nucleotide sequence (SEQ ID NO:13) of a native sequence PRO218 cDNA, wherein SEQ ID NO:13 is a clone designated herein as "DNA30867-1335".

Figure 14 shows the amino acid sequence (SEQ ID NO:14) derived from the coding sequence of SEQ ID NO:13 shown in Figure 13.

Figure 15 shows a nucleotide sequence (SEQ ID NO:15) of a native sequence PRO260 cDNA, wherein SEQ ID NO:15 is a clone designated herein as "DNA33470-1175".

10 Figure 16 shows the amino acid sequence (SEQ ID NO:16) derived from the coding sequence of SEQ ID NO:15 shown in Figure 15.

Figure 17 shows a nucleotide sequence (SEQ ID NO:17) of a native sequence PRO233 cDNA, wherein SEQ ID NO:17 is a clone designated herein as "DNA34436-1238".

15 Figure 18 shows the amino acid sequence (SEQ ID NO:18) derived from the coding sequence of SEQ ID NO:17 shown in Figure 17.

Figure 19 shows a nucleotide sequence (SEQ ID NO:19) of a native sequence PRO234 cDNA, wherein SEQ ID NO:19 is a clone designated herein as "DNA35557-1137".

Figure 20 shows the amino acid sequence (SEQ ID NO:20) derived from the coding sequence of SEQ ID NO:19 shown in Figure 19.

20 Figure 21 shows a nucleotide sequence (SEQ ID NO:21) of a native sequence PRO236 cDNA, wherein SEQ ID NO:21 is a clone designated herein as "DNA35599-1168".

Figure 22 shows the amino acid sequence (SEQ ID NO:22) derived from the coding sequence of SEQ ID NO:21 shown in Figure 21.

25 Figure 23 shows a nucleotide sequence (SEQ ID NO:23) of a native sequence PRO244 cDNA, wherein SEQ ID NO:23 is a clone designated herein as "DNA35668-1171".

Figure 24 shows the amino acid sequence (SEQ ID NO:24) derived from the coding sequence of SEQ ID NO:23 shown in Figure 23.

Figure 25 shows a nucleotide sequence (SEQ ID NO:25) of a native sequence PRO262 cDNA, wherein SEQ ID NO:25 is a clone designated herein as "DNA36992-1168".

30 Figure 26 shows the amino acid sequence (SEQ ID NO:26) derived from the coding sequence of SEQ ID NO:25 shown in Figure 25.

Figure 27 shows a nucleotide sequence (SEQ ID NO:27) of a native sequence PRO271 cDNA, wherein SEQ ID NO:27 is a clone designated herein as "DNA39423-1182".

35 Figure 28 shows the amino acid sequence (SEQ ID NO:28) derived from the coding sequence of SEQ ID NO:27 shown in Figure 27.

Figure 29 shows a nucleotide sequence (SEQ ID NO:29) of a native sequence PRO268 cDNA, wherein SEQ ID NO:29 is a clone designated herein as "DNA39427-1179".

Figure 30 shows the amino acid sequence (SEQ ID NO:30) derived from the coding sequence of SEQ ID NO:29 shown in Figure 29.

Figure 31 shows a nucleotide sequence (SEQ ID NO:31) of a native sequence PRO270 cDNA, wherein SEQ ID NO:31 is a clone designated herein as "DNA39510-1181".

5 Figure 32 shows the amino acid sequence (SEQ ID NO:32) derived from the coding sequence of SEQ ID NO:31 shown in Figure 31.

Figure 33 shows a nucleotide sequence (SEQ ID NO:33) of a native sequence PRO355 cDNA, wherein SEQ ID NO:33 is a clone designated herein as "DNA39518-1247".

Figure 34 shows the amino acid sequence (SEQ ID NO:34) derived from the coding sequence of SEQ ID NO:33 shown in Figure 33.

10 Figure 35 shows a nucleotide sequence (SEQ ID NO:35) of a native sequence PRO298 cDNA, wherein SEQ ID NO:35 is a clone designated herein as "DNA39975-1210".

Figure 36 shows the amino acid sequence (SEQ ID NO:36) derived from the coding sequence of SEQ ID NO:35 shown in Figure 35.

15 Figure 37 shows a nucleotide sequence (SEQ ID NO:37) of a native sequence PRO299 cDNA, wherein SEQ ID NO:37 is a clone designated herein as "DNA39976-1215".

Figure 38 shows the amino acid sequence (SEQ ID NO:38) derived from the coding sequence of SEQ ID NO:37 shown in Figure 37.

Figure 39 shows a nucleotide sequence (SEQ ID NO:39) of a native sequence PRO296 cDNA, wherein SEQ ID NO:39 is a clone designated herein as "DNA39979-1213".

20 Figure 40 shows the amino acid sequence (SEQ ID NO:40) derived from the coding sequence of SEQ ID NO:39 shown in Figure 39.

Figure 41 shows a nucleotide sequence (SEQ ID NO:41) of a native sequence PRO329 cDNA, wherein SEQ ID NO:41 is a clone designated herein as "DNA40594-1233".

25 Figure 42 shows the amino acid sequence (SEQ ID NO:42) derived from the coding sequence of SEQ ID NO:41 shown in Figure 41.

Figure 43 shows a nucleotide sequence (SEQ ID NO:43) of a native sequence PRO330 cDNA, wherein SEQ ID NO:43 is a clone designated herein as "DNA40603-1232".

Figure 44 shows the amino acid sequence (SEQ ID NO:44) derived from the coding sequence of SEQ ID NO:43 shown in Figure 43.

30 Figure 45 shows a nucleotide sequence (SEQ ID NO:45) of a native sequence PRO294 cDNA, wherein SEQ ID NO:45 is a clone designated herein as "DNA40604-1187".

Figure 46 shows the amino acid sequence (SEQ ID NO:46) derived from the coding sequence of SEQ ID NO:45 shown in Figure 45.

35 Figure 47 shows a nucleotide sequence (SEQ ID NO:47) of a native sequence PRO300 cDNA, wherein SEQ ID NO:47 is a clone designated herein as "DNA40625-1189".

Figure 48 shows the amino acid sequence (SEQ ID NO:48) derived from the coding sequence of SEQ ID NO:47 shown in Figure 47.

Figure 49 shows a nucleotide sequence (SEQ ID NO:49) of a native sequence PRO307 cDNA, wherein SEQ ID NO:49 is a clone designated herein as "DNA41225-1217".

Figure 50 shows the amino acid sequence (SEQ ID NO:50) derived from the coding sequence of SEQ ID NO:49 shown in Figure 49.

5 Figure 51 shows a nucleotide sequence (SEQ ID NO:51) of a native sequence PRO334 cDNA, wherein SEQ ID NO:51 is a clone designated herein as "DNA41379-1236".

Figure 52 shows the amino acid sequence (SEQ ID NO:52) derived from the coding sequence of SEQ ID NO:51 shown in Figure 51.

Figure 53 shows a nucleotide sequence (SEQ ID NO:53) of a native sequence PRO352 cDNA, wherein SEQ ID NO:53 is a clone designated herein as "DNA41386-1316".

10 Figure 54 shows the amino acid sequence (SEQ ID NO:54) derived from the coding sequence of SEQ ID NO:53 shown in Figure 53.

Figure 55 shows a nucleotide sequence (SEQ ID NO:55) of a native sequence PRO710 cDNA, wherein SEQ ID NO:55 is a clone designated herein as "DNA44161-1434".

15 Figure 56 shows the amino acid sequence (SEQ ID NO:56) derived from the coding sequence of SEQ ID NO:55 shown in Figure 55.

Figure 57 shows a nucleotide sequence (SEQ ID NO:57) of a native sequence PRO873 cDNA, wherein SEQ ID NO:57 is a clone designated herein as "DNA44179-1362".

Figure 58 shows the amino acid sequence (SEQ ID NO:58) derived from the coding sequence of SEQ ID NO:57 shown in Figure 57.

20 Figure 59 shows a nucleotide sequence (SEQ ID NO:59) of a native sequence PRO354 cDNA, wherein SEQ ID NO:59 is a clone designated herein as "DNA44192-1246".

Figure 60 shows the amino acid sequence (SEQ ID NO:60) derived from the coding sequence of SEQ ID NO:59 shown in Figure 59.

25 Figure 61 shows a nucleotide sequence (SEQ ID NO:61) of a native sequence PRO1151 cDNA, wherein SEQ ID NO:61 is a clone designated herein as "DNA44694-1500".

Figure 62 shows the amino acid sequence (SEQ ID NO:62) derived from the coding sequence of SEQ ID NO:61 shown in Figure 61.

Figure 63 shows a nucleotide sequence (SEQ ID NO:63) of a native sequence PRO382 cDNA, wherein SEQ ID NO:63 is a clone designated herein as "DNA45234-1277".

30 Figure 64 shows the amino acid sequence (SEQ ID NO:64) derived from the coding sequence of SEQ ID NO:63 shown in Figure 63.

Figure 65 shows a nucleotide sequence (SEQ ID NO:65) of a native sequence PRO1864 cDNA, wherein SEQ ID NO:65 is a clone designated herein as "DNA45409-2511".

35 Figure 66 shows the amino acid sequence (SEQ ID NO:66) derived from the coding sequence of SEQ ID NO:65 shown in Figure 65.

Figure 67 shows a nucleotide sequence (SEQ ID NO:67) of a native sequence PRO386 cDNA, wherein SEQ ID NO:67 is a clone designated herein as "DNA45415-1318".

Figure 68 shows the amino acid sequence (SEQ ID NO:68) derived from the coding sequence of SEQ ID NO:67 shown in Figure 67.

Figure 69 shows a nucleotide sequence (SEQ ID NO:69) of a native sequence PRO541 cDNA, wherein SEQ ID NO:69 is a clone designated herein as "DNA45417-1432".

5 Figure 70 shows the amino acid sequence (SEQ ID NO:70) derived from the coding sequence of SEQ ID NO:69 shown in Figure 69.

Figure 71 shows a nucleotide sequence (SEQ ID NO:71) of a native sequence PRO852 cDNA, wherein SEQ ID NO:71 is a clone designated herein as "DNA45493-1349".

Figure 72 shows the amino acid sequence (SEQ ID NO:72) derived from the coding sequence of SEQ ID NO:71 shown in Figure 71.

10 Figure 73 shows a nucleotide sequence (SEQ ID NO:73) of a native sequence PRO700 cDNA, wherein SEQ ID NO:73 is a clone designated herein as "DNA46776-1284".

Figure 74 shows the amino acid sequence (SEQ ID NO:74) derived from the coding sequence of SEQ ID NO:73 shown in Figure 73.

15 Figures 75A-75B show a nucleotide sequence (SEQ ID NO:75) of a native sequence PRO708 cDNA, wherein SEQ ID NO:75 is a clone designated herein as "DNA48296-1292".

Figure 76 shows the amino acid sequence (SEQ ID NO:76) derived from the coding sequence of SEQ ID NO:75 shown in Figures 75A-75B.

Figure 77 shows a nucleotide sequence (SEQ ID NO:77) of a native sequence PRO707 cDNA, wherein SEQ ID NO:77 is a clone designated herein as "DNA48306-1291".

20 Figure 78 shows the amino acid sequence (SEQ ID NO:78) derived from the coding sequence of SEQ ID NO:77 shown in Figure 77.

Figure 79 shows a nucleotide sequence (SEQ ID NO:79) of a native sequence PRO864 cDNA, wherein SEQ ID NO:79 is a clone designated herein as "DNA48328-1355".

25 Figure 80 shows the amino acid sequence (SEQ ID NO:80) derived from the coding sequence of SEQ ID NO:79 shown in Figure 79.

Figure 81 shows a nucleotide sequence (SEQ ID NO:81) of a native sequence PRO706 cDNA, wherein SEQ ID NO:81 is a clone designated herein as "DNA48329-1290".

Figure 82 shows the amino acid sequence (SEQ ID NO:82) derived from the coding sequence of SEQ ID NO:81 shown in Figure 81.

30 Figure 83 shows a nucleotide sequence (SEQ ID NO:83) of a native sequence PRO732 cDNA, wherein SEQ ID NO:83 is a clone designated herein as "DNA48334-1435".

Figure 84 shows the amino acid sequence (SEQ ID NO:84) derived from the coding sequence of SEQ ID NO:83 shown in Figure 83.

35 Figure 85 shows a nucleotide sequence (SEQ ID NO:85) of a native sequence PRO537 cDNA, wherein SEQ ID NO:85 is a clone designated herein as "DNA49141-1431".

Figure 86 shows the amino acid sequence (SEQ ID NO:86) derived from the coding sequence of SEQ ID NO:85 shown in Figure 85.

Figure 87 shows a nucleotide sequence (SEQ ID NO:87) of a native sequence PRO545 cDNA, wherein SEQ ID NO:87 is a clone designated herein as "DNA49624-1279".

Figure 88 shows the amino acid sequence (SEQ ID NO:88) derived from the coding sequence of SEQ ID NO:87 shown in Figure 87.

5 Figure 89 shows a nucleotide sequence (SEQ ID NO:89) of a native sequence PRO718 cDNA, wherein SEQ ID NO:89 is a clone designated herein as "DNA49647-1398".

Figure 90 shows the amino acid sequence (SEQ ID NO:90) derived from the coding sequence of SEQ ID NO:89 shown in Figure 89.

Figure 91 shows a nucleotide sequence (SEQ ID NO:91) of a native sequence PRO872 cDNA, wherein SEQ ID NO:91 is a clone designated herein as "DNA49819-1439".

10 Figure 92 shows the amino acid sequence (SEQ ID NO:92) derived from the coding sequence of SEQ ID NO:91 shown in Figure 91.

Figure 93 shows a nucleotide sequence (SEQ ID NO:93) of a native sequence PRO704 cDNA, wherein SEQ ID NO:93 is a clone designated herein as "DNA50911-1288".

15 Figure 94 shows the amino acid sequence (SEQ ID NO:94) derived from the coding sequence of SEQ ID NO:93 shown in Figure 93.

Figure 95 shows a nucleotide sequence (SEQ ID NO:95) of a native sequence PRO705 cDNA, wherein SEQ ID NO:95 is a clone designated herein as "DNA50914-1289".

Figure 96 shows the amino acid sequence (SEQ ID NO:96) derived from the coding sequence of SEQ ID NO:95 shown in Figure 95.

20 Figure 97 shows a nucleotide sequence (SEQ ID NO:97) of a native sequence PRO871 cDNA, wherein SEQ ID NO:97 is a clone designated herein as "DNA50919-1361".

Figure 98 shows the amino acid sequence (SEQ ID NO:98) derived from the coding sequence of SEQ ID NO:97 shown in Figure 97.

25 Figure 99 shows a nucleotide sequence (SEQ ID NO:99) of a native sequence PRO702 cDNA, wherein SEQ ID NO:99 is a clone designated herein as "DNA50980-1286".

Figure 100 shows the amino acid sequence (SEQ ID NO:100) derived from the coding sequence of SEQ ID NO:99 shown in Figure 99.

Figure 101 shows a nucleotide sequence (SEQ ID NO:101) of a native sequence PRO944 cDNA, wherein SEQ ID NO:101 is a clone designated herein as "DNA52185-1370".

30 Figure 102 shows the amino acid sequence (SEQ ID NO:102) derived from the coding sequence of SEQ ID NO:101 shown in Figure 101.

Figure 103 shows a nucleotide sequence (SEQ ID NO:103) of a native sequence PRO739 cDNA, wherein SEQ ID NO:103 is a clone designated herein as "DNA52756".

35 Figure 104 shows the amino acid sequence (SEQ ID NO:104) derived from the coding sequence of SEQ ID NO:103 shown in Figure 103.

Figure 105 shows a nucleotide sequence (SEQ ID NO:105) of a native sequence PRO941 cDNA, wherein SEQ ID NO:105 is a clone designated herein as "DNA53906-1368".

Figure 106 shows the amino acid sequence (SEQ ID NO:106) derived from the coding sequence of SEQ ID NO:105 shown in Figure 105.

Figure 107 shows a nucleotide sequence (SEQ ID NO:107) of a native sequence PRO1082 cDNA, wherein SEQ ID NO:107 is a clone designated herein as "DNA53912-1457".

5 Figure 108 shows the amino acid sequence (SEQ ID NO:108) derived from the coding sequence of SEQ ID NO:107 shown in Figure 107.

Figure 109 shows a nucleotide sequence (SEQ ID NO:109) of a native sequence PRO1133 cDNA, wherein SEQ ID NO:109 is a clone designated herein as "DNA53913-1490".

Figure 110 shows the amino acid sequence (SEQ ID NO:110) derived from the coding sequence of SEQ ID NO:109 shown in Figure 109.

10 Figure 111 shows a nucleotide sequence (SEQ ID NO:111) of a native sequence PRO983 cDNA, wherein SEQ ID NO:111 is a clone designated herein as "DNA53977-1371".

Figure 112 shows the amino acid sequence (SEQ ID NO:112) derived from the coding sequence of SEQ ID NO:111 shown in Figure 111.

15 Figure 113 shows a nucleotide sequence (SEQ ID NO:113) of a native sequence PRO784 cDNA, wherein SEQ ID NO:113 is a clone designated herein as "DNA53978-1443".

Figure 114 shows the amino acid sequence (SEQ ID NO:114) derived from the coding sequence of SEQ ID NO:113 shown in Figure 113.

Figure 115 shows a nucleotide sequence (SEQ ID NO:115) of a native sequence PRO783 cDNA, wherein SEQ ID NO:115 is a clone designated herein as "DNA53996-1442".

20 Figure 116 shows the amino acid sequence (SEQ ID NO:116) derived from the coding sequence of SEQ ID NO:115 shown in Figure 115.

Figure 117 shows a nucleotide sequence (SEQ ID NO:117) of a native sequence PRO940 cDNA, wherein SEQ ID NO:117 is a clone designated herein as "DNA54002-1367".

25 Figure 118 shows the amino acid sequence (SEQ ID NO:118) derived from the coding sequence of SEQ ID NO:117 shown in Figure 117.

Figure 119 shows a nucleotide sequence (SEQ ID NO:119) of a native sequence PRO768 cDNA, wherein SEQ ID NO:119 is a clone designated herein as "DNA55737-1345".

Figure 120 shows the amino acid sequence (SEQ ID NO:120) derived from the coding sequence of SEQ ID NO:119 shown in Figure 119.

30 Figure 121 shows a nucleotide sequence (SEQ ID NO:121) of a native sequence PRO1079 cDNA, wherein SEQ ID NO:121 is a clone designated herein as "DNA56050-1455".

Figure 122 shows the amino acid sequence (SEQ ID NO:122) derived from the coding sequence of SEQ ID NO:121 shown in Figure 121.

35 Figure 123 shows a nucleotide sequence (SEQ ID NO:123) of a native sequence PRO1078 cDNA, wherein SEQ ID NO:123 is a clone designated herein as "DNA56052-1454".

Figure 124 shows the amino acid sequence (SEQ ID NO:124) derived from the coding sequence of SEQ ID NO:123 shown in Figure 123.

Figure 125 shows a nucleotide sequence (SEQ ID NO:125) of a native sequence PRO1018 cDNA, wherein SEQ ID NO:125 is a clone designated herein as "DNA56107-1415".

Figure 126 shows the amino acid sequence (SEQ ID NO:126) derived from the coding sequence of SEQ ID NO:125 shown in Figure 125.

5 Figure 127 shows a nucleotide sequence (SEQ ID NO:127) of a native sequence PRO793 cDNA, wherein SEQ ID NO:127 is a clone designated herein as "DNA56110-1437".

Figure 128 shows the amino acid sequence (SEQ ID NO:128) derived from the coding sequence of SEQ ID NO:127 shown in Figure 127.

Figure 129 shows a nucleotide sequence (SEQ ID NO:129) of a native sequence PRO1773 cDNA, wherein SEQ ID NO:129 is a clone designated herein as "DNA56406-1704".

10 Figure 130 shows the amino acid sequence (SEQ ID NO:130) derived from the coding sequence of SEQ ID NO:129 shown in Figure 129.

Figure 131 shows a nucleotide sequence (SEQ ID NO:131) of a native sequence PRO1014 cDNA, wherein SEQ ID NO:131 is a clone designated herein as "DNA56409-1377".

15 Figure 132 shows the amino acid sequence (SEQ ID NO:132) derived from the coding sequence of SEQ ID NO:131 shown in Figure 131.

Figure 133 shows a nucleotide sequence (SEQ ID NO:133) of a native sequence PRO1013 cDNA, wherein SEQ ID NO:133 is a clone designated herein as "DNA56410-1414".

Figure 134 shows the amino acid sequence (SEQ ID NO:134) derived from the coding sequence of SEQ ID NO:133 shown in Figure 133.

20 Figure 135 shows a nucleotide sequence (SEQ ID NO:135) of a native sequence PRO937 cDNA, wherein SEQ ID NO:135 is a clone designated herein as "DNA56436-1448".

Figure 136 shows the amino acid sequence (SEQ ID NO:136) derived from the coding sequence of SEQ ID NO:135 shown in Figure 135.

25 Figure 137 shows a nucleotide sequence (SEQ ID NO:137) of a native sequence PRO1477 cDNA, wherein SEQ ID NO:137 is a clone designated herein as "DNA56529-1647".

Figure 138 shows the amino acid sequence (SEQ ID NO:138) derived from the coding sequence of SEQ ID NO:137 shown in Figure 137.

Figure 139 shows a nucleotide sequence (SEQ ID NO:139) of a native sequence PRO842 cDNA, wherein SEQ ID NO:139 is a clone designated herein as "DNA56855-1447".

30 Figure 140 shows the amino acid sequence (SEQ ID NO:140) derived from the coding sequence of SEQ ID NO:139 shown in Figure 139.

Figure 141 shows a nucleotide sequence (SEQ ID NO:141) of a native sequence PRO839 cDNA, wherein SEQ ID NO:141 is a clone designated herein as "DNA56859-1445".

35 Figure 142 shows the amino acid sequence (SEQ ID NO:142) derived from the coding sequence of SEQ ID NO:141 shown in Figure 141.

Figure 143 shows a nucleotide sequence (SEQ ID NO:143) of a native sequence PRO1180 cDNA, wherein SEQ ID NO:143 is a clone designated herein as "DNA56860-1510".

Figure 144 shows the amino acid sequence (SEQ ID NO:144) derived from the coding sequence of SEQ ID NO:143 shown in Figure 143.

Figure 145 shows a nucleotide sequence (SEQ ID NO:145) of a native sequence PRO1134 cDNA, wherein SEQ ID NO:145 is a clone designated herein as "DNA56865-1491".

5 Figure 146 shows the amino acid sequence (SEQ ID NO:146) derived from the coding sequence of SEQ ID NO:145 shown in Figure 145.

Figure 147 shows a nucleotide sequence (SEQ ID NO:147) of a native sequence PRO1115 cDNA, wherein SEQ ID NO:147 is a clone designated herein as "DNA56868-1478".

Figure 148 shows the amino acid sequence (SEQ ID NO:148) derived from the coding sequence of SEQ ID NO:147 shown in Figure 147.

10 Figure 149 shows a nucleotide sequence (SEQ ID NO:149) of a native sequence PRO1277 cDNA, wherein SEQ ID NO:149 is a clone designated herein as "DNA56869-1545".

Figure 150 shows the amino acid sequence (SEQ ID NO:150) derived from the coding sequence of SEQ ID NO:149 shown in Figure 149.

15 Figure 151 shows a nucleotide sequence (SEQ ID NO:151) of a native sequence PRO1135 cDNA, wherein SEQ ID NO:151 is a clone designated herein as "DNA56870-1492".

Figure 152 shows the amino acid sequence (SEQ ID NO:152) derived from the coding sequence of SEQ ID NO:151 shown in Figure 151.

Figure 153 shows a nucleotide sequence (SEQ ID NO:153) of a native sequence PRO827 cDNA, wherein SEQ ID NO:153 is a clone designated herein as "DNA57039-1402".

20 Figure 154 shows the amino acid sequence (SEQ ID NO:154) derived from the coding sequence of SEQ ID NO:153 shown in Figure 153.

Figure 155 shows a nucleotide sequence (SEQ ID NO:155) of a native sequence PRO1057 cDNA, wherein SEQ ID NO:155 is a clone designated herein as "DNA57253-1382".

25 Figure 156 shows the amino acid sequence (SEQ ID NO:156) derived from the coding sequence of SEQ ID NO:155 shown in Figure 155.

Figure 157 shows a nucleotide sequence (SEQ ID NO:157) of a native sequence PRO1113 cDNA, wherein SEQ ID NO:157 is a clone designated herein as "DNA57254-1477".

Figure 158 shows the amino acid sequence (SEQ ID NO:158) derived from the coding sequence of SEQ ID NO:157 shown in Figure 157.

30 Figure 159 shows a nucleotide sequence (SEQ ID NO:159) of a native sequence PRO1006 cDNA, wherein SEQ ID NO:159 is a clone designated herein as "DNA57699-1412".

Figure 160 shows the amino acid sequence (SEQ ID NO:160) derived from the coding sequence of SEQ ID NO:159 shown in Figure 159.

35 Figure 161 shows a nucleotide sequence (SEQ ID NO:161) of a native sequence PRO1074 cDNA, wherein SEQ ID NO:161 is a clone designated herein as "DNA57704-1452".

Figure 162 shows the amino acid sequence (SEQ ID NO:162) derived from the coding sequence of SEQ ID NO:161 shown in Figure 161.

Figure 163 shows a nucleotide sequence (SEQ ID NO:163) of a native sequence PRO1073 cDNA, wherein SEQ ID NO:163 is a clone designated herein as "DNA57710-1451".

Figure 164 shows the amino acid sequence (SEQ ID NO:164) derived from the coding sequence of SEQ ID NO:163 shown in Figure 163.

5 Figure 165 shows a nucleotide sequence (SEQ ID NO:165) of a native sequence PRO1136 cDNA, wherein SEQ ID NO:165 is a clone designated herein as "DNA57827-1493".

Figure 166 shows the amino acid sequence (SEQ ID NO:166) derived from the coding sequence of SEQ ID NO:165 shown in Figure 165.

Figure 167 shows a nucleotide sequence (SEQ ID NO:167) of a native sequence PRO1004 cDNA, wherein SEQ ID NO:167 is a clone designated herein as "DNA57844-1410".

10 Figure 168 shows the amino acid sequence (SEQ ID NO:168) derived from the coding sequence of SEQ ID NO:167 shown in Figure 167.

Figure 169 shows a nucleotide sequence (SEQ ID NO:169) of a native sequence PRO1344 cDNA, wherein SEQ ID NO:169 is a clone designated herein as "DNA58723-1588".

15 Figure 170 shows the amino acid sequence (SEQ ID NO:170) derived from the coding sequence of SEQ ID NO:169 shown in Figure 169.

Figure 171 shows a nucleotide sequence (SEQ ID NO:171) of a native sequence PRO1110 cDNA, wherein SEQ ID NO:171 is a clone designated herein as "DNA58727-1474".

Figure 172 shows the amino acid sequence (SEQ ID NO:172) derived from the coding sequence of SEQ ID NO:171 shown in Figure 171.

20 Figure 173 shows a nucleotide sequence (SEQ ID NO:173) of a native sequence PRO1378 cDNA, wherein SEQ ID NO:173 is a clone designated herein as "DNA58730-1607".

Figure 174 shows the amino acid sequence (SEQ ID NO:174) derived from the coding sequence of SEQ ID NO:173 shown in Figure 173.

25 Figure 175 shows a nucleotide sequence (SEQ ID NO:175) of a native sequence PRO1481 cDNA, wherein SEQ ID NO:175 is a clone designated herein as "DNA58732-1650".

Figure 176 shows the amino acid sequence (SEQ ID NO:176) derived from the coding sequence of SEQ ID NO:175 shown in Figure 175.

Figure 177 shows a nucleotide sequence (SEQ ID NO:177) of a native sequence PRO1109 cDNA, wherein SEQ ID NO:177 is a clone designated herein as "DNA58737-1473".

30 Figure 178 shows the amino acid sequence (SEQ ID NO:178) derived from the coding sequence of SEQ ID NO:177 shown in Figure 177.

Figure 179 shows a nucleotide sequence (SEQ ID NO:179) of a native sequence PRO1383 cDNA, wherein SEQ ID NO:179 is a clone designated herein as "DNA58743-1609".

35 Figure 180 shows the amino acid sequence (SEQ ID NO:180) derived from the coding sequence of SEQ ID NO:179 shown in Figure 179.

Figure 181 shows a nucleotide sequence (SEQ ID NO:181) of a native sequence PRO1072 cDNA, wherein SEQ ID NO:181 is a clone designated herein as "DNA58747-1384".

Figure 182 shows the amino acid sequence (SEQ ID NO:182) derived from the coding sequence of SEQ ID NO:181 shown in Figure 181.

Figure 183 shows a nucleotide sequence (SEQ ID NO:183) of a native sequence PRO1189 cDNA, wherein SEQ ID NO:183 is a clone designated herein as "DNA58828-1519".

5 Figure 184 shows the amino acid sequence (SEQ ID NO:184) derived from the coding sequence of SEQ ID NO:183 shown in Figure 183.

Figure 185 shows a nucleotide sequence (SEQ ID NO:185) of a native sequence PRO1003 cDNA, wherein SEQ ID NO:185 is a clone designated herein as "DNA58846-1409".

Figure 186 shows the amino acid sequence (SEQ ID NO:186) derived from the coding sequence of SEQ ID NO:185 shown in Figure 185.

10 Figure 187 shows a nucleotide sequence (SEQ ID NO:187) of a native sequence PRO1108 cDNA, wherein SEQ ID NO:187 is a clone designated herein as "DNA58848-1472".

Figure 188 shows the amino acid sequence (SEQ ID NO:188) derived from the coding sequence of SEQ ID NO:187 shown in Figure 187.

15 Figure 189 shows a nucleotide sequence (SEQ ID NO:189) of a native sequence PRO1137 cDNA, wherein SEQ ID NO:189 is a clone designated herein as "DNA58849-1494".

Figure 190 shows the amino acid sequence (SEQ ID NO:190) derived from the coding sequence of SEQ ID NO:189 shown in Figure 189.

Figure 191 shows a nucleotide sequence (SEQ ID NO:191) of a native sequence PRO1138 cDNA, wherein SEQ ID NO:191 is a clone designated herein as "DNA58850-1495".

20 Figure 192 shows the amino acid sequence (SEQ ID NO:192) derived from the coding sequence of SEQ ID NO:191 shown in Figure 191.

Figure 193 shows a nucleotide sequence (SEQ ID NO:193) of a native sequence PRO1415 cDNA, wherein SEQ ID NO:193 is a clone designated herein as "DNA58852-1637".

25 Figure 194 shows the amino acid sequence (SEQ ID NO:194) derived from the coding sequence of SEQ ID NO:193 shown in Figure 193.

Figure 195 shows a nucleotide sequence (SEQ ID NO:195) of a native sequence PRO1054 cDNA, wherein SEQ ID NO:195 is a clone designated herein as "DNA58853-1423".

Figure 196 shows the amino acid sequence (SEQ ID NO:196) derived from the coding sequence of SEQ ID NO:195 shown in Figure 195.

30 Figure 197 shows a nucleotide sequence (SEQ ID NO:197) of a native sequence PRO994 cDNA, wherein SEQ ID NO:197 is a clone designated herein as "DNA58855-1422".

Figure 198 shows the amino acid sequence (SEQ ID NO:198) derived from the coding sequence of SEQ ID NO:197 shown in Figure 197.

35 Figure 199 shows a nucleotide sequence (SEQ ID NO:199) of a native sequence PRO1069 cDNA, wherein SEQ ID NO:199 is a clone designated herein as "DNA59211-1450".

Figure 200 shows the amino acid sequence (SEQ ID NO:200) derived from the coding sequence of SEQ ID NO:199 shown in Figure 199.

Figure 201 shows a nucleotide sequence (SEQ ID NO:201) of a native sequence PRO1411 cDNA, wherein SEQ ID NO:201 is a clone designated herein as "DNA59212-1627".

Figure 202 shows the amino acid sequence (SEQ ID NO:202) derived from the coding sequence of SEQ ID NO:201 shown in Figure 201.

5 Figure 203 shows a nucleotide sequence (SEQ ID NO:203) of a native sequence PRO1129 cDNA, wherein SEQ ID NO:203 is a clone designated herein as "DNA59213-1487".

Figure 204 shows the amino acid sequence (SEQ ID NO:204) derived from the coding sequence of SEQ ID NO:203 shown in Figure 203.

Figure 205 shows a nucleotide sequence (SEQ ID NO:205) of a native sequence PRO1359 cDNA, wherein SEQ ID NO:205 is a clone designated herein as "DNA59219-1613".

10 Figure 206 shows the amino acid sequence (SEQ ID NO:206) derived from the coding sequence of SEQ ID NO:205 shown in Figure 205.

Figure 207 shows a nucleotide sequence (SEQ ID NO:207) of a native sequence PRO1139 cDNA, wherein SEQ ID NO:207 is a clone designated herein as "DNA59497-1496".

15 Figure 208 shows the amino acid sequence (SEQ ID NO:208) derived from the coding sequence of SEQ ID NO:207 shown in Figure 207.

Figure 209 shows a nucleotide sequence (SEQ ID NO:209) of a native sequence PRO1065 cDNA, wherein SEQ ID NO:209 is a clone designated herein as "DNA59602-1436".

Figure 210 shows the amino acid sequence (SEQ ID NO:210) derived from the coding sequence of SEQ ID NO:209 shown in Figure 209.

20 Figure 211 shows a nucleotide sequence (SEQ ID NO:211) of a native sequence PRO1028 cDNA, wherein SEQ ID NO:211 is a clone designated herein as "DNA59603-1419".

Figure 212 shows the amino acid sequence (SEQ ID NO:212) derived from the coding sequence of SEQ ID NO:211 shown in Figure 211.

25 Figure 213 shows a nucleotide sequence (SEQ ID NO:213) of a native sequence PRO1027 cDNA, wherein SEQ ID NO:213 is a clone designated herein as "DNA59605-1418".

Figure 214 shows the amino acid sequence (SEQ ID NO:214) derived from the coding sequence of SEQ ID NO:213 shown in Figure 213.

Figure 215 shows a nucleotide sequence (SEQ ID NO:215) of a native sequence PRO1140 cDNA, wherein SEQ ID NO:215 is a clone designated herein as "DNA59607-1497".

30 Figure 216 shows the amino acid sequence (SEQ ID NO:216) derived from the coding sequence of SEQ ID NO:215 shown in Figure 215.

Figure 217 shows a nucleotide sequence (SEQ ID NO:217) of a native sequence PRO1291 cDNA, wherein SEQ ID NO:217 is a clone designated herein as "DNA59610-1556".

35 Figure 218 shows the amino acid sequence (SEQ ID NO:218) derived from the coding sequence of SEQ ID NO:217 shown in Figure 217.

Figure 219 shows a nucleotide sequence (SEQ ID NO:219) of a native sequence PRO1105 cDNA, wherein SEQ ID NO:219 is a clone designated herein as "DNA59612-1466".

Figure 220 shows the amino acid sequence (SEQ ID NO:220) derived from the coding sequence of SEQ ID NO:219 shown in Figure 219.

Figure 221 shows a nucleotide sequence (SEQ ID NO:221) of a native sequence PRO1026 cDNA, wherein SEQ ID NO:221 is a clone designated herein as "DNA59613-1417".

5 Figure 222 shows the amino acid sequence (SEQ ID NO:222) derived from the coding sequence of SEQ ID NO:221 shown in Figure 221.

Figure 223 shows a nucleotide sequence (SEQ ID NO:223) of a native sequence PRO1104 cDNA, wherein SEQ ID NO:223 is a clone designated herein as "DNA59616-1465".

Figure 224 shows the amino acid sequence (SEQ ID NO:224) derived from the coding sequence of SEQ ID NO:223 shown in Figure 223.

10 Figure 225 shows a nucleotide sequence (SEQ ID NO:225) of a native sequence PRO1100 cDNA, wherein SEQ ID NO:225 is a clone designated herein as "DNA59619-1464".

Figure 226 shows the amino acid sequence (SEQ ID NO:226) derived from the coding sequence of SEQ ID NO:225 shown in Figure 225.

15 Figure 227 shows a nucleotide sequence (SEQ ID NO:227) of a native sequence PRO1141 cDNA, wherein SEQ ID NO:227 is a clone designated herein as "DNA59625-1498".

Figure 228 shows the amino acid sequence (SEQ ID NO:228) derived from the coding sequence of SEQ ID NO:227 shown in Figure 227.

Figure 229 shows a nucleotide sequence (SEQ ID NO:229) of a native sequence PRO1772 cDNA, wherein SEQ ID NO:229 is a clone designated herein as "DNA59817-1703".

20 Figure 230 shows the amino acid sequence (SEQ ID NO:230) derived from the coding sequence of SEQ ID NO:229 shown in Figure 229.

Figure 231 shows a nucleotide sequence (SEQ ID NO:231) of a native sequence PRO1064 cDNA, wherein SEQ ID NO:231 is a clone designated herein as "DNA59827-1426".

25 Figure 232 shows the amino acid sequence (SEQ ID NO:232) derived from the coding sequence of SEQ ID NO:231 shown in Figure 231.

Figure 233 shows a nucleotide sequence (SEQ ID NO:233) of a native sequence PRO1379 cDNA, wherein SEQ ID NO:233 is a clone designated herein as "DNA59828-1608".

Figure 234 shows the amino acid sequence (SEQ ID NO:234) derived from the coding sequence of SEQ ID NO:233 shown in Figure 233.

30 Figure 235 shows a nucleotide sequence (SEQ ID NO:235) of a native sequence PRO3573 cDNA, wherein SEQ ID NO:235 is a clone designated herein as "DNA59837-2545".

Figure 236 shows the amino acid sequence (SEQ ID NO:236) derived from the coding sequence of SEQ ID NO:235 shown in Figure 235.

35 Figure 237 shows a nucleotide sequence (SEQ ID NO:237) of a native sequence PRO3566 cDNA, wherein SEQ ID NO:237 is a clone designated herein as "DNA59844-2542".

Figure 238 shows the amino acid sequence (SEQ ID NO:238) derived from the coding sequence of SEQ ID NO:237 shown in Figure 237.

Figure 239 shows a nucleotide sequence (SEQ ID NO:239) of a native sequence PRO1156 cDNA, wherein SEQ ID NO:239 is a clone designated herein as "DNA59853-1505".

Figure 240 shows the amino acid sequence (SEQ ID NO:240) derived from the coding sequence of SEQ ID NO:239 shown in Figure 239.

5 Figure 241 shows a nucleotide sequence (SEQ ID NO:241) of a native sequence PRO1098 cDNA, wherein SEQ ID NO:241 is a clone designated herein as "DNA59854-1459".

Figure 242 shows the amino acid sequence (SEQ ID NO:242) derived from the coding sequence of SEQ ID NO:241 shown in Figure 241.

Figure 243 shows a nucleotide sequence (SEQ ID NO:243) of a native sequence PRO1128 cDNA, wherein SEQ ID NO:243 is a clone designated herein as "DNA59855-1485".

10 Figure 244 shows the amino acid sequence (SEQ ID NO:244) derived from the coding sequence of SEQ ID NO:243 shown in Figure 243.

Figure 245 shows a nucleotide sequence (SEQ ID NO:245) of a native sequence PRO1248 cDNA, wherein SEQ ID NO:245 is a clone designated herein as "DNA60278-1530".

15 Figure 246 shows the amino acid sequence (SEQ ID NO:246) derived from the coding sequence of SEQ ID NO:245 shown in Figure 245.

Figure 247 shows a nucleotide sequence (SEQ ID NO:247) of a native sequence PRO1127 cDNA, wherein SEQ ID NO:247 is a clone designated herein as "DNA60283-1484".

Figure 248 shows the amino acid sequence (SEQ ID NO:248) derived from the coding sequence of SEQ ID NO:247 shown in Figure 247.

20 Figure 249 shows a nucleotide sequence (SEQ ID NO:249) of a native sequence PRO1316 cDNA, wherein SEQ ID NO:249 is a clone designated herein as "DNA60608-1577".

Figure 250 shows the amino acid sequence (SEQ ID NO:250) derived from the coding sequence of SEQ ID NO:249 shown in Figure 249.

25 Figure 251 shows a nucleotide sequence (SEQ ID NO:251) of a native sequence PRO1197 cDNA, wherein SEQ ID NO:251 is a clone designated herein as "DNA60611-1524".

Figure 252 shows the amino acid sequence (SEQ ID NO:252) derived from the coding sequence of SEQ ID NO:251 shown in Figure 251.

Figure 253 shows a nucleotide sequence (SEQ ID NO:253) of a native sequence PRO1125 cDNA, wherein SEQ ID NO:253 is a clone designated herein as "DNA60619-1482".

30 Figure 254 shows the amino acid sequence (SEQ ID NO:254) derived from the coding sequence of SEQ ID NO:253 shown in Figure 253.

Figure 255 shows a nucleotide sequence (SEQ ID NO:255) of a native sequence PRO1158 cDNA, wherein SEQ ID NO:255 is a clone designated herein as "DNA60625-1507".

35 Figure 256 shows the amino acid sequence (SEQ ID NO:256) derived from the coding sequence of SEQ ID NO:255 shown in Figure 255.

Figure 257 shows a nucleotide sequence (SEQ ID NO:257) of a native sequence PRO1124 cDNA, wherein SEQ ID NO:257 is a clone designated herein as "DNA60629-1481".

Figure 258 shows the amino acid sequence (SEQ ID NO:258) derived from the coding sequence of SEQ ID NO:257 shown in Figure 257.

Figure 259 shows a nucleotide sequence (SEQ ID NO:259) of a native sequence PRO1380 cDNA, wherein SEQ ID NO:259 is a clone designated herein as "DNA60740-1615".

5 Figure 260 shows the amino acid sequence (SEQ ID NO:260) derived from the coding sequence of SEQ ID NO:259 shown in Figure 259.

Figure 261 shows a nucleotide sequence (SEQ ID NO:261) of a native sequence PRO1377 cDNA, wherein SEQ ID NO:261 is a clone designated herein as "DNA61608-1606".

Figure 262 shows the amino acid sequence (SEQ ID NO:262) derived from the coding sequence of SEQ ID NO:261 shown in Figure 261.

10 Figure 263 shows a nucleotide sequence (SEQ ID NO:263) of a native sequence PRO1287 cDNA, wherein SEQ ID NO:263 is a clone designated herein as "DNA61755-1554".

Figure 264 shows the amino acid sequence (SEQ ID NO:264) derived from the coding sequence of SEQ ID NO:263 shown in Figure 263.

15 Figure 265 shows a nucleotide sequence (SEQ ID NO:265) of a native sequence PRO1249 cDNA, wherein SEQ ID NO:265 is a clone designated herein as "DNA62809-1531".

Figure 266 shows the amino acid sequence (SEQ ID NO:266) derived from the coding sequence of SEQ ID NO:265 shown in Figure 265.

Figure 267 shows a nucleotide sequence (SEQ ID NO:267) of a native sequence PRO1335 cDNA, wherein SEQ ID NO:267 is a clone designated herein as "DNA62812-1594".

20 Figure 268 shows the amino acid sequence (SEQ ID NO:268) derived from the coding sequence of SEQ ID NO:267 shown in Figure 267.

Figure 269 shows a nucleotide sequence (SEQ ID NO:269) of a native sequence PRO3572 cDNA, wherein SEQ ID NO:269 is a clone designated herein as "DNA62813-2544".

25 Figure 270 shows the amino acid sequence (SEQ ID NO:270) derived from the coding sequence of SEQ ID NO:269 shown in Figure 269.

Figure 271 shows a nucleotide sequence (SEQ ID NO:271) of a native sequence PRO1599 cDNA, wherein SEQ ID NO:271 is a clone designated herein as "DNA62845-1684".

Figure 272 shows the amino acid sequence (SEQ ID NO:272) derived from the coding sequence of SEQ ID NO:271 shown in Figure 271.

30 Figure 273 shows a nucleotide sequence (SEQ ID NO:273) of a native sequence PRO1374 cDNA, wherein SEQ ID NO:273 is a clone designated herein as "DNA64849-1604".

Figure 274 shows the amino acid sequence (SEQ ID NO:274) derived from the coding sequence of SEQ ID NO:273 shown in Figure 273.

35 Figure 275 shows a nucleotide sequence (SEQ ID NO:275) of a native sequence PRO1345 cDNA, wherein SEQ ID NO:275 is a clone designated herein as "DNA64852-1589".

Figure 276 shows the amino acid sequence (SEQ ID NO:276) derived from the coding sequence of SEQ ID NO:275 shown in Figure 275.

Figure 277 shows a nucleotide sequence (SEQ ID NO:277) of a native sequence PRO1311 cDNA, wherein SEQ ID NO:277 is a clone designated herein as "DNA64863-1573".

Figure 278 shows the amino acid sequence (SEQ ID NO:278) derived from the coding sequence of SEQ ID NO:277 shown in Figure 277.

5 Figure 279 shows a nucleotide sequence (SEQ ID NO:279) of a native sequence PRO1357 cDNA, wherein SEQ ID NO:279 is a clone designated herein as "DNA64881-1602".

Figure 280 shows the amino acid sequence (SEQ ID NO:280) derived from the coding sequence of SEQ ID NO:279 shown in Figure 279.

Figure 281 shows a nucleotide sequence (SEQ ID NO:281) of a native sequence PRO1557 cDNA, wherein SEQ ID NO:281 is a clone designated herein as "DNA64902-1667".

10 Figure 282 shows the amino acid sequence (SEQ ID NO:282) derived from the coding sequence of SEQ ID NO:281 shown in Figure 281.

Figure 283 shows a nucleotide sequence (SEQ ID NO:283) of a native sequence PRO1305 cDNA, wherein SEQ ID NO:283 is a clone designated herein as "DNA64952-1568".

15 Figure 284 shows the amino acid sequence (SEQ ID NO:284) derived from the coding sequence of SEQ ID NO:283 shown in Figure 283.

Figure 285 shows a nucleotide sequence (SEQ ID NO:285) of a native sequence PRO1302 cDNA, wherein SEQ ID NO:285 is a clone designated herein as "DNA65403-1565".

Figure 286 shows the amino acid sequence (SEQ ID NO:286) derived from the coding sequence of SEQ ID NO:285 shown in Figure 285.

20 Figure 287 shows a nucleotide sequence (SEQ ID NO:287) of a native sequence PRO1266 cDNA, wherein SEQ ID NO:287 is a clone designated herein as "DNA65413-1534".

Figure 288 shows the amino acid sequence (SEQ ID NO:288) derived from the coding sequence of SEQ ID NO:287 shown in Figure 287.

25 Figures 289A-289B show a nucleotide sequence (SEQ ID NO:289) of a native sequence PRO1336 cDNA, wherein SEQ ID NO:289 is a clone designated herein as "DNA65423-1595".

Figure 290 shows the amino acid sequence (SEQ ID NO:290) derived from the coding sequence of SEQ ID NO:289 shown in Figures 289A-289B.

Figure 291 shows a nucleotide sequence (SEQ ID NO:291) of a native sequence PRO1278 cDNA, wherein SEQ ID NO:291 is a clone designated herein as "DNA66304-1546".

30 Figure 292 shows the amino acid sequence (SEQ ID NO:292) derived from the coding sequence of SEQ ID NO:291 shown in Figure 291.

Figure 293 shows a nucleotide sequence (SEQ ID NO:293) of a native sequence PRO1270 cDNA, wherein SEQ ID NO:293 is a clone designated herein as "DNA66308-1537".

35 Figure 294 shows the amino acid sequence (SEQ ID NO:294) derived from the coding sequence of SEQ ID NO:293 shown in Figure 293.

Figure 295 shows a nucleotide sequence (SEQ ID NO:295) of a native sequence PRO1298 cDNA, wherein SEQ ID NO:295 is a clone designated herein as "DNA66511-1563".

Figure 296 shows the amino acid sequence (SEQ ID NO:296) derived from the coding sequence of SEQ ID NO:295 shown in Figure 295.

Figure 297 shows a nucleotide sequence (SEQ ID NO:297) of a native sequence PRO1301 cDNA, wherein SEQ ID NO:297 is a clone designated herein as "DNA66512-1564".

5 Figure 298 shows the amino acid sequence (SEQ ID NO:298) derived from the coding sequence of SEQ ID NO:297 shown in Figure 297.

Figure 299 shows a nucleotide sequence (SEQ ID NO:299) of a native sequence PRO1268 cDNA, wherein SEQ ID NO:299 is a clone designated herein as "DNA66519-1535".

Figure 300 shows the amino acid sequence (SEQ ID NO:300) derived from the coding sequence of SEQ ID NO:299 shown in Figure 299.

10 Figure 301 shows a nucleotide sequence (SEQ ID NO:301) of a native sequence PRO1327 cDNA, wherein SEQ ID NO:301 is a clone designated herein as "DNA66521-1583".

Figure 302 shows the amino acid sequence (SEQ ID NO:302) derived from the coding sequence of SEQ ID NO:301 shown in Figure 301.

15 Figure 303 shows a nucleotide sequence (SEQ ID NO:303) of a native sequence PRO1328 cDNA, wherein SEQ ID NO:303 is a clone designated herein as "DNA66658-1584".

Figure 304 shows the amino acid sequence (SEQ ID NO:304) derived from the coding sequence of SEQ ID NO:303 shown in Figure 303.

Figure 305 shows a nucleotide sequence (SEQ ID NO:305) of a native sequence PRO1329 cDNA, wherein SEQ ID NO:305 is a clone designated herein as "DNA66660-1585".

20 Figure 306 shows the amino acid sequence (SEQ ID NO:306) derived from the coding sequence of SEQ ID NO:305 shown in Figure 305.

Figure 307 shows a nucleotide sequence (SEQ ID NO:307) of a native sequence PRO1339 cDNA, wherein SEQ ID NO:307 is a clone designated herein as "DNA66669-1597".

25 Figure 308 shows the amino acid sequence (SEQ ID NO:308) derived from the coding sequence of SEQ ID NO:307 shown in Figure 307.

Figure 309 shows a nucleotide sequence (SEQ ID NO:309) of a native sequence PRO1342 cDNA, wherein SEQ ID NO:309 is a clone designated herein as "DNA66674-1599".

Figure 310 shows the amino acid sequence (SEQ ID NO:310) derived from the coding sequence of SEQ ID NO:309 shown in Figure 309.

30 Figures 311A-311B show a nucleotide sequence (SEQ ID NO:311) of a native sequence PRO1487 cDNA, wherein SEQ ID NO:311 is a clone designated herein as "DNA68836-1656".

Figure 312 shows the amino acid sequence (SEQ ID NO:312) derived from the coding sequence of SEQ ID NO:311 shown in Figures 311A-311B.

35 Figure 313 shows a nucleotide sequence (SEQ ID NO:313) of a native sequence PRO3579 cDNA, wherein SEQ ID NO:313 is a clone designated herein as "DNA68862-2546".

Figure 314 shows the amino acid sequence (SEQ ID NO:314) derived from the coding sequence of SEQ ID NO:313 shown in Figure 313.

Figure 315 shows a nucleotide sequence (SEQ ID NO:315) of a native sequence PRO1472 cDNA, wherein SEQ ID NO:315 is a clone designated herein as "DNA68866-1644".

Figure 316 shows the amino acid sequence (SEQ ID NO:316) derived from the coding sequence of SEQ ID NO:315 shown in Figure 315.

5 Figure 317 shows a nucleotide sequence (SEQ ID NO:317) of a native sequence PRO1385 cDNA, wherein SEQ ID NO:317 is a clone designated herein as "DNA68869-1610".

Figure 318 shows the amino acid sequence (SEQ ID NO:318) derived from the coding sequence of SEQ ID NO:317 shown in Figure 317.

Figure 319 shows a nucleotide sequence (SEQ ID NO:319) of a native sequence PRO1461 cDNA, wherein SEQ ID NO:319 is a clone designated herein as "DNA68871-1638".

10 Figure 320 shows the amino acid sequence (SEQ ID NO:320) derived from the coding sequence of SEQ ID NO:319 shown in Figure 319.

Figure 321 shows a nucleotide sequence (SEQ ID NO:321) of a native sequence PRO1429 cDNA, wherein SEQ ID NO:321 is a clone designated herein as "DNA68879-1631".

15 Figure 322 shows the amino acid sequence (SEQ ID NO:322) derived from the coding sequence of SEQ ID NO:321 shown in Figure 321.

Figure 323 shows a nucleotide sequence (SEQ ID NO:323) of a native sequence PRO1568 cDNA, wherein SEQ ID NO:323 is a clone designated herein as "DNA68880-1676".

Figure 324 shows the amino acid sequence (SEQ ID NO:324) derived from the coding sequence of SEQ ID NO:323 shown in Figure 323.

20 Figure 325 shows a nucleotide sequence (SEQ ID NO:325) of a native sequence PRO1569 cDNA, wherein SEQ ID NO:325 is a clone designated herein as "DNA68882-1677".

Figure 326 shows the amino acid sequence (SEQ ID NO:326) derived from the coding sequence of SEQ ID NO:325 shown in Figure 325.

25 Figure 327 shows a nucleotide sequence (SEQ ID NO:327) of a native sequence PRO1753 cDNA, wherein SEQ ID NO:327 is a clone designated herein as "DNA68883-1691".

Figure 328 shows the amino acid sequence (SEQ ID NO:328) derived from the coding sequence of SEQ ID NO:327 shown in Figure 327.

Figure 329 shows a nucleotide sequence (SEQ ID NO:329) of a native sequence PRO1570 cDNA, wherein SEQ ID NO:329 is a clone designated herein as "DNA68885-1678".

30 Figure 330 shows the amino acid sequence (SEQ ID NO:330) derived from the coding sequence of SEQ ID NO:329 shown in Figure 329.

Figure 331 shows a nucleotide sequence (SEQ ID NO:331) of a native sequence PRO1559 cDNA, wherein SEQ ID NO:331 is a clone designated herein as "DNA68886".

35 Figure 332 shows the amino acid sequence (SEQ ID NO:332) derived from the coding sequence of SEQ ID NO:331 shown in Figure 331.

Figure 333 shows a nucleotide sequence (SEQ ID NO:333) of a native sequence PRO1486 cDNA, wherein SEQ ID NO:333 is a clone designated herein as "DNA71180-1655".

Figure 334 shows the amino acid sequence (SEQ ID NO:334) derived from the coding sequence of SEQ ID NO:333 shown in Figure 333.

Figure 335 shows a nucleotide sequence (SEQ ID NO:335) of a native sequence PRO1433 cDNA, wherein SEQ ID NO:335 is a clone designated herein as "DNA71184-1634".

5 Figure 336 shows the amino acid sequence (SEQ ID NO:336) derived from the coding sequence of SEQ ID NO:335 shown in Figure 335.

Figure 337 shows a nucleotide sequence (SEQ ID NO:337) of a native sequence PRO1490 cDNA, wherein SEQ ID NO:337 is a clone designated herein as "DNA71213-1659".

Figure 338 shows the amino acid sequence (SEQ ID NO:338) derived from the coding sequence of SEQ ID NO:337 shown in Figure 337.

10 Figure 339 shows a nucleotide sequence (SEQ ID NO:339) of a native sequence PRO1482 cDNA, wherein SEQ ID NO:339 is a clone designated herein as "DNA71234-1651".

Figure 340 shows the amino acid sequence (SEQ ID NO:340) derived from the coding sequence of SEQ ID NO:339 shown in Figure 339.

15 Figure 341 shows a nucleotide sequence (SEQ ID NO:341) of a native sequence PRO1409 cDNA, wherein SEQ ID NO:341 is a clone designated herein as "DNA71269-1621".

Figure 342 shows the amino acid sequence (SEQ ID NO:342) derived from the coding sequence of SEQ ID NO:341 shown in Figure 341.

Figure 343 shows a nucleotide sequence (SEQ ID NO:343) of a native sequence PRO1446 cDNA, wherein SEQ ID NO:343 is a clone designated herein as "DNA71277-1636".

20 Figure 344 shows the amino acid sequence (SEQ ID NO:344) derived from the coding sequence of SEQ ID NO:343 shown in Figure 343.

Figure 345 shows a nucleotide sequence (SEQ ID NO:345) of a native sequence PRO1604 cDNA, wherein SEQ ID NO:345 is a clone designated herein as "DNA71286-1687".

25 Figure 346 shows the amino acid sequence (SEQ ID NO:346) derived from the coding sequence of SEQ ID NO:345 shown in Figure 345.

Figure 347 shows a nucleotide sequence (SEQ ID NO:347) of a native sequence PRO1491 cDNA, wherein SEQ ID NO:347 is a clone designated herein as "DNA71883-1660".

Figure 348 shows the amino acid sequence (SEQ ID NO:348) derived from the coding sequence of SEQ ID NO:347 shown in Figure 347.

30 Figure 349 shows a nucleotide sequence (SEQ ID NO:349) of a native sequence PRO1431 cDNA, wherein SEQ ID NO:349 is a clone designated herein as "DNA73401-1633".

Figure 350 shows the amino acid sequence (SEQ ID NO:350) derived from the coding sequence of SEQ ID NO:349 shown in Figure 349.

35 Figures 351A-351B show a nucleotide sequence (SEQ ID NO:351) of a native sequence PRO1563 cDNA, wherein SEQ ID NO:351 is a clone designated herein as "DNA73492-1671".

Figure 352 shows the amino acid sequence (SEQ ID NO:352) derived from the coding sequence of SEQ ID NO:351 shown in Figures 351A-351B.

Figure 353 shows a nucleotide sequence (SEQ ID NO:353) of a native sequence PRO1571 cDNA, wherein SEQ ID NO:353 is a clone designated herein as "DNA73730-1679".

Figure 354 shows the amino acid sequence (SEQ ID NO:354) derived from the coding sequence of SEQ ID NO:353 shown in Figure 353.

5 Figure 355 shows a nucleotide sequence (SEQ ID NO:355) of a native sequence PRO1572 cDNA, wherein SEQ ID NO:355 is a clone designated herein as "DNA73734-1680".

Figure 356 shows the amino acid sequence (SEQ ID NO:356) derived from the coding sequence of SEQ ID NO:355 shown in Figure 355.

Figure 357 shows a nucleotide sequence (SEQ ID NO:357) of a native sequence PRO1573 cDNA, wherein SEQ ID NO:357 is a clone designated herein as "DNA73735-1681".

10 Figure 358 shows the amino acid sequence (SEQ ID NO:358) derived from the coding sequence of SEQ ID NO:357 shown in Figure 357.

Figure 359 shows a nucleotide sequence (SEQ ID NO:359) of a native sequence PRO1508 cDNA, wherein SEQ ID NO:359 is a clone designated herein as "DNA73742-1662".

15 Figure 360 shows the amino acid sequence (SEQ ID NO:360) derived from the coding sequence of SEQ ID NO:359 shown in Figure 359.

Figure 361 shows a nucleotide sequence (SEQ ID NO:361) of a native sequence PRO1485 cDNA, wherein SEQ ID NO:361 is a clone designated herein as "DNA73746-1654".

Figure 362 shows the amino acid sequence (SEQ ID NO:362) derived from the coding sequence of SEQ ID NO:361 shown in Figure 361.

20 Figure 363 shows a nucleotide sequence (SEQ ID NO:363) of a native sequence PRO1564 cDNA, wherein SEQ ID NO:363 is a clone designated herein as "DNA73760-1672".

Figure 364 shows the amino acid sequence (SEQ ID NO:364) derived from the coding sequence of SEQ ID NO:363 shown in Figure 363.

25 Figure 365 shows a nucleotide sequence (SEQ ID NO:365) of a native sequence PRO1550 cDNA, wherein SEQ ID NO:365 is a clone designated herein as "DNA76393-1664".

Figure 366 shows the amino acid sequence (SEQ ID NO:366) derived from the coding sequence of SEQ ID NO:365 shown in Figure 365.

Figure 367 shows a nucleotide sequence (SEQ ID NO:367) of a native sequence PRO1757 cDNA, wherein SEQ ID NO:367 is a clone designated herein as "DNA76398-1699".

30 Figure 368 shows the amino acid sequence (SEQ ID NO:368) derived from the coding sequence of SEQ ID NO:367 shown in Figure 367.

Figure 369 shows a nucleotide sequence (SEQ ID NO:369) of a native sequence PRO1758 cDNA, wherein SEQ ID NO:369 is a clone designated herein as "DNA76399-1700".

35 Figure 370 shows the amino acid sequence (SEQ ID NO:370) derived from the coding sequence of SEQ ID NO:369 shown in Figure 369.

Figure 371 shows a nucleotide sequence (SEQ ID NO:371) of a native sequence PRO1781 cDNA, wherein SEQ ID NO:371 is a clone designated herein as "DNA76522-2500".

Figure 372 shows the amino acid sequence (SEQ ID NO:372) derived from the coding sequence of SEQ ID NO:371 shown in Figure 371.

Figure 373 shows a nucleotide sequence (SEQ ID NO:373) of a native sequence PRO1606 cDNA, wherein SEQ ID NO:373 is a clone designated herein as "DNA76533-1689".

5 Figure 374 shows the amino acid sequence (SEQ ID NO:374) derived from the coding sequence of SEQ ID NO:373 shown in Figure 373.

Figure 375 shows a nucleotide sequence (SEQ ID NO:375) of a native sequence PRO1784 cDNA, wherein SEQ ID NO:375 is a clone designated herein as "DNA77303-2502".

Figure 376 shows the amino acid sequence (SEQ ID NO:376) derived from the coding sequence of SEQ ID NO:375 shown in Figure 375.

10 Figure 377 shows a nucleotide sequence (SEQ ID NO:377) of a native sequence PRO1774 cDNA, wherein SEQ ID NO:377 is a clone designated herein as "DNA77626-1705".

Figure 378 shows the amino acid sequence (SEQ ID NO:378) derived from the coding sequence of SEQ ID NO:377 shown in Figure 377.

15 Figure 379 shows a nucleotide sequence (SEQ ID NO:379) of a native sequence PRO1605 cDNA, wherein SEQ ID NO:379 is a clone designated herein as "DNA77648-1688".

Figure 380 shows the amino acid sequence (SEQ ID NO:380) derived from the coding sequence of SEQ ID NO:379 shown in Figure 379.

Figure 381 shows a nucleotide sequence (SEQ ID NO:381) of a native sequence PRO1928 cDNA, wherein SEQ ID NO:381 is a clone designated herein as "DNA81754-2532".

20 Figure 382 shows the amino acid sequence (SEQ ID NO:382) derived from the coding sequence of SEQ ID NO:381 shown in Figure 381.

Figure 383 shows a nucleotide sequence (SEQ ID NO:383) of a native sequence PRO1865 cDNA, wherein SEQ ID NO:383 is a clone designated herein as "DNA81757-2512".

25 Figure 384 shows the amino acid sequence (SEQ ID NO:384) derived from the coding sequence of SEQ ID NO:383 shown in Figure 383.

Figure 385 shows a nucleotide sequence (SEQ ID NO:385) of a native sequence PRO1925 cDNA, wherein SEQ ID NO:385 is a clone designated herein as "DNA82302-2529".

Figure 386 shows the amino acid sequence (SEQ ID NO:386) derived from the coding sequence of SEQ ID NO:385 shown in Figure 385.

30 Figure 387 shows a nucleotide sequence (SEQ ID NO:387) of a native sequence PRO1926 cDNA, wherein SEQ ID NO:387 is a clone designated herein as "DNA82340-2530".

Figure 388 shows the amino acid sequence (SEQ ID NO:388) derived from the coding sequence of SEQ ID NO:387 shown in Figure 387.

35 Figure 389 shows a nucleotide sequence (SEQ ID NO:389) of a native sequence PRO2630 cDNA, wherein SEQ ID NO:389 is a clone designated herein as "DNA83551".

Figure 390 shows the amino acid sequence (SEQ ID NO:390) derived from the coding sequence of SEQ ID NO:389 shown in Figure 389.

Figure 391 shows a nucleotide sequence (SEQ ID NO:391) of a native sequence PRO3443 cDNA, wherein SEQ ID NO:391 is a clone designated herein as "DNA87991-2540".

Figure 392 shows the amino acid sequence (SEQ ID NO:392) derived from the coding sequence of SEQ ID NO:391 shown in Figure 391.

5 Figure 393 shows a nucleotide sequence (SEQ ID NO:393) of a native sequence PRO3301 cDNA, wherein SEQ ID NO:393 is a clone designated herein as "DNA88002".

Figure 394 shows the amino acid sequence (SEQ ID NO:394) derived from the coding sequence of SEQ ID NO:393 shown in Figure 393.

Figure 395 shows a nucleotide sequence (SEQ ID NO:395) of a native sequence PRO3442 cDNA, wherein SEQ ID NO:395 is a clone designated herein as "DNA92238-2539".

10 Figure 396 shows the amino acid sequence (SEQ ID NO:396) derived from the coding sequence of SEQ ID NO:395 shown in Figure 395.

Figure 397 shows a nucleotide sequence (SEQ ID NO:397) of a native sequence PRO4978 cDNA, wherein SEQ ID NO:397 is a clone designated herein as "DNA95930".

15 Figure 398 shows the amino acid sequence (SEQ ID NO:398) derived from the coding sequence of SEQ ID NO:397 shown in Figure 397.

Figure 399 shows a nucleotide sequence (SEQ ID NO:399) of a native sequence PRO5801 cDNA, wherein SEQ ID NO:399 is a clone designated herein as "DNA115291-2681".

Figure 400 shows the amino acid sequence (SEQ ID NO:400) derived from the coding sequence of SEQ ID NO:399 shown in Figure 399.

20 Figure 401 shows a nucleotide sequence (SEQ ID NO:401) of a native sequence PRO19630 cDNA, wherein SEQ ID NO:401 is a clone designated herein as "DNA23336-2861".

Figure 402 shows the amino acid sequence (SEQ ID NO:402) derived from the coding sequence of SEQ ID NO:401 shown in Figure 401.

25 Figure 403 shows a nucleotide sequence (SEQ ID NO:403) of a native sequence PRO203 cDNA, wherein SEQ ID NO:403 is a clone designated herein as "DNA30862-1396".

Figure 404 shows the amino acid sequence (SEQ ID NO:404) derived from the coding sequence of SEQ ID NO:403 shown in Figure 403.

Figure 405 shows a nucleotide sequence (SEQ ID NO:405) of a native sequence PRO204 cDNA, wherein SEQ ID NO:405 is a clone designated herein as "DNA30871-1157".

30 Figure 406 shows the amino acid sequence (SEQ ID NO:406) derived from the coding sequence of SEQ ID NO:405 shown in Figure 405.

Figure 407 shows a nucleotide sequence (SEQ ID NO:407) of a native sequence PRO210 cDNA, wherein SEQ ID NO:407 is a clone designated herein as "DNA32279-1131".

35 Figure 408 shows the amino acid sequence (SEQ ID NO:408) derived from the coding sequence of SEQ ID NO:407 shown in Figure 407.

Figure 409 shows a nucleotide sequence (SEQ ID NO:409) of a native sequence PRO223 cDNA, wherein SEQ ID NO:409 is a clone designated herein as "DNA33206-1165".

Figure 410 shows the amino acid sequence (SEQ ID NO:410) derived from the coding sequence of SEQ ID NO:409 shown in Figure 409.

Figure 411 shows a nucleotide sequence (SEQ ID NO:411) of a native sequence PRO247 cDNA, wherein SEQ ID NO:411 is a clone designated herein as "DNA35673-1201".

5 Figure 412 shows the amino acid sequence (SEQ ID NO:412) derived from the coding sequence of SEQ ID NO:411 shown in Figure 411.

Figure 413 shows a nucleotide sequence (SEQ ID NO:413) of a native sequence PRO358 cDNA, wherein SEQ ID NO:413 is a clone designated herein as "DNA47361-1154-2".

Figure 414 shows the amino acid sequence (SEQ ID NO:414) derived from the coding sequence of SEQ ID NO:413 shown in Figure 413.

10 Figure 415 shows a nucleotide sequence (SEQ ID NO:415) of a native sequence PRO724 cDNA, wherein SEQ ID NO:415 is a clone designated herein as "DNA49631-1328".

Figure 416 shows the amino acid sequence (SEQ ID NO:416) derived from the coding sequence of SEQ ID NO:415 shown in Figure 415.

15 Figure 417 shows a nucleotide sequence (SEQ ID NO:417) of a native sequence PRO868 cDNA, wherein SEQ ID NO:417 is a clone designated herein as "DNA52594-1270".

Figure 418 shows the amino acid sequence (SEQ ID NO:418) derived from the coding sequence of SEQ ID NO:417 shown in Figure 417.

Figure 419 shows a nucleotide sequence (SEQ ID NO:419) of a native sequence PRO740 cDNA, wherein SEQ ID NO:419 is a clone designated herein as "DNA55800-1263".

20 Figure 420 shows the amino acid sequence (SEQ ID NO:420) derived from the coding sequence of SEQ ID NO:419 shown in Figure 419.

Figure 421 shows a nucleotide sequence (SEQ ID NO:421) of a native sequence PRO1478 cDNA, wherein SEQ ID NO:421 is a clone designated herein as "DNA56531-1648".

25 Figure 422 shows the amino acid sequence (SEQ ID NO:422) derived from the coding sequence of SEQ ID NO:421 shown in Figure 421.

Figure 423 shows a nucleotide sequence (SEQ ID NO:423) of a native sequence PRO162 cDNA, wherein SEQ ID NO:423 is a clone designated herein as "DNA56965-1356".

Figure 424 shows the amino acid sequence (SEQ ID NO:424) derived from the coding sequence of SEQ ID NO:423 shown in Figure 423.

30 Figure 425 shows a nucleotide sequence (SEQ ID NO:425) of a native sequence PRO828 cDNA, wherein SEQ ID NO:425 is a clone designated herein as "DNA57037-1444".

Figure 426 shows the amino acid sequence (SEQ ID NO:426) derived from the coding sequence of SEQ ID NO:425 shown in Figure 425.

35 Figure 427 shows a nucleotide sequence (SEQ ID NO:427) of a native sequence PRO819 cDNA, wherein SEQ ID NO:427 is a clone designated herein as "DNA57695-1340".

Figure 428 shows the amino acid sequence (SEQ ID NO:428) derived from the coding sequence of SEQ ID NO:427 shown in Figure 427.

Figure 429 shows a nucleotide sequence (SEQ ID NO:429) of a native sequence PRO813 cDNA, wherein SEQ ID NO:429 is a clone designated herein as "DNA57834-1339".

Figure 430 shows the amino acid sequence (SEQ ID NO:430) derived from the coding sequence of SEQ ID NO:429 shown in Figure 429.

5 Figure 431 shows a nucleotide sequence (SEQ ID NO:431) of a native sequence PRO1194 cDNA, wherein SEQ ID NO:431 is a clone designated herein as "DNA57841-1522".

Figure 432 shows the amino acid sequence (SEQ ID NO:432) derived from the coding sequence of SEQ ID NO:431 shown in Figure 431.

Figure 433 shows a nucleotide sequence (SEQ ID NO:433) of a native sequence PRO887 cDNA, wherein SEQ ID NO:433 is a clone designated herein as "DNA58130".

10 Figure 434 shows the amino acid sequence (SEQ ID NO:434) derived from the coding sequence of SEQ ID NO:433 shown in Figure 433.

Figure 435 shows a nucleotide sequence (SEQ ID NO:435) of a native sequence PRO1071 cDNA, wherein SEQ ID NO:435 is a clone designated herein as "DNA58847-1383".

15 Figure 436 shows the amino acid sequence (SEQ ID NO:436) derived from the coding sequence of SEQ ID NO:435 shown in Figure 435.

Figure 437 shows a nucleotide sequence (SEQ ID NO:437) of a native sequence PRO1029 cDNA, wherein SEQ ID NO:437 is a clone designated herein as "DNA59493-1420".

Figure 438 shows the amino acid sequence (SEQ ID NO:438) derived from the coding sequence of SEQ ID NO:437 shown in Figure 437.

20 Figure 439 shows a nucleotide sequence (SEQ ID NO:439) of a native sequence PRO1190 cDNA, wherein SEQ ID NO:439 is a clone designated herein as "DNA59586-1520".

Figure 440 shows the amino acid sequence (SEQ ID NO:440) derived from the coding sequence of SEQ ID NO:439 shown in Figure 439.

25 Figure 441 shows a nucleotide sequence (SEQ ID NO:441) of a native sequence PRO4334 cDNA, wherein SEQ ID NO:441 is a clone designated herein as "DNA59608-2577".

Figure 442 shows the amino acid sequence (SEQ ID NO:442) derived from the coding sequence of SEQ ID NO:441 shown in Figure 441.

Figure 443 shows a nucleotide sequence (SEQ ID NO:443) of a native sequence PRO1155 cDNA, wherein SEQ ID NO:443 is a clone designated herein as "DNA59849-1504".

30 Figure 444 shows the amino acid sequence (SEQ ID NO:444) derived from the coding sequence of SEQ ID NO:443 shown in Figure 443.

Figure 445 shows a nucleotide sequence (SEQ ID NO:445) of a native sequence PRO1157 cDNA, wherein SEQ ID NO:445 is a clone designated herein as "DNA60292-1506".

35 Figure 446 shows the amino acid sequence (SEQ ID NO:446) derived from the coding sequence of SEQ ID NO:445 shown in Figure 445.

Figure 447 shows a nucleotide sequence (SEQ ID NO:447) of a native sequence PRO1122 cDNA, wherein SEQ ID NO:447 is a clone designated herein as "DNA62377-1381-1".

Figure 448 shows the amino acid sequence (SEQ ID NO:448) derived from the coding sequence of SEQ ID NO:447 shown in Figure 447.

Figure 449 shows a nucleotide sequence (SEQ ID NO:449) of a native sequence PRO1183 cDNA, wherein SEQ ID NO:449 is a clone designated herein as "DNA62880-1513".

5 Figure 450 shows the amino acid sequence (SEQ ID NO:450) derived from the coding sequence of SEQ ID NO:449 shown in Figure 449.

Figure 451 shows a nucleotide sequence (SEQ ID NO:451) of a native sequence PRO1337 cDNA, wherein SEQ ID NO:451 is a clone designated herein as "DNA66672-1586".

Figure 452 shows the amino acid sequence (SEQ ID NO:452) derived from the coding sequence of SEQ ID NO:451 shown in Figure 451.

10 Figure 453 shows a nucleotide sequence (SEQ ID NO:453) of a native sequence PRO1480 cDNA, wherein SEQ ID NO:453 is a clone designated herein as "DNA67962-1649".

Figure 454 shows the amino acid sequence (SEQ ID NO:454) derived from the coding sequence of SEQ ID NO:453 shown in Figure 453.

15 Figure 455 shows a nucleotide sequence (SEQ ID NO:455) of a native sequence PRO19645 cDNA, wherein SEQ ID NO:455 is a clone designated herein as "DNA69555-2867".

Figure 456 shows the amino acid sequence (SEQ ID NO:456) derived from the coding sequence of SEQ ID NO:455 shown in Figure 455.

Figure 457 shows a nucleotide sequence (SEQ ID NO:457) of a native sequence PRO9782 cDNA, wherein SEQ ID NO:457 is a clone designated herein as "DNA71162-2764".

20 Figure 458 shows the amino acid sequence (SEQ ID NO:458) derived from the coding sequence of SEQ ID NO:457 shown in Figure 457.

Figure 459 shows a nucleotide sequence (SEQ ID NO:459) of a native sequence PRO1419 cDNA, wherein SEQ ID NO:459 is a clone designated herein as "DNA71290-1630".

25 Figure 460 shows the amino acid sequence (SEQ ID NO:460) derived from the coding sequence of SEQ ID NO:459 shown in Figure 459.

Figure 461 shows a nucleotide sequence (SEQ ID NO:461) of a native sequence PRO1575 cDNA, wherein SEQ ID NO:461 is a clone designated herein as "DNA76401-1683".

Figure 462 shows the amino acid sequence (SEQ ID NO:462) derived from the coding sequence of SEQ ID NO:461 shown in Figure 461.

30 Figure 463 shows a nucleotide sequence (SEQ ID NO:463) of a native sequence PRO1567 cDNA, wherein SEQ ID NO:463 is a clone designated herein as "DNA76541-1675".

Figure 464 shows the amino acid sequence (SEQ ID NO:464) derived from the coding sequence of SEQ ID NO:463 shown in Figure 463.

35 Figure 465 shows a nucleotide sequence (SEQ ID NO:465) of a native sequence PRO1891 cDNA, wherein SEQ ID NO:465 is a clone designated herein as "DNA76788-2526".

Figure 466 shows the amino acid sequence (SEQ ID NO:466) derived from the coding sequence of SEQ ID NO:465 shown in Figure 465.

Figure 467 shows a nucleotide sequence (SEQ ID NO:467) of a native sequence PRO1889 cDNA, wherein SEQ ID NO:467 is a clone designated herein as "DNA77623-2524".

Figure 468 shows the amino acid sequence (SEQ ID NO:468) derived from the coding sequence of SEQ ID NO:467 shown in Figure 467.

5 Figure 469 shows a nucleotide sequence (SEQ ID NO:469) of a native sequence PRO1785 cDNA, wherein SEQ ID NO:469 is a clone designated herein as "DNA80136-2503".

Figure 470 shows the amino acid sequence (SEQ ID NO:470) derived from the coding sequence of SEQ ID NO:469 shown in Figure 469.

Figure 471 shows a nucleotide sequence (SEQ ID NO:471) of a native sequence PRO6003 cDNA, wherein SEQ ID NO:471 is a clone designated herein as "DNA83568-2692".

10 Figure 472 shows the amino acid sequence (SEQ ID NO:472) derived from the coding sequence of SEQ ID NO:471 shown in Figure 471.

Figure 473 shows a nucleotide sequence (SEQ ID NO:473) of a native sequence PRO4333 cDNA, wherein SEQ ID NO:473 is a clone designated herein as "DNA84210-2576".

15 Figure 474 shows the amino acid sequence (SEQ ID NO:474) derived from the coding sequence of SEQ ID NO:473 shown in Figure 473.

Figure 475 shows a nucleotide sequence (SEQ ID NO:475) of a native sequence PRO4356 cDNA, wherein SEQ ID NO:475 is a clone designated herein as "DNA86576-2595".

Figure 476 shows the amino acid sequence (SEQ ID NO:476) derived from the coding sequence of SEQ ID NO:475 shown in Figure 475.

20 Figure 477 shows a nucleotide sequence (SEQ ID NO:477) of a native sequence PRO4352 cDNA, wherein SEQ ID NO:477 is a clone designated herein as "DNA87976-2593".

Figure 478 shows the amino acid sequence (SEQ ID NO:478) derived from the coding sequence of SEQ ID NO:477 shown in Figure 477.

25 Figure 479 shows a nucleotide sequence (SEQ ID NO:479) of a native sequence PRO4354 cDNA, wherein SEQ ID NO:479 is a clone designated herein as "DNA92256-2596".

Figure 480 shows the amino acid sequence (SEQ ID NO:480) derived from the coding sequence of SEQ ID NO:479 shown in Figure 479.

Figure 481 shows a nucleotide sequence (SEQ ID NO:481) of a native sequence PRO4369 cDNA, wherein SEQ ID NO:481 is a clone designated herein as "DNA92289-2598".

30 Figure 482 shows the amino acid sequence (SEQ ID NO:482) derived from the coding sequence of SEQ ID NO:481 shown in Figure 481.

Figure 483 shows a nucleotide sequence (SEQ ID NO:483) of a native sequence PRO6030 cDNA, wherein SEQ ID NO:483 is a clone designated herein as "DNA96850-2705".

35 Figure 484 shows the amino acid sequence (SEQ ID NO:484) derived from the coding sequence of SEQ ID NO:483 shown in Figure 483.

Figure 485 shows a nucleotide sequence (SEQ ID NO:485) of a native sequence PRO4433 cDNA, wherein SEQ ID NO:485 is a clone designated herein as "DNA96855-2629".

Figure 486 shows the amino acid sequence (SEQ ID NO:486) derived from the coding sequence of SEQ ID NO:485 shown in Figure 485.

Figure 487 shows a nucleotide sequence (SEQ ID NO:487) of a native sequence PRO4424 cDNA, wherein SEQ ID NO:487 is a clone designated herein as "DNA96857-2636".

5 Figure 488 shows the amino acid sequence (SEQ ID NO:488) derived from the coding sequence of SEQ ID NO:487 shown in Figure 487.

Figure 489 shows a nucleotide sequence (SEQ ID NO:489) of a native sequence PRO6017 cDNA, wherein SEQ ID NO:489 is a clone designated herein as "DNA96860-2700".

Figure 490 shows the amino acid sequence (SEQ ID NO:490) derived from the coding sequence of SEQ ID NO:489 shown in Figure 489.

10 Figure 491 shows a nucleotide sequence (SEQ ID NO:491) of a native sequence PRO19563 cDNA, wherein SEQ ID NO:491 is a clone designated herein as "DNA96861-2844".

Figure 492 shows the amino acid sequence (SEQ ID NO:492) derived from the coding sequence of SEQ ID NO:491 shown in Figure 491.

15 Figure 493 shows a nucleotide sequence (SEQ ID NO:493) of a native sequence PRO6015 cDNA, wherein SEQ ID NO:493 is a clone designated herein as "DNA96866-2698".

Figure 494 shows the amino acid sequence (SEQ ID NO:494) derived from the coding sequence of SEQ ID NO:493 shown in Figure 493.

Figure 495 shows a nucleotide sequence (SEQ ID NO:495) of a native sequence PRO5779 cDNA, wherein SEQ ID NO:495 is a clone designated herein as "DNA96870-2676".

20 Figure 496 shows the amino acid sequence (SEQ ID NO:496) derived from the coding sequence of SEQ ID NO:495 shown in Figure 495.

Figure 497 shows a nucleotide sequence (SEQ ID NO:497) of a native sequence PRO5776 cDNA, wherein SEQ ID NO:497 is a clone designated herein as "DNA96872-2674".

25 Figure 498 shows the amino acid sequence (SEQ ID NO:498) derived from the coding sequence of SEQ ID NO:497 shown in Figure 497.

Figure 499 shows a nucleotide sequence (SEQ ID NO:499) of a native sequence PRO4430 cDNA, wherein SEQ ID NO:499 is a clone designated herein as "DNA96878-2626".

Figure 500 shows the amino acid sequence (SEQ ID NO:500) derived from the coding sequence of SEQ ID NO:499 shown in Figure 499.

30 Figure 501 shows a nucleotide sequence (SEQ ID NO:501) of a native sequence PRO4421 cDNA, wherein SEQ ID NO:501 is a clone designated herein as "DNA96879-2619".

Figure 502 shows the amino acid sequence (SEQ ID NO:502) derived from the coding sequence of SEQ ID NO:501 shown in Figure 501.

35 Figure 503 shows a nucleotide sequence (SEQ ID NO:503) of a native sequence PRO4499 cDNA, wherein SEQ ID NO:503 is a clone designated herein as "DNA96889-2641".

Figure 504 shows the amino acid sequence (SEQ ID NO:504) derived from the coding sequence of SEQ ID NO:503 shown in Figure 503.

Figure 505 shows a nucleotide sequence (SEQ ID NO:505) of a native sequence PRO4423 cDNA, wherein SEQ ID NO:505 is a clone designated herein as "DNA96893-2621".

Figure 506 shows the amino acid sequence (SEQ ID NO:506) derived from the coding sequence of SEQ ID NO:505 shown in Figure 505.

5 Figure 507 shows a nucleotide sequence (SEQ ID NO:507) of a native sequence PRO5998 cDNA, wherein SEQ ID NO:507 is a clone designated herein as "DNA96897-2688".

Figure 508 shows the amino acid sequence (SEQ ID NO:508) derived from the coding sequence of SEQ ID NO:507 shown in Figure 507.

Figure 509 shows a nucleotide sequence (SEQ ID NO:509) of a native sequence PRO4501 cDNA, wherein SEQ ID NO:509 is a clone designated herein as "DNA98564-2643".

10 Figure 510 shows the amino acid sequence (SEQ ID NO:510) derived from the coding sequence of SEQ ID NO:509 shown in Figure 509.

Figure 511 shows a nucleotide sequence (SEQ ID NO:511) of a native sequence PRO6240 cDNA, wherein SEQ ID NO:511 is a clone designated herein as "DNA107443-2718".

15 Figure 512 shows the amino acid sequence (SEQ ID NO:512) derived from the coding sequence of SEQ ID NO:511 shown in Figure 511.

Figure 513 shows a nucleotide sequence (SEQ ID NO:513) of a native sequence PRO6245 cDNA, wherein SEQ ID NO:513 is a clone designated herein as "DNA107786-2723".

Figure 514 shows the amino acid sequence (SEQ ID NO:514) derived from the coding sequence of SEQ ID NO:513 shown in Figure 513.

20 Figure 515 shows a nucleotide sequence (SEQ ID NO:515) of a native sequence PRO6175 cDNA, wherein SEQ ID NO:515 is a clone designated herein as "DNA108682-2712".

Figure 516 shows the amino acid sequence (SEQ ID NO:516) derived from the coding sequence of SEQ ID NO:515 shown in Figure 515.

25 Figure 517 shows a nucleotide sequence (SEQ ID NO:517) of a native sequence PRO9742 cDNA, wherein SEQ ID NO:517 is a clone designated herein as "DNA108684-2761".

Figure 518 shows the amino acid sequence (SEQ ID NO:518) derived from the coding sequence of SEQ ID NO:517 shown in Figure 517.

Figure 519 shows a nucleotide sequence (SEQ ID NO:519) of a native sequence PRO7179 cDNA, wherein SEQ ID NO:519 is a clone designated herein as "DNA108701-2749".

30 Figure 520 shows the amino acid sequence (SEQ ID NO:520) derived from the coding sequence of SEQ ID NO:519 shown in Figure 519.

Figure 521 shows a nucleotide sequence (SEQ ID NO:521) of a native sequence PRO6239 cDNA, wherein SEQ ID NO:521 is a clone designated herein as "DNA108720-2717".

35 Figure 522 shows the amino acid sequence (SEQ ID NO:522) derived from the coding sequence of SEQ ID NO:521 shown in Figure 521.

Figure 523 shows a nucleotide sequence (SEQ ID NO:523) of a native sequence PRO6493 cDNA, wherein SEQ ID NO:523 is a clone designated herein as "DNA108726-2729".

Figure 524 shows the amino acid sequence (SEQ ID NO:524) derived from the coding sequence of SEQ ID NO:523 shown in Figure 523.

Figures 525A-525B show a nucleotide sequence (SEQ ID NO:525) of a native sequence PRO9741 cDNA, wherein SEQ ID NO:525 is a clone designated herein as "DNA108728-2760".

5 Figure 526 shows the amino acid sequence (SEQ ID NO:526) derived from the coding sequence of SEQ ID NO:525 shown in Figures 525A-525B.

Figure 527 shows a nucleotide sequence (SEQ ID NO:527) of a native sequence PRO9822 cDNA, wherein SEQ ID NO:527 is a clone designated herein as "DNA108738-2767".

Figure 528 shows the amino acid sequence (SEQ ID NO:528) derived from the coding sequence of SEQ ID NO:527 shown in Figure 527.

10 Figure 529 shows a nucleotide sequence (SEQ ID NO:529) of a native sequence PRO6244 cDNA, wherein SEQ ID NO:529 is a clone designated herein as "DNA108743-2722".

Figure 530 shows the amino acid sequence (SEQ ID NO:530) derived from the coding sequence of SEQ ID NO:529 shown in Figure 529.

15 Figure 531 shows a nucleotide sequence (SEQ ID NO:531) of a native sequence PRO9740 cDNA, wherein SEQ ID NO:531 is a clone designated herein as "DNA108758-2759".

Figure 532 shows the amino acid sequence (SEQ ID NO:532) derived from the coding sequence of SEQ ID NO:531 shown in Figure 531.

Figure 533 shows a nucleotide sequence (SEQ ID NO:533) of a native sequence PRO9739 cDNA, wherein SEQ ID NO:533 is a clone designated herein as "DNA108765-2758".

20 Figure 534 shows the amino acid sequence (SEQ ID NO:534) derived from the coding sequence of SEQ ID NO:533 shown in Figure 533.

Figure 535 shows a nucleotide sequence (SEQ ID NO:535) of a native sequence PRO7177 cDNA, wherein SEQ ID NO:535 is a clone designated herein as "DNA108783-2747".

25 Figure 536 shows the amino acid sequence (SEQ ID NO:536) derived from the coding sequence of SEQ ID NO:535 shown in Figure 535.

Figure 537 shows a nucleotide sequence (SEQ ID NO:537) of a native sequence PRO7178 cDNA, wherein SEQ ID NO:537 is a clone designated herein as "DNA108789-2748".

Figure 538 shows the amino acid sequence (SEQ ID NO:538) derived from the coding sequence of SEQ ID NO:537 shown in Figure 537.

30 Figure 539 shows a nucleotide sequence (SEQ ID NO:539) of a native sequence PRO6246 cDNA, wherein SEQ ID NO:539 is a clone designated herein as "DNA108806-2724".

Figure 540 shows the amino acid sequence (SEQ ID NO:540) derived from the coding sequence of SEQ ID NO:539 shown in Figure 539.

35 Figure 541 shows a nucleotide sequence (SEQ ID NO:541) of a native sequence PRO6241 cDNA, wherein SEQ ID NO:541 is a clone designated herein as "DNA108936-2719".

Figure 542 shows the amino acid sequence (SEQ ID NO:542) derived from the coding sequence of SEQ ID NO:541 shown in Figure 541.

Figure 543 shows a nucleotide sequence (SEQ ID NO:543) of a native sequence PRO9835 cDNA, wherein SEQ ID NO:543 is a clone designated herein as "DNA119510-2771".

Figure 544 shows the amino acid sequence (SEQ ID NO:544) derived from the coding sequence of SEQ ID NO:543 shown in Figure 543.

5 Figure 545 shows a nucleotide sequence (SEQ ID NO:545) of a native sequence PRO9857 cDNA, wherein SEQ ID NO:545 is a clone designated herein as "DNA119517-2778".

Figure 546 shows the amino acid sequence (SEQ ID NO:546) derived from the coding sequence of SEQ ID NO:545 shown in Figure 545.

Figure 547 shows a nucleotide sequence (SEQ ID NO:547) of a native sequence PRO7436 cDNA, wherein SEQ ID NO:547 is a clone designated herein as "DNA119535-2756".

10 Figure 548 shows the amino acid sequence (SEQ ID NO:548) derived from the coding sequence of SEQ ID NO:547 shown in Figure 547.

Figure 549 shows a nucleotide sequence (SEQ ID NO:549) of a native sequence PRO9856 cDNA, wherein SEQ ID NO:549 is a clone designated herein as "DNA119537-2777".

15 Figure 550 shows the amino acid sequence (SEQ ID NO:550) derived from the coding sequence of SEQ ID NO:549 shown in Figure 549.

Figure 551 shows a nucleotide sequence (SEQ ID NO:551) of a native sequence PRO19605 cDNA, wherein SEQ ID NO:551 is a clone designated herein as "DNA119714-2851".

Figure 552 shows the amino acid sequence (SEQ ID NO:552) derived from the coding sequence of SEQ ID NO:551 shown in Figure 551.

20 Figure 553 shows a nucleotide sequence (SEQ ID NO:553) of a native sequence PRO9859 cDNA, wherein SEQ ID NO:553 is a clone designated herein as "DNA125170-2780".

Figure 554 shows the amino acid sequence (SEQ ID NO:554) derived from the coding sequence of SEQ ID NO:553 shown in Figure 553.

25 Figure 555 shows a nucleotide sequence (SEQ ID NO:555) of a native sequence PRO12970 cDNA, wherein SEQ ID NO:555 is a clone designated herein as "DNA129594-2841".

Figure 556 shows the amino acid sequence (SEQ ID NO:556) derived from the coding sequence of SEQ ID NO:555 shown in Figure 555.

Figure 557 shows a nucleotide sequence (SEQ ID NO:557) of a native sequence PRO19626 cDNA, wherein SEQ ID NO:557 is a clone designated herein as "DNA129793-2857".

30 Figure 558 shows the amino acid sequence (SEQ ID NO:558) derived from the coding sequence of SEQ ID NO:557 shown in Figure 557.

Figure 559 shows a nucleotide sequence (SEQ ID NO:559) of a native sequence PRO9833 cDNA, wherein SEQ ID NO:559 is a clone designated herein as "DNA130809-2769".

35 Figure 560 shows the amino acid sequence (SEQ ID NO:560) derived from the coding sequence of SEQ ID NO:559 shown in Figure 559.

Figure 561 shows a nucleotide sequence (SEQ ID NO:561) of a native sequence PRO19670 cDNA, wherein SEQ ID NO:561 is a clone designated herein as "DNA131639-2874".

Figure 562 shows the amino acid sequence (SEQ ID NO:562) derived from the coding sequence of SEQ ID NO:561 shown in Figure 561.

Figure 563 shows a nucleotide sequence (SEQ ID NO:563) of a native sequence PRO19624 cDNA, wherein SEQ ID NO:563 is a clone designated herein as "DNA131649-2855".

5 Figure 564 shows the amino acid sequence (SEQ ID NO:564) derived from the coding sequence of SEQ ID NO:563 shown in Figure 563.

Figure 565 shows a nucleotide sequence (SEQ ID NO:565) of a native sequence PRO19680 cDNA, wherein SEQ ID NO:565 is a clone designated herein as "DNA131652-2876".

Figure 566 shows the amino acid sequence (SEQ ID NO:566) derived from the coding sequence of SEQ ID NO:565 shown in Figure 565.

10 Figure 567 shows a nucleotide sequence (SEQ ID NO:567) of a native sequence PRO19675 cDNA, wherein SEQ ID NO:567 is a clone designated herein as "DNA131658-2875".

Figure 568 shows the amino acid sequence (SEQ ID NO:568) derived from the coding sequence of SEQ ID NO:567 shown in Figure 567.

15 Figure 569 shows a nucleotide sequence (SEQ ID NO:569) of a native sequence PRO9834 cDNA, wherein SEQ ID NO:569 is a clone designated herein as "DNA132162-2770".

Figure 570 shows the amino acid sequence (SEQ ID NO:570) derived from the coding sequence of SEQ ID NO:569 shown in Figure 569.

Figure 571 shows a nucleotide sequence (SEQ ID NO:571) of a native sequence PRO9744 cDNA, wherein SEQ ID NO:571 is a clone designated herein as "DNA136110-2763".

20 Figure 572 shows the amino acid sequence (SEQ ID NO:572) derived from the coding sequence of SEQ ID NO:571 shown in Figure 571.

Figure 573 shows a nucleotide sequence (SEQ ID NO:573) of a native sequence PRO19644 cDNA, wherein SEQ ID NO:573 is a clone designated herein as "DNA139592-2866".

25 Figure 574 shows the amino acid sequence (SEQ ID NO:574) derived from the coding sequence of SEQ ID NO:573 shown in Figure 573.

Figure 575 shows a nucleotide sequence (SEQ ID NO:575) of a native sequence PRO19625 cDNA, wherein SEQ ID NO:575 is a clone designated herein as "DNA139608-2856".

Figure 576 shows the amino acid sequence (SEQ ID NO:576) derived from the coding sequence of SEQ ID NO:575 shown in Figure 575.

30 Figure 577 shows a nucleotide sequence (SEQ ID NO:577) of a native sequence PRO19597 cDNA, wherein SEQ ID NO:577 is a clone designated herein as "DNA143292-2848".

Figure 578 shows the amino acid sequence (SEQ ID NO:578) derived from the coding sequence of SEQ ID NO:577 shown in Figure 577.

35 Figure 579 shows a nucleotide sequence (SEQ ID NO:579) of a native sequence PRO16090 cDNA, wherein SEQ ID NO:579 is a clone designated herein as "DNA144844-2843".

Figure 580 shows the amino acid sequence (SEQ ID NO:580) derived from the coding sequence of SEQ ID NO:579 shown in Figure 579.

Figure 581 shows a nucleotide sequence (SEQ ID NO:581) of a native sequence PRO19576 cDNA, wherein SEQ ID NO:581 is a clone designated herein as "DNA144857-2845".

Figure 582 shows the amino acid sequence (SEQ ID NO:582) derived from the coding sequence of SEQ ID NO:581 shown in Figure 581.

5 Figure 583 shows a nucleotide sequence (SEQ ID NO:583) of a native sequence PRO19646 cDNA, wherein SEQ ID NO:583 is a clone designated herein as "DNA145841-2868".

Figure 584 shows the amino acid sequence (SEQ ID NO:584) derived from the coding sequence of SEQ ID NO:583 shown in Figure 583.

Figure 585 shows a nucleotide sequence (SEQ ID NO:585) of a native sequence PRO19814 cDNA, wherein SEQ ID NO:585 is a clone designated herein as "DNA148004-2882".

10 Figure 586 shows the amino acid sequence (SEQ ID NO:586) derived from the coding sequence of SEQ ID NO:585 shown in Figure 585.

Figure 587 shows a nucleotide sequence (SEQ ID NO:587) of a native sequence PRO19669 cDNA, wherein SEQ ID NO:587 is a clone designated herein as "DNA149893-2873".

15 Figure 588 shows the amino acid sequence (SEQ ID NO:588) derived from the coding sequence of SEQ ID NO:587 shown in Figure 587.

Figure 589 shows a nucleotide sequence (SEQ ID NO:589) of a native sequence PRO19818 cDNA, wherein SEQ ID NO:589 is a clone designated herein as "DNA149930-2884".

Figure 590 shows the amino acid sequence (SEQ ID NO:590) derived from the coding sequence of SEQ ID NO:589 shown in Figure 589.

20 Figure 591 shows a nucleotide sequence (SEQ ID NO:591) of a native sequence PRO20088 cDNA, wherein SEQ ID NO:591 is a clone designated herein as "DNA150157-2898".

Figure 592 shows the amino acid sequence (SEQ ID NO:592) derived from the coding sequence of SEQ ID NO:591 shown in Figure 591.

25 Figure 593 shows a nucleotide sequence (SEQ ID NO:593) of a native sequence PRO16089 cDNA, wherein SEQ ID NO:593 is a clone designated herein as "DNA150163-2842".

Figure 594 shows the amino acid sequence (SEQ ID NO:594) derived from the coding sequence of SEQ ID NO:593 shown in Figure 593.

Figure 595 shows a nucleotide sequence (SEQ ID NO:595) of a native sequence PRO20025 cDNA, wherein SEQ ID NO:595 is a clone designated herein as "DNA153579-2894".

30 Figure 596 shows the amino acid sequence (SEQ ID NO:596) derived from the coding sequence of SEQ ID NO:595 shown in Figure 595.

Figure 597 shows a nucleotide sequence (SEQ ID NO:597) of a native sequence PRO20040 cDNA, wherein SEQ ID NO:597 is a clone designated herein as "DNA164625-2890".

35 Figure 598 shows the amino acid sequence (SEQ ID NO:598) derived from the coding sequence of SEQ ID NO:597 shown in Figure 597.

Figure 599 shows a nucleotide sequence (SEQ ID NO:599) of a native sequence PRO791 cDNA, wherein SEQ ID NO:599 is a clone designated herein as "DNA57838-1337".

Figure 600 shows the amino acid sequence (SEQ ID NO:600) derived from the coding sequence of SEQ ID NO:599 shown in Figure 599.

Figure 601 shows a nucleotide sequence (SEQ ID NO:601) of a native sequence PRO1131 cDNA, wherein SEQ ID NO:601 is a clone designated herein as "DNA59777-1480".

5 Figure 602 shows the amino acid sequence (SEQ ID NO:602) derived from the coding sequence of SEQ ID NO:601 shown in Figure 601.

Figure 603 shows a nucleotide sequence (SEQ ID NO:603) of a native sequence PRO1343 cDNA, wherein SEQ ID NO:603 is a clone designated herein as "DNA66675-1587".

Figure 604 shows the amino acid sequence (SEQ ID NO:604) derived from the coding sequence of SEQ ID NO:603 shown in Figure 603.

10 Figure 605 shows a nucleotide sequence (SEQ ID NO:605) of a native sequence PRO1760 cDNA, wherein SEQ ID NO:605 is a clone designated herein as "DNA76532-1702".

Figure 606 shows the amino acid sequence (SEQ ID NO:606) derived from the coding sequence of SEQ ID NO:605 shown in Figure 605.

15 Figure 607 shows a nucleotide sequence (SEQ ID NO:607) of a native sequence PRO6029 cDNA, wherein SEQ ID NO:607 is a clone designated herein as "DNA105849-2704".

Figure 608 shows the amino acid sequence (SEQ ID NO:608) derived from the coding sequence of SEQ ID NO:607 shown in Figure 607.

Figure 609 shows a nucleotide sequence (SEQ ID NO:609) of a native sequence PRO1801 cDNA, wherein SEQ ID NO:609 is a clone designated herein as "DNA83500-2506".

20 Figure 610 shows the amino acid sequence (SEQ ID NO:610) derived from the coding sequence of SEQ ID NO:609 shown in Figure 609.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

I. Definitions

25 The terms "PRO polypeptide" and "PRO" as used herein and when immediately followed by a numerical designation refer to various polypeptides, wherein the complete designation (i.e., PRO/number) refers to specific polypeptide sequences as described herein. The terms "PRO/number polypeptide" and "PRO/number" wherein the term "number" is provided as an actual numerical designation as used herein encompass native sequence polypeptides and polypeptide variants (which are further defined herein). The PRO polypeptides described herein
30 may be isolated from a variety of sources, such as from human tissue types or from another source, or prepared by recombinant or synthetic methods. The term "PRO polypeptide" refers to each individual PRO/number polypeptide disclosed herein. All disclosures in this specification which refer to the "PRO polypeptide" refer to each of the polypeptides individually as well as jointly. For example, descriptions of the preparation of, purification of, derivation of, formation of antibodies to or against, administration of, compositions containing,
35 treatment of a disease with, etc., pertain to each polypeptide of the invention individually. The term "PRO polypeptide" also includes variants of the PRO/number polypeptides disclosed herein.

A "native sequence PRO polypeptide" comprises a polypeptide having the same amino acid sequence as

the corresponding PRO polypeptide derived from nature. Such native sequence PRO polypeptides can be isolated from nature or can be produced by recombinant or synthetic means. The term "native sequence PRO polypeptide" specifically encompasses naturally-occurring truncated or secreted forms of the specific PRO polypeptide (*e.g.*, an extracellular domain sequence), naturally-occurring variant forms (*e.g.*, alternatively spliced forms) and naturally-occurring allelic variants of the polypeptide. In various embodiments of the invention, the native sequence PRO polypeptides disclosed herein are mature or full-length native sequence polypeptides comprising the full-length amino acids sequences shown in the accompanying figures. Start and stop codons are shown in bold font and underlined in the figures. However, while the PRO polypeptide disclosed in the accompanying figures are shown to begin with methionine residues designated herein as amino acid position 1 in the figures, it is conceivable and possible that other methionine residues located either upstream or downstream from the amino acid position 1 in the figures may be employed as the starting amino acid residue for the PRO polypeptides.

The PRO polypeptide "extracellular domain" or "ECD" refers to a form of the PRO polypeptide which is essentially free of the transmembrane and cytoplasmic domains. Ordinarily, a PRO polypeptide ECD will have less than 1% of such transmembrane and/or cytoplasmic domains and preferably, will have less than 0.5% of such domains. It will be understood that any transmembrane domains identified for the PRO polypeptides of the present invention are identified pursuant to criteria routinely employed in the art for identifying that type of hydrophobic domain. The exact boundaries of a transmembrane domain may vary but most likely by no more than about 5 amino acids at either end of the domain as initially identified herein. Optionally, therefore, an extracellular domain of a PRO polypeptide may contain from about 5 or fewer amino acids on either side of the transmembrane domain/extracellular domain boundary as identified in the Examples or specification and such polypeptides, with or without the associated signal peptide, and nucleic acid encoding them, are contemplated by the present invention.

The approximate location of the "signal peptides" of the various PRO polypeptides disclosed herein are shown in the present specification and/or the accompanying figures. It is noted, however, that the C-terminal boundary of a signal peptide may vary, but most likely by no more than about 5 amino acids on either side of the signal peptide C-terminal boundary as initially identified herein, wherein the C-terminal boundary of the signal peptide may be identified pursuant to criteria routinely employed in the art for identifying that type of amino acid sequence element (*e.g.*, Nielsen et al., Prot. Eng. 10:1-6 (1997) and von Heinje et al., Nucl. Acids. Res. 14:4683-4690 (1986)). Moreover, it is also recognized that, in some cases, cleavage of a signal sequence from a secreted polypeptide is not entirely uniform, resulting in more than one secreted species. These mature polypeptides, where the signal peptide is cleaved within no more than about 5 amino acids on either side of the C-terminal boundary of the signal peptide as identified herein, and the polynucleotides encoding them, are contemplated by the present invention.

"PRO polypeptide variant" means an active PRO polypeptide as defined above or below having at least about 80% amino acid sequence identity with a full-length native sequence PRO polypeptide sequence as disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Such PRO polypeptide variants include, for instance, PRO

polypeptides wherein one or more amino acid residues are added, or deleted, at the N- or C-terminus of the full-length native amino acid sequence. Ordinarily, a PRO polypeptide variant will have at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a full-length native sequence PRO polypeptide sequence as disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, PRO variant polypeptides are at least about 10 amino acids in length, alternatively at least about 20 amino acids in length, alternatively at least about 30 amino acids in length, alternatively at least about 40 amino acids in length, alternatively at least about 50 amino acids in length, alternatively at least about 60 amino acids in length, alternatively at least about 70 amino acids in length, alternatively at least about 80 amino acids in length, alternatively at least about 90 amino acids in length, alternatively at least about 100 amino acids in length, alternatively at least about 150 amino acids in length, alternatively at least about 200 amino acids in length, alternatively at least about 300 amino acids in length, or more.

"Percent (%) amino acid sequence identity" with respect to the PRO polypeptide sequences identified herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the specific PRO polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For purposes herein, however, % amino acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through

Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

$$100 \text{ times the fraction } X/Y$$

where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A. As examples of % amino acid sequence identity calculations using this method, Tables 2 and 3 demonstrate how to calculate the % amino acid sequence identity of the amino acid sequence designated "Comparison Protein" to the amino acid sequence designated "PRO", wherein "PRO" represents the amino acid sequence of a hypothetical PRO polypeptide of interest, "Comparison Protein" represents the amino acid sequence of a polypeptide against which the "PRO" polypeptide of interest is being compared, and "X", "Y" and "Z" each represent different hypothetical amino acid residues.

Unless specifically stated otherwise, all % amino acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % amino acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer program (Altschul et al., Methods in Enzymology 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span = 1, overlap fraction = 0.125, word threshold (T) = 11, and scoring matrix = BLOSUM62. When WU-BLAST-2 is employed, a % amino acid sequence identity value is determined by dividing (a) the number of matching identical amino acid residues between the amino acid sequence of the PRO polypeptide of interest having a sequence derived from the native PRO polypeptide and the comparison amino acid sequence of interest (i.e., the sequence against which the PRO polypeptide of interest is being compared which may be a PRO variant polypeptide) as determined by WU-BLAST-2 by (b) the total number of amino acid residues of the PRO polypeptide of interest. For example, in the statement "a polypeptide comprising an the amino acid sequence A which has or having at least 80% amino acid sequence identity to the amino acid sequence B", the amino acid sequence A is the comparison amino acid sequence of interest and the amino acid sequence B is the amino acid sequence of the PRO polypeptide of interest.

Percent amino acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from <http://www.ncbi.nlm.nih.gov> or otherwise obtained from the

National Institute of Health, Bethesda, MD. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

In situations where NCBI-BLAST2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

$$100 \text{ times the fraction } X/Y$$

where X is the number of amino acid residues scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A.

"PRO variant polynucleotide" or "PRO variant nucleic acid sequence" means a nucleic acid molecule which encodes an active PRO polypeptide as defined below and which has at least about 80% nucleic acid sequence identity with a nucleotide acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, a PRO variant polynucleotide will have at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity with a nucleic acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal sequence, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Variants do not encompass the native nucleotide sequence.

Ordinarily, PRO variant polynucleotides are at least about 30 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 120 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 210 nucleotides in length, alternatively at least about 240 nucleotides in length, alternatively at least about 270 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 900 nucleotides in length, or more.

"Percent (%) nucleic acid sequence identity" with respect to PRO-encoding nucleic acid sequences identified herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the PRO nucleic acid sequence of interest, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent nucleic acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. For purposes herein, however, % nucleic acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for nucleic acid sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

$$100 \text{ times the fraction } W/Z$$

where W is the number of nucleotides scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C. As examples of % nucleic acid sequence identity calculations, Tables 4 and 5, demonstrate how to calculate the % nucleic acid sequence identity of the nucleic acid sequence designated "Comparison DNA" to the nucleic acid sequence designated "PRO-DNA", wherein "PRO-DNA" represents a hypothetical PRO-encoding nucleic acid sequence of interest, "Comparison DNA" represents the nucleotide sequence of a nucleic acid molecule against which the "PRO-DNA" nucleic acid molecule of interest is being compared, and "N", "L" and "V" each represent

different hypothetical nucleotides.

Unless specifically stated otherwise, all % nucleic acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % nucleic acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer program (Altschul et al., Methods in Enzymology 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span = 1, overlap fraction = 0.125, word threshold (T) = 11, and scoring matrix = BLOSUM62. When WU-BLAST-2 is employed, a % nucleic acid sequence identity value is determined by dividing (a) the number of matching identical nucleotides between the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest having a sequence derived from the native sequence PRO polypeptide-encoding nucleic acid and the comparison nucleic acid molecule of interest (i.e., the sequence against which the PRO polypeptide-encoding nucleic acid molecule of interest is being compared which may be a variant PRO polynucleotide) as determined by WU-BLAST-2 by (b) the total number of nucleotides of the PRO polypeptide-encoding nucleic acid molecule of interest. For example, in the statement "an isolated nucleic acid molecule comprising a nucleic acid sequence A which has or having at least 80% nucleic acid sequence identity to the nucleic acid sequence B", the nucleic acid sequence A is the comparison nucleic acid molecule of interest and the nucleic acid sequence B is the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest.

Percent nucleic acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from <http://www.ncbi.nlm.nih.gov> or otherwise obtained from the National Institute of Health, Bethesda, MD. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

In situations where NCBI-BLAST2 is employed for sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

100 times the fraction W/Z

where W is the number of nucleotides scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C.

In other embodiments, PRO variant polynucleotides are nucleic acid molecules that encode an active PRO polypeptide and which are capable of hybridizing, preferably under stringent hybridization and wash conditions,

to nucleotide sequences encoding a full-length PRO polypeptide as disclosed herein. PRO variant polypeptides may be those that are encoded by a PRO variant polynucleotide.

5 "Isolated," when used to describe the various polypeptides disclosed herein, means polypeptide that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would typically interfere with diagnostic or therapeutic
10 uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In preferred embodiments, the polypeptide will be purified (1) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or, preferably, silver stain. Isolated polypeptide includes polypeptide *in situ* within recombinant cells, since at least one
15 component of the PRO polypeptide natural environment will not be present. Ordinarily, however, isolated polypeptide will be prepared by at least one purification step.

An "isolated" PRO polypeptide-encoding nucleic acid or other polypeptide-encoding nucleic acid is a nucleic acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the natural source of the polypeptide-encoding nucleic acid. An isolated
20 polypeptide-encoding nucleic acid molecule is other than in the form or setting in which it is found in nature. Isolated polypeptide-encoding nucleic acid molecules therefore are distinguished from the specific polypeptide-encoding nucleic acid molecule as it exists in natural cells. However, an isolated polypeptide-encoding nucleic acid molecule includes polypeptide-encoding nucleic acid molecules contained in cells that ordinarily express the polypeptide where, for example, the nucleic acid molecule is in a chromosomal location different from that of
25 natural cells.

The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

25 Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked"
30 means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

The term "antibody" is used in the broadest sense and specifically covers, for example, single anti-PRO
35 monoclonal antibodies (including agonist, antagonist, and neutralizing antibodies), anti-PRO antibody compositions with polypeptopic specificity, single chain anti-PRO antibodies, and fragments of anti-PRO antibodies (see below). The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially

homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally-occurring mutations that may be present in minor amounts.

"Stringency" of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration. In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends on the ability of denatured DNA to reanneal when complementary strands are present in an environment below their melting temperature. The higher the degree of desired homology between the probe and hybridizable sequence, the higher the relative temperature which can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so. For additional details and explanation of stringency of hybridization reactions, see Ausubel et al., Current Protocols in Molecular Biology, Wiley Interscience Publishers, (1995).

"Stringent conditions" or "high stringency conditions", as defined herein, may be identified by those that: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50°C; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42°C; or (3) employ 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 µg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC (sodium chloride/sodium citrate) and 50% formamide at 55°C, followed by a high-stringency wash consisting of 0.1 x SSC containing EDTA at 55°C.

"Moderately stringent conditions" may be identified as described by Sambrook et al., Molecular Cloning: A Laboratory Manual, New York: Cold Spring Harbor Press, 1989, and include the use of washing solution and hybridization conditions (e.g., temperature, ionic strength and %SDS) less stringent than those described above. An example of moderately stringent conditions is overnight incubation at 37°C in a solution comprising: 20% formamide, 5 x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5 x Denhardt's solution, 10% dextran sulfate, and 20 mg/ml denatured sheared salmon sperm DNA, followed by washing the filters in 1 x SSC at about 37-50°C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

The term "epitope tagged" when used herein refers to a chimeric polypeptide comprising a PRO polypeptide fused to a "tag polypeptide". The tag polypeptide has enough residues to provide an epitope against which an antibody can be made, yet is short enough such that it does not interfere with activity of the polypeptide to which it is fused. The tag polypeptide preferably also is fairly unique so that the antibody does not substantially cross-react with other epitopes. Suitable tag polypeptides generally have at least six amino acid residues and usually between about 8 and 50 amino acid residues (preferably, between about 10 and 20 amino acid residues).

As used herein, the term "immunoadhesin" designates antibody-like molecules which combine the binding specificity of a heterologous protein (an "adhesin") with the effector functions of immunoglobulin constant domains. Structurally, the immunoadhesins comprise a fusion of an amino acid sequence with the desired binding

specificity which is other than the antigen recognition and binding site of an antibody (i.e., is "heterologous"), and an immunoglobulin constant domain sequence. The adhesin part of an immunoadhesin molecule typically is a contiguous amino acid sequence comprising at least the binding site of a receptor or a ligand. The immunoglobulin constant domain sequence in the immunoadhesin may be obtained from any immunoglobulin, such as IgG-1, IgG-2, IgG-3, or IgG-4 subtypes, IgA (including IgA-1 and IgA-2), IgE, IgD or IgM.

5 "Active" or "activity" for the purposes herein refers to form(s) of a PRO polypeptide which retain a biological and/or an immunological activity of native or naturally-occurring PRO, wherein "biological" activity refers to a biological function (either inhibitory or stimulatory) caused by a native or naturally-occurring PRO other than the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring PRO and an "immunological" activity refers to the ability to induce the production of an
10 antibody against an antigenic epitope possessed by a native or naturally-occurring PRO.

The term "antagonist" is used in the broadest sense, and includes any molecule that partially or fully blocks, inhibits, or neutralizes a biological activity of a native PRO polypeptide disclosed herein. In a similar manner, the term "agonist" is used in the broadest sense and includes any molecule that mimics a biological activity of a native PRO polypeptide disclosed herein. Suitable agonist or antagonist molecules specifically
15 include agonist or antagonist antibodies or antibody fragments, fragments or amino acid sequence variants of native PRO polypeptides, peptides, antisense oligonucleotides, small organic molecules, etc. Methods for identifying agonists or antagonists of a PRO polypeptide may comprise contacting a PRO polypeptide with a candidate agonist or antagonist molecule and measuring a detectable change in one or more biological activities normally associated with the PRO polypeptide.

20 "Treatment" refers to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen) the targeted pathologic condition or disorder. Those in need of treatment include those already with the disorder as well as those prone to have the disorder or those in whom the disorder is to be prevented.

"Chronic" administration refers to administration of the agent(s) in a continuous mode as opposed to an
25 acute mode, so as to maintain the initial therapeutic effect (activity) for an extended period of time. "Intermittent" administration is treatment that is not consecutively done without interruption, but rather is cyclic in nature.

"Mammal" for purposes of treatment refers to any animal classified as a mammal, including humans, domestic and farm animals, and zoo, sports, or pet animals, such as dogs, cats, cattle, horses, sheep, pigs, goats, rabbits, etc. Preferably, the mammal is human.

30 Administration "in combination with" one or more further therapeutic agents includes simultaneous (concurrent) and consecutive administration in any order.

"Carriers" as used herein include pharmaceutically acceptable carriers, excipients, or stabilizers which are nontoxic to the cell or mammal being exposed thereto at the dosages and concentrations employed. Often the physiologically acceptable carrier is an aqueous pH buffered solution. Examples of physiologically acceptable
35 carriers include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptide; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine,

asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN™, polyethylene glycol (PEG), and PLURONICS™.

5 "Antibody fragments" comprise a portion of an intact antibody, preferably the antigen binding or variable region of the intact antibody. Examples of antibody fragments include Fab, Fab', F(ab')₂, and Fv fragments; diabodies; linear antibodies (Zapata et al., Protein Eng. 8(10): 1057-1062 [1995]); single-chain antibody molecules; and multispecific antibodies formed from antibody fragments.

10 Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, each with a single antigen-binding site, and a residual "Fc" fragment, a designation reflecting the ability to crystallize readily. Pepsin treatment yields an F(ab')₂ fragment that has two antigen-combining sites and is still capable of cross-linking antigen.

"Fv" is the minimum antibody fragment which contains a complete antigen-recognition and -binding site. This region consists of a dimer of one heavy- and one light-chain variable domain in tight, non-covalent association. It is in this configuration that the three CDRs of each variable domain interact to define an antigen-binding site on the surface of the V_H-V_L dimer. Collectively, the six CDRs confer antigen-binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

15 The Fab fragment also contains the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab fragments differ from Fab' fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group. F(ab')₂ antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

20 The "light chains" of antibodies (immunoglobulins) from any vertebrate species can be assigned to one of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains.

Depending on the amino acid sequence of the constant domain of their heavy chains, immunoglobulins can be assigned to different classes. There are five major classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, and several of these may be further divided into subclasses (isotypes), e.g., IgG1, IgG2, IgG3, IgG4, IgA, and IgA2.

30 "Single-chain Fv" or "sFv" antibody fragments comprise the V_H and V_L domains of antibody, wherein these domains are present in a single polypeptide chain. Preferably, the Fv polypeptide further comprises a polypeptide linker between the V_H and V_L domains which enables the sFv to form the desired structure for antigen binding. For a review of sFv, see Pluckthun in The Pharmacology of Monoclonal Antibodies, vol. 113, Rosenberg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994).

35 The term "diabodies" refers to small antibody fragments with two antigen-binding sites, which fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) in the same

polypeptide chain (V_H - V_L). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Diabodies are described more fully in, for example, EP 404,097; WO 93/11161; and Hollinger et al., Proc. Natl. Acad. Sci. USA, 90:6444-6448 (1993).

5 An "isolated" antibody is one which has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the antibody will be purified (1) to greater than 95% by weight of antibody as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence
10 by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing conditions using Coomassie blue or, preferably, silver stain. Isolated antibody includes the antibody in situ within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

15 An antibody that "specifically binds to" or is "specific for" a particular polypeptide or an epitope on a particular polypeptide is one that binds to that particular polypeptide or epitope on a particular polypeptide without substantially binding to any other polypeptide or polypeptide epitope.

The word "label" when used herein refers to a detectable compound or composition which is conjugated directly or indirectly to the antibody so as to generate a "labeled" antibody. The label may be detectable by itself (e.g. radioisotope labels or fluorescent labels) or, in the case of an enzymatic label, may catalyze chemical
20 alteration of a substrate compound or composition which is detectable.

By "solid phase" is meant a non-aqueous matrix to which the antibody of the present invention can adhere. Examples of solid phases encompassed herein include those formed partially or entirely of glass (e.g., controlled pore glass), polysaccharides (e.g., agarose), polyacrylamides, polystyrene, polyvinyl alcohol and silicones. In certain embodiments, depending on the context, the solid phase can comprise the well of an assay
25 plate; in others it is a purification column (e.g., an affinity chromatography column). This term also includes a discontinuous solid phase of discrete particles, such as those described in U.S. Patent No. 4,275,149.

A "liposome" is a small vesicle composed of various types of lipids, phospholipids and/or surfactant which is useful for delivery of a drug (such as a PRO polypeptide or antibody thereto) to a mammal. The components of the liposome are commonly arranged in a bilayer formation, similar to the lipid arrangement of
30 biological membranes.

A "small molecule" is defined herein to have a molecular weight below about 500 Daltons.

An "effective amount" of a polypeptide disclosed herein or an agonist or antagonist thereof is an amount sufficient to carry out a specifically stated purpose. An "effective amount" may be determined empirically and in a routine manner, in relation to the stated purpose.
35

Table 1

```

/*
*
* C-C increased from 12 to 15
* Z is average of EQ
5  * B is average of ND
* match with stop is _M; stop-stop = 0; J (joker) match = 0
*/
#define _M      -8      /* value of a match with a stop */

10 int _day[26][26] = {
/*  A B C D E F G H I J K L M N O P Q R S T U V W X Y Z */
/* A */ { 2, 0, -2, 0, 0, -4, 1, -1, -1, 0, -1, -2, -1, 0, _M, 1, 0, -2, 1, 1, 0, 0, -6, 0, -3, 0},
/* B */ { 0, 3, -4, 3, 2, -5, 0, 1, -2, 0, 0, -3, -2, 2, _M, -1, 1, 0, 0, 0, 0, -2, -5, 0, -3, 1},
/* C */ {-2, -4, 15, -5, -5, -4, -3, -3, -2, 0, -5, -6, -5, -4, _M, -3, -5, -4, 0, -2, 0, -2, -8, 0, 0, -5},
15 /* D */ { 0, 3, -5, 4, 3, -6, 1, 1, -2, 0, 0, -4, -3, 2, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 2},
/* E */ { 0, 2, -5, 3, 4, -5, 0, 1, -2, 0, 0, -3, -2, 1, _M, -1, 2, -1, 0, 0, 0, -2, -7, 0, -4, 3},
/* F */ {-4, -5, -4, -6, -5, 9, -5, -2, 1, 0, -5, 2, 0, -4, _M, -5, -5, -4, -3, -3, 0, -1, 0, 0, 7, -5},
/* G */ { 1, 0, -3, 1, 0, -5, 5, -2, -3, 0, -2, -4, -3, 0, _M, -1, -1, -3, 1, 0, 0, -1, -7, 0, -5, 0},
/* H */ {-1, 1, -3, 1, 1, -2, -2, 6, -2, 0, 0, -2, -2, 2, _M, 0, 3, 2, -1, -1, 0, -2, -3, 0, 0, 2},
20 /* I */ {-1, -2, -2, -2, -2, 1, -3, -2, 5, 0, -2, 2, 2, -2, _M, -2, -2, -2, -1, 0, 0, 4, -5, 0, -1, -2},
/* J */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* K */ {-1, 0, -5, 0, 0, -5, -2, 0, -2, 0, 5, -3, 0, 1, _M, -1, 1, 3, 0, 0, 0, -2, -3, 0, -4, 0},
/* L */ {-2, -3, -6, -4, -3, 2, -4, -2, 2, 0, -3, 6, 4, -3, _M, -3, -2, -3, -3, -1, 0, 2, -2, 0, -1, -2},
/* M */ {-1, -2, -5, -3, -2, 0, -3, -2, 2, 0, 0, 4, 6, -2, _M, -2, -1, 0, -2, -1, 0, 2, -4, 0, -2, -1},
25 /* N */ { 0, 2, -4, 2, 1, -4, 0, 2, -2, 0, 1, -3, -2, 2, _M, -1, 1, 0, 1, 0, 0, -2, -4, 0, -2, 1},
/* O */ { _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, _M, 0, _M, _M, _M, _M, _M, _M, _M, _M, _M},
/* P */ { 1, -1, -3, -1, -1, -5, -1, 0, -2, 0, -1, -3, -2, -1, _M, 6, 0, 0, 1, 0, 0, -1, -6, 0, -5, 0},
/* Q */ { 0, 1, -5, 2, 2, -5, -1, 3, -2, 0, 1, -2, -1, 1, _M, 0, 4, 1, -1, -1, 0, -2, -5, 0, -4, 3},
/* R */ {-2, 0, -4, -1, -1, -4, -3, 2, -2, 0, 3, -3, 0, 0, _M, 0, 1, 6, 0, -1, 0, -2, 2, 0, -4, 0},
30 /* S */ { 1, 0, 0, 0, 0, -3, 1, -1, -1, 0, 0, -3, -2, 1, _M, 1, -1, 0, 2, 1, 0, -1, -2, 0, -3, 0},
/* T */ { 1, 0, -2, 0, 0, -3, 0, -1, 0, 0, 0, -1, -1, 0, _M, 0, -1, -1, 1, 3, 0, 0, -5, 0, -3, 0},
/* U */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* V */ { 0, -2, -2, -2, -2, -1, -1, -2, 4, 0, -2, 2, 2, -2, _M, -1, -2, -2, -1, 0, 0, 4, -6, 0, -2, -2},
/* W */ {-6, -5, -8, -7, -7, 0, -7, -3, -5, 0, -3, -2, -4, -4, _M, -6, -5, 2, -2, -5, 0, -6, 17, 0, 0, -6},
35 /* X */ { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, _M, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* Y */ {-3, -3, 0, -4, -4, 7, -5, 0, -1, 0, -4, -1, -2, -2, _M, -5, -4, -4, -3, -3, 0, -2, 0, 0, 10, -4},
/* Z */ { 0, 1, -5, 2, 3, -5, 0, 2, -2, 0, 0, -2, -1, 1, _M, 0, 3, 0, 0, 0, 0, -2, -6, 0, -4, 4}
};

40

45

50

55

```

Table 1 (cont')

```

/*
*/
#include <stdio.h>
#include <ctype.h>

5
#define MAXJMP      16      /* max jumps in a diag */
#define MAXGAP      24      /* don't continue to penalize gaps larger than this */
#define JMPS        1024    /* max jmps in an path */
10
#define MX           4      /* save if there's at least MX-1 bases since last jmp */

#define DMAT         3      /* value of matching bases */
#define DMIS         0      /* penalty for mismatched bases */
#define DINS0        8      /* penalty for a gap */
15
#define DINS1         1      /* penalty per base */
#define PINS0         8      /* penalty for a gap */
#define PINS1         4      /* penalty per residue */

struct jmp {
20
    short            n[MAXJMP]; /* size of jmp (neg for dely) */
    unsigned short   x[MAXJMP]; /* base no. of jmp in seq x */
}; /* limits seq to 2^16 -1 */

struct diag {
25
    int              score;      /* score at last jmp */
    long             offset;     /* offset of prev block */
    short            ijmp;       /* current jmp index */
    struct jmp        jp;        /* list of jmps */
};

30
struct path {
    int              spc;         /* number of leading spaces */
    short            n[JMPS]; /* size of jmp (gap) */
    int              x[JMPS]; /* loc of jmp (last elem before gap) */
35
};

char          *ofile;           /* output file name */
char          *namex[2];        /* seq names: getseqs() */
char          *prog;            /* prog name for err msgs */
char          *seqx[2];         /* seqs: getseqs() */
40
int           dmax;             /* best diag: nw() */
int           dmax0;            /* final diag */
int           dna;              /* set if dna: main() */
int           endgaps;          /* set if penalizing end gaps */
int           gapx, gapy;        /* total gaps in seqs */
45
int           len0, len1;        /* seq lens */
int           ngapx, ngapy;      /* total size of gaps */
int           smax;             /* max score: nw() */
int           *xbm;             /* bitmap for matching */
long          offset;           /* current offset in jmp file */
50
struct        diag              *dx; /* holds diagonals */
struct        path              pp[2]; /* holds path for seqs */

char          *calloc(), *malloc(), *index(), *strcpy();
55
char          *getseq(), *g_calloc();

```

60

Table 1 (cont')

```

/* Needleman-Wunsch alignment program
*
* usage: progs file1 file2
* where file1 and file2 are two dna or two protein sequences.
5 * The sequences can be in upper- or lower-case and may contain ambiguity
* Any lines beginning with ';', '>' or '<' are ignored
* Max file length is 65535 (limited by unsigned short x in the jmp struct)
* A sequence with 1/3 or more of its elements ACGTU is assumed to be DNA
10 * Output is in the file "align.out"
*
* The program may create a tmp file in /tmp to hold info about traceback.
* Original version developed under BSD 4.3 on a vax 8650
*/
15 #include "nw.h"
#include "day.h"

static _dbval[26] = {
    1,14,2,13,0,0,4,11,0,0,12,0,3,15,0,0,0,5,6,8,8,7,9,0,10,0
20 };

static _pbval[26] = {
    1,2|(1<<('D'-'A'))|(1<<('N'-'A')), 4, 8, 16, 32, 64,
    128, 256, 0xFFFFFFFF, 1<<10, 1<<11, 1<<12, 1<<13, 1<<14,
    1<<15, 1<<16, 1<<17, 1<<18, 1<<19, 1<<20, 1<<21, 1<<22,
25 1<<23, 1<<24, 1<<25|(1<<('E'-'A'))|(1<<('Q'-'A'))
};

main(ac, av)
30     int      ac;
     char     *av[];
{
    prog = av[0];
    if (ac != 3) {
35         fprintf(stderr, "usage: %s file1 file2\n", prog);
        fprintf(stderr, "where file1 and file2 are two dna or two protein sequences.\n");
        fprintf(stderr, "The sequences can be in upper- or lower-case\n");
        fprintf(stderr, "Any lines beginning with ';' or '<' are ignored\n");
        fprintf(stderr, "Output is in the file \"align.out\"\n");
        exit(1);
40     }
    namex[0] = av[1];
    namex[1] = av[2];
    seqx[0] = getseq(namex[0], &len0);
    seqx[1] = getseq(namex[1], &len1);
45     xbm = (dna)? _dbval : _pbval;

    endgaps = 0; /* 1 to penalize endgaps */
    ofile = "align.out"; /* output file */

50     nw(); /* fill in the matrix, get the possible jumps */
    readjumps(); /* get the actual jumps */
    print(); /* print stats, alignment */

    cleanup(0); /* unlink any tmp files */
55 }

```

main

Table 1 (cont')

```

/* do the alignment, return best score: main()
* dna: values in Fitch and Smith, PNAS, 80, 1382-1386, 1983
* pro: PAM 250 values
5  * When scores are equal, we prefer mismatches to any gap, prefer
* a new gap to extending an ongoing gap, and prefer a gap in seqx
* to a gap in seq y.
*/
nw()
{
10      char      *px, *py;          /* seqs and ptrs */
      int        *ndely, *dely;     /* keep track of dely */
      int        ndelx, delx;       /* keep track of delx */
      int        *tmp;              /* for swapping row0, row1 */
15      int        mis;              /* score for each type */
      int        ins0, ins1;        /* insertion penalties */
      register   id;                /* diagonal index */
      register   ij;                /* jmp index */
      register   *col0, *col1;      /* score for curr, last row */
20      register   xx, yy;           /* index into seqs */

      dx = (struct diag *)g_calloc("to get diags", len0+len1+1, sizeof(struct diag));

      ndely = (int *)g_calloc("to get ndely", len1+1, sizeof(int));
      dely = (int *)g_calloc("to get dely", len1+1, sizeof(int));
25      col0 = (int *)g_calloc("to get col0", len1+1, sizeof(int));
      col1 = (int *)g_calloc("to get col1", len1+1, sizeof(int));
      ins0 = (dna)? DINS0 : PINS0;
      ins1 = (dna)? DINS1 : PINS1;

30      smax = -10000;
      if (endgaps) {
          for (col0[0] = dely[0] = -ins0, yy = 1; yy <= len1; yy++) {
              col0[yy] = dely[yy] = col0[yy-1] - ins1;
              ndely[yy] = yy;
35          }
          col0[0] = 0;          /* Waterman Bull Math Biol 84 */
      }
      else
40          for (yy = 1; yy <= len1; yy++)
              dely[yy] = -ins0;

      /* fill in match matrix
      */
45      for (px = seqx[0], xx = 1; xx <= len0; px++, xx++) {
          /* initialize first entry in col
          */
          if (endgaps) {
              if (xx == 1)
50                  col1[0] = delx = -(ins0+ins1);
              else
                  col1[0] = delx = col0[0] - ins1;
              ndelx = xx;
          }
          else {
55              col1[0] = 0;
              delx = -ins0;
              ndelx = 0;
          }
      }
60

```

Table 1 (cont')**...nw**

```

5      for (py = seqx[1], yy = 1; yy <= len1; py++, yy++) {
        mis = col0[yy-1];
        if (dna)
            mis += (xbm[*px-'A']&xbm[*py-'A'])? DMAT : DMIS;
        else
            mis += _day[*px-'A'][*py-'A'];

10      /* update penalty for del in x seq;
        * favor new del over ongong del
        * ignore MAXGAP if weighting endgaps
        */
        if (endgaps || ndely[yy] < MAXGAP) {
15            if (col0[yy] - ins0 >= dely[yy]) {
                dely[yy] = col0[yy] - (ins0+ins1);
                ndely[yy] = 1;
            } else {
                dely[yy] -= ins1;
                ndely[yy]++;
20            }
        } else {
            if (col0[yy] - (ins0+ins1) >= dely[yy]) {
                dely[yy] = col0[yy] - (ins0+ins1);
                ndely[yy] = 1;
25            } else
                ndely[yy]++;
        }

        /* update penalty for del in y seq;
        * favor new del over ongong del
        */
        if (endgaps || ndelx < MAXGAP) {
30            if (col1[yy-1] - ins0 >= delx) {
                delx = col1[yy-1] - (ins0+ins1);
                ndelx = 1;
35            } else {
                delx -= ins1;
                ndelx++;
            }
        } else {
40            if (col1[yy-1] - (ins0+ins1) >= delx) {
                delx = col1[yy-1] - (ins0+ins1);
                ndelx = 1;
            } else
45                ndelx++;
        }

        /* pick the maximum score; we're favoring
50        * mis over any del and delx over dely
        */
55
60

```

Table 1 (cont')

...nw

```

0      id = xx - yy + len1 - 1;
      if (mis >= delx && mis >= dely[yy])
          col1[yy] = mis;
5      else if (delx >= dely[yy]) {
          col1[yy] = delx;
          ij = dx[id].ijmp;
          if (dx[id].jp.n[0] && (!dna || (ndelx >= MAXJMP
10      && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
              dx[id].ijmp++;
              if (++ij >= MAXJMP) {
                  writejumps(id);
                  ij = dx[id].ijmp = 0;
                  dx[id].offset = offset;
15      offset += sizeof(struct jmp) + sizeof(offset);
              }
          }
          dx[id].jp.n[ij] = ndelx;
          dx[id].jp.x[ij] = xx;
          dx[id].score = delx;
20      }
      else {
          col1[yy] = dely[yy];
          ij = dx[id].ijmp;
25      if (dx[id].jp.n[0] && (!dna || (ndely[yy] >= MAXJMP
          && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
              dx[id].ijmp++;
              if (++ij >= MAXJMP) {
                  writejumps(id);
                  ij = dx[id].ijmp = 0;
                  dx[id].offset = offset;
30      offset += sizeof(struct jmp) + sizeof(offset);
              }
          }
          dx[id].jp.n[ij] = -ndely[yy];
          dx[id].jp.x[ij] = xx;
          dx[id].score = dely[yy];
35      }
      if (xx == len0 && yy < len1) {
          /* last col
          */
          if (endgaps)
              col1[yy] -= ins0+ins1*(len1-yy);
          if (col1[yy] > smax) {
45      smax = col1[yy];
              dmax = id;
          }
      }
50      if (endgaps && xx < len0)
          col1[yy-1] -= ins0+ins1*(len0-xx);
      if (col1[yy-1] > smax) {
          smax = col1[yy-1];
          dmax = id;
55      }
      tmp = col0; col0 = col1; col1 = tmp;
  }
  (void) free((char *)ndely);
  (void) free((char *)dely);
60  (void) free((char *)col0);
  (void) free((char *)col1);
  }

```

Table 1 (cont')

```

/*
 *
 * print() -- only routine visible outside this module
 *
5  * static:
 * getmat() -- trace back best path, count matches: print()
 * pr_align() -- print alignment of described in array p[]: print()
 * dumpblock() -- dump a block of lines with numbers, stars: pr_align()
 * nums() -- put out a number line: dumpblock()
10 * putline() -- put out a line (name, [num], seq, [num]): dumpblock()
 * stars() -- put a line of stars: dumpblock()
 * stripname() -- strip any path and prefix from a seqname
 */

15 #include "nw.h"

#define SPC      3
#define P_LINE  256 /* maximum output line */
#define P_SPC    3   /* space between name or num and seq */

20 extern _day[26][26];
int olen; /* set output line length */
FILE *fx; /* output file */

25 print()
{
    int lx, ly, firstgap, lastgap; /* overlap */

    if ((fx = fopen(ofile, "w")) == 0) {
30         fprintf(stderr, "%s: can't write %s\n", prog, ofile);
        cleanup(1);
    }
    fprintf(fx, "< first sequence: %s (length = %d)\n", namex[0], len0);
    fprintf(fx, "< second sequence: %s (length = %d)\n", namex[1], len1);
35     olen = 60;
    lx = len0;
    ly = len1;
    firstgap = lastgap = 0;
    if (dmax < len1 - 1) { /* leading gap in x */
40         pp[0].spc = firstgap = len1 - dmax - 1;
        ly -= pp[0].spc;
    }
    else if (dmax > len1 - 1) { /* leading gap in y */
45         pp[1].spc = firstgap = dmax - (len1 - 1);
        lx -= pp[1].spc;
    }
    if (dmax0 < len0 - 1) { /* trailing gap in x */
50         lastgap = len0 - dmax0 - 1;
        lx -= lastgap;
    }
    else if (dmax0 > len0 - 1) { /* trailing gap in y */
55         lastgap = dmax0 - (len0 - 1);
        ly -= lastgap;
    }
    getmat(lx, ly, firstgap, lastgap);
    pr_align();
}

60

```

print

Table 1 (cont')

```

/*
 * trace back the best path, count matches
 */
static
5 getmat(lx, ly, firstgap, lastgap)                                getmat
    int    lx, ly;          /* "core" (minus endgaps) */
    int    firstgap, lastgap; /* leading trailing overlap */
{
    int      nm, i0, i1, siz0, siz1;
10    char     outx[32];
    double    pct;
    register  n0, n1;
    register char *p0, *p1;

15    /* get total matches, score
    */
    i0 = i1 = siz0 = siz1 = 0;
    p0 = seqx[0] + pp[1].spc;
    p1 = seqx[1] + pp[0].spc;
20    n0 = pp[1].spc + 1;
    n1 = pp[0].spc + 1;

    nm = 0;
    while ( *p0 && *p1 ) {
25         if (siz0) {
             p1++;
             n1++;
             siz0--;
         }
30         else if (siz1) {
             p0++;
             n0++;
             siz1--;
         }
35         else {
             if (xbm[*p0-'A']&xbm[*p1-'A'])
                 nm++;
             if (n0++ == pp[0].x[i0])
                 siz0 = pp[0].n[i0++];
40             if (n1++ == pp[1].x[i1])
                 siz1 = pp[1].n[i1++];
             p0++;
             p1++;
         }
45     }

    /* pct homology:
    * if penalizing endgaps, base is the shorter seq
    * else, knock off overhangs and take shorter core
    */
50    if (endgaps)
        lx = (len0 < len1)? len0 : len1;
    else
        lx = (lx < ly)? lx : ly;
55    pct = 100.*(double)nm/(double)lx;
    fprintf(fx, "\n");
    fprintf(fx, "< %d match%s in an overlap of %d: %.2f percent similarity\n",
        nm, (nm == 1)? "" : "es", lx, pct);
60

```

Table 1 (cont')

```

fprintf(fx, "< gaps in first sequence: %d", gapx);
if (gapx) {
    (void) sprintf(outx, " (%d %s%s)",
        ngapx, (dna)? "base":"residue", (ngapx == 1)? "" : "s");
    fprintf(fx, "%s", outx);

    fprintf(fx, ", gaps in second sequence: %d", gapy);
    if (gapy) {
        (void) sprintf(outx, " (%d %s%s)",
            ngapy, (dna)? "base":"residue", (ngapy == 1)? "" : "s");
        fprintf(fx, "%s", outx);
    }
    if (dna)
        fprintf(fx,
            "\n<score: %d (match = %d, mismatch = %d, gap penalty = %d + %d per base)\n",
            smax, DMAT, DMIS, DINS0, DINS1);
    else
        fprintf(fx,
            "\n<score: %d (Dayhoff PAM 250 matrix, gap penalty = %d + %d per residue)\n",
            smax, PINS0, PINS1);
    if (endgaps)
        fprintf(fx,
            "<endgaps penalized. left endgap: %d %s%s, right endgap: %d %s%s\n",
            firstgap, (dna)? "base" : "residue", (firstgap == 1)? "" : "s",
            lastgap, (dna)? "base" : "residue", (lastgap == 1)? "" : "s");
    else
        fprintf(fx, "<endgaps not penalized\n");
}

static      nm;          /* matches in core -- for checking */
static      lmax;        /* lengths of stripped file names */
static      ij[2];       /* jmp index for a path */
static      nc[2];       /* number at start of current line */
static      ni[2];       /* current elem number -- for gapping */
static      siz[2];
static char *ps[2];      /* ptr to current element */
static char *po[2];      /* ptr to next output char slot */
static char out[2][P_LINE]; /* output line */
static char star[P_LINE]; /* set by stars() */

/*
 * print alignment of described in struct path pp[]
 */
static
pr_align()
{
    int      nn;          /* char count */
    int      more;
    register i;

    for (i = 0, lmax = 0; i < 2; i++) {
        nn = stripname(namex[i]);
        if (nn > lmax)
            lmax = nn;

        nc[i] = 1;
        ni[i] = 1;
        siz[i] = ij[i] = 0;
        ps[i] = seqx[i];
        po[i] = out[i];
    }
}

```

...getmat

pr_align

Table 1 (cont')

```

for (nn = nm = 0, more = 1; more; ) {
    for (i = more = 0; i < 2; i++) {
        /*
5         * do we have more of this sequence?
        */
        if (!*ps[i])
            continue;

10         more++;

        if (pp[i].spc) { /* leading space */
            *po[i]++ = ' ';
            pp[i].spc--;
15         }
        else if (siz[i]) { /* in a gap */
            *po[i]++ = '-';
            siz[i]--;
20         }
        else { /* we're putting a seq element
            */
            *po[i] = *ps[i];
            if (islower(*ps[i]))
                *ps[i] = toupper(*ps[i]);
25             po[i]++;
            ps[i]++;

            /*
30             * are we at next gap for this seq?
            */
            if (ni[i] == pp[i].x[ij[i]]) {
                /*
                * we need to merge all gaps
                * at this location
35                 */
                siz[i] = pp[i].n[ij[i]++];
                while (ni[i] == pp[i].x[ij[i]])
                    siz[i] += pp[i].n[ij[i]++];
40                 }
                ni[i]++;
            }
        }
        if (++nn == olen || !more && nn) {
45             dumpblock();
            for (i = 0; i < 2; i++)
                po[i] = out[i];
            nn = 0;
        }
50     }
}

/*
 * dump a block of lines, including numbers, stars: pr_align()
 */
55 static
dumpblock()
{
    register i;

60     for (i = 0; i < 2; i++)
        *po[i] = '\0';

```

dumpblock

Table 1 (cont')

...dumpblock

```

5      (void)putc('\n', fx);
      for (i = 0; i < 2; i++) {
          if (*out[i] && (*out[i] != ' ' || *(po[i]) != ' ')) {
              if (i == 0)
                  nums(i);
              if (i == 0 && *out[1])
                  stars();
10         putline(i);
              if (i == 0 && *out[1])
                  fprintf(fx, star);
              if (i == 1)
                  nums(i);
15         }
      }
  }

/*
20  * put out a number line: dumpblock()
  */
  static
  nums(ix)
25  {
      int      ix;      /* index in out[] holding seq line */

      char      nline[P_LINE];
      register  i, j;
      register char *pn, *px, *py;

30      for (pn = nline, i = 0; i < lmax+P_SPC; i++, pn++)
          *pn = ' ';
      for (i = nc[ix], py = out[ix]; *py; py++, pn++) {
          if (*py == ' ' || *py == '-')
              *pn = ' ';
35          else {
              if (i%10 == 0 || (i == 1 && nc[ix] != 1)) {
                  j = (i < 0)? -i : i;
                  for (px = pn; j /= 10, px--)
                      *px = j%10 + '0';
40                  if (i < 0)
                      *px = '-';
              }
              else
                  *pn = ' ';
45              i++;
          }
      }
      *pn = '\0';
      nc[ix] = i;
50      for (pn = nline; *pn; pn++)
          (void)putc(*pn, fx);
      (void)putc('\n', fx);
  }

55  /*
  * put out a line (name, [num], seq, [num]): dumpblock()
  */
  static
  putline(ix)
60      int      ix;      {

```

nums

putline

Table 1 (cont')

...putline

```

5      int          i;
      register char *px;

      for (px = namex[ix], i = 0; *px && *px != ':'; px++, i++)
          (void) putc(*px, fx);
      for (; i < lmax+P_SPC; i++)
          (void) putc(' ', fx);

10     /* these count from 1:
       * ni[] is current element (from 1)
       * nc[] is number at start of current line
       */
15     for (px = out[ix]; *px; px++)
          (void) putc(*px&0x7F, fx);
      (void) putc('\n', fx);
  }

20  /*
   * put a line of stars (seqs always in out[0], out[1]): dumpblock()
   */
   static
25  stars()
  {
      int          i;
      register char *p0, *p1, cx, *px;

30     if (!*out[0] || (*out[0] == ' ' && *(po[0]) == ' ') ||
        !*out[1] || (*out[1] == ' ' && *(po[1]) == ' '))
          return;
      px = star;
      for (i = lmax+P_SPC; i; i--)
35         *px++ = ' ';

      for (p0 = out[0], p1 = out[1]; *p0 && *p1; p0++, p1++) {
          if (isalpha(*p0) && isalpha(*p1)) {
40             if (xbm[*p0-'A']&xbm[*p1-'A']) {
                 cx = '*';
                 nm++;
             }
             else if (!dna && _day[*p0-'A'][*p1-'A'] > 0)
45                 cx = '.';
             else
                 cx = ' ';
          }
          else
50             cx = ' ';
          *px++ = cx;
      }
      *px++ = '\n';
      *px = '\0';
55  }

```

stars

60

Table 1 (cont')

```

/*
 * strip path or prefix from pn, return len: pr_align()
 */
static
5 stripname(pn)                                stripname
    char    *pn;    /* file name (may be path) */
    {
        register char    *px, *py;
10        py = 0;
        for (px = pn; *px; px++)
            if (*px == '/')
                py = px + 1;
15        if (py)
            (void) strcpy(pn, py);
        return(strlen(pn));
    }
20
25
30
35
40
45
50
55
60

```

Table 1 (cont')

```

/*
 * cleanup() -- cleanup any tmp file
 * getseq() -- read in seq, set dna, len, maxlen
 * g_calloc() -- calloc() with error checkin
5  * readjumps() -- get the good jumps; from tmp file if necessary
 * writejumps() -- write a filled array of jumps to a tmp file: nw()
 */
#include "nw.h"
#include <sys/file.h>

10 char *jname = "/tmp/homgXXXXXX"; /* tmp file for jumps */
FILE *fj;

int cleanup(); /* cleanup tmp file */
15 long lseek();

/*
 * remove any tmp file if we blow
 */
20 cleanup(i)
    int i;
{
    if (fj)
        (void) unlink(jname);
25 exit(i);
}

/*
 * read, return ptr to seq, set dna, len, maxlen
 * skip lines starting with ';', '<', or '>'
 * seq in upper or lower case
 */
30 char *
getseq(file, len)
35 char *file; /* file name */
    int *len; /* seq len */
{
    char line[1024], *pseq;
    register char *px, *py;
    int natgc, tlen;
    FILE *fp;

    if ((fp = fopen(file, "r")) == 0) {
        fprintf(stderr, "%s: can't read %s\n", prog, file);
        exit(1);
    }
    tlen = natgc = 0;
    while (fgets(line, 1024, fp)) {
        if (*line == ';' || *line == '<' || *line == '>')
            continue;
        for (px = line; *px != '\n'; px++)
            if (isupper(*px) || islower(*px))
                tlen++;
    }
    if ((pseq = malloc((unsigned)(tlen+6))) == 0) {
        fprintf(stderr, "%s: malloc() failed to get %d bytes for %s\n", prog, tlen+6, file);
        exit(1);
    }
    pseq[0] = pseq[1] = pseq[2] = pseq[3] = '\0';
60

```

Table 1 (cont')

...getseq

```

py = pseq + 4;
*len = tlen;
rewind(fp);
5
while (fgets(line, 1024, fp)) {
    if (*line == ';' || *line == '<' || *line == '>')
        continue;
    for (px = line; *px != '\n'; px++) {
10        if (isupper(*px))
            *py++ = *px;
        else if (islower(*px))
            *py++ = toupper(*px);
        if (index("ATGCU", *(py-1)))
15            natgc++;
    }
    *py++ = '\0';
    *py = '\0';
20    (void) fclose(fp);
    dna = natgc > (tlen/3);
    return(pseq+4);
}

25 char *
g_alloc(msg, nx, sz)
char *msg; /* program, calling routine */
int nx, sz; /* number and size of elements */
{
30     char *px, *calloc();

    if ((px = calloc((unsigned)nx, (unsigned)sz)) == 0) {
        if (*msg) {
35             fprintf(stderr, "%s: g_alloc() failed %s (n=%d, sz=%d)\n", prog, msg, nx, sz);
            exit(1);
        }
    }
    return(px);
40 }

/*
 * get final jmps from dx[] or tmp file, set pp[], reset dmax: main()
 */
readjmps()
45 {
    int fd = -1;
    int siz, i0, i1;
    register i, j, xx;

50     if (fj) {
        (void) fclose(fj);
        if ((fd = open(jname, O_RDONLY, 0)) < 0) {
            fprintf(stderr, "%s: can't open() %s\n", prog, jname);
            cleanup(1);
55         }
    }
    for (i = i0 = i1 = 0, dmax0 = dmax, xx = len0; i++) {
        while (1) {
60             for (j = dx[dmax].ijmp; j >= 0 && dx[dmax].jp.x[j] >= xx; j--)
                ;

```

g_alloc

readjmps

Table 1 (cont')**...readjumps**

```

5         if (j < 0 && dx[dmax].offset && fj) {
            (void) lseek(fd, dx[dmax].offset, 0);
            (void) read(fd, (char *)&dx[dmax].jp, sizeof(struct jmp));
            (void) read(fd, (char *)&dx[dmax].offset, sizeof(dx[dmax].offset));
            dx[dmax].ijmp = MAXJMP-1;
        }
        else
10             break;
    }
    if (i >= JMPS) {
        fprintf(stderr, "%s: too many gaps in alignment\n", prog);
        cleanup(1);
    }
15    if (j >= 0) {
        siz = dx[dmax].jp.n[j];
        xx = dx[dmax].jp.x[j];
        dmax += siz;
        if (siz < 0) { /* gap in second seq */
20             pp[1].n[i1] = -siz;
             xx += siz;
             /* id = xx - yy + len1 - 1
              */
             pp[1].x[i1] = xx - dmax + len1 - 1;
             gapy++;
             ngapy -= siz;
            /* ignore MAXGAP when doing endgaps */
            siz = (-siz < MAXGAP || endgaps)? -siz : MAXGAP;
            i1++;
30         }
        else if (siz > 0) { /* gap in first seq */
            pp[0].n[i0] = siz;
            pp[0].x[i0] = xx;
            gapx++;
            ngapx += siz;
35            /* ignore MAXGAP when doing endgaps */
            siz = (siz < MAXGAP || endgaps)? siz : MAXGAP;
            i0++;
        }
40    }
    else
        break;
}

45    /* reverse the order of jumps
    */
    for (j = 0, i0--; j < i0; j++, i0--) {
        i = pp[0].n[j]; pp[0].n[j] = pp[0].n[i0]; pp[0].n[i0] = i;
        i = pp[0].x[j]; pp[0].x[j] = pp[0].x[i0]; pp[0].x[i0] = i;
50    }
    for (j = 0, i1--; j < i1; j++, i1--) {
        i = pp[1].n[j]; pp[1].n[j] = pp[1].n[i1]; pp[1].n[i1] = i;
        i = pp[1].x[j]; pp[1].x[j] = pp[1].x[i1]; pp[1].x[i1] = i;
55    }
    if (fd >= 0)
        (void) close(fd);
    if (fj) {
        (void) unlink(jname);
        fj = 0;
60        offset = 0;
    }
}

```

Table 1 (cont')

```

/*
 * write a filled jmp struct offset of the prev one (if any): nw()
 */
5  writejumps(ix)                                writejumps
    int    ix;
    {
        char    *mktemp();
10         if (!fj) {
            if (mktemp(jname) < 0) {
                fprintf(stderr, "%s: can't mktemp() %s\n", prog, jname);
                cleanup(1);
            }
15             if ((fj = fopen(jname, "w")) == 0) {
                fprintf(stderr, "%s: can't write %s\n", prog, jname);
                exit(1);
            }
20         }
        (void) fwrite((char *)&dx[ix].jp, sizeof(struct jmp), 1, fj);
        (void) fwrite((char *)&dx[ix].offset, sizeof(dx[ix].offset), 1, fj);
    }
}
25
30
35
40
45
50
55
60

```

Table 2

PRO	XXXXXXXXXXXXXXXXXX	(Length = 15 amino acids)
Comparison Protein	XXXXXXXXYYYYYY	(Length = 12 amino acids)

5 % amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =

10 5 divided by 15 = 33.3%

Table 3

PRO	XXXXXXXXXX	(Length = 10 amino acids)
15 Comparison Protein	XXXXXXXXYYYYYYZZYZ	(Length = 15 amino acids)

% amino acid sequence identity =

20 (the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =

5 divided by 10 = 50%

Table 4

25 PRO-DNA	NNNNNNNNNNNNNN	(Length = 14 nucleotides)
Comparison DNA	NNNNNNLLLLLLLLLL	(Length = 16 nucleotides)

% nucleic acid sequence identity =

30

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) =

6 divided by 14 = 42.9%

35

Table 5

PRO-DNA	NNNNNNNNNNNN	(Length = 12 nucleotides)
Comparison DNA	NNNNLLLTVV	(Length = 9 nucleotides)

5 % nucleic acid sequence identity =

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) =

10 4 divided by 12 = 33.3%

II. Compositions and Methods of the Invention

A. Full-Length PRO Polypeptides

15 The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO polypeptides. In particular, cDNAs encoding various PRO polypeptides have been identified and isolated, as disclosed in further detail in the Examples below. It is noted that proteins produced in separate expression rounds may be given different PRO numbers but the UNQ number is unique for any given DNA and the encoded protein, and will not be changed. However, for sake of simplicity, in the present specification the protein encoded by the full length native nucleic acid molecules disclosed herein as well as all further native homologues and variants included in the foregoing definition of PRO, will be referred to as "PRO/number", regardless of their origin or mode of preparation.

20 As disclosed in the Examples below, various cDNA clones have been deposited with the ATCC. The actual nucleotide sequences of those clones can readily be determined by the skilled artisan by sequencing of the deposited clone using routine methods in the art. The predicted amino acid sequence can be determined from the nucleotide sequence using routine skill. For the PRO polypeptides and encoding nucleic acids described herein, Applicants have identified what is believed to be the reading frame best identifiable with the sequence information available at the time.

B. PRO Polypeptide Variants

30 In addition to the full-length native sequence PRO polypeptides described herein, it is contemplated that PRO variants can be prepared. PRO variants can be prepared by introducing appropriate nucleotide changes into the PRO DNA, and/or by synthesis of the desired PRO polypeptide. Those skilled in the art will appreciate that amino acid changes may alter post-translational processes of the PRO, such as changing the number or position of glycosylation sites or altering the membrane anchoring characteristics.

35 Variations in the native full-length sequence PRO or in various domains of the PRO described herein, can be made, for example, using any of the techniques and guidelines for conservative and non-conservative

mutations set forth, for instance, in U.S. Patent No. 5,364,934. Variations may be a substitution, deletion or insertion of one or more codons encoding the PRO that results in a change in the amino acid sequence of the PRO as compared with the native sequence PRO. Optionally the variation is by substitution of at least one amino acid with any other amino acid in one or more of the domains of the PRO. Guidance in determining which amino acid residue may be inserted, substituted or deleted without adversely affecting the desired activity may be found by
5 comparing the sequence of the PRO with that of homologous known protein molecules and minimizing the number of amino acid sequence changes made in regions of high homology. Amino acid substitutions can be the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, such as the replacement of a leucine with a serine, i.e., conservative amino acid replacements. Insertions or deletions may optionally be in the range of about 1 to 5 amino acids. The variation allowed may be determined by
10 systematically making insertions, deletions or substitutions of amino acids in the sequence and testing the resulting variants for activity exhibited by the full-length or mature native sequence.

PRO polypeptide fragments are provided herein. Such fragments may be truncated at the N-terminus or C-terminus, or may lack internal residues, for example, when compared with a full length native protein. Certain fragments lack amino acid residues that are not essential for a desired biological activity of the PRO
15 polypeptide.

PRO fragments may be prepared by any of a number of conventional techniques. Desired peptide fragments may be chemically synthesized. An alternative approach involves generating PRO fragments by enzymatic digestion, e.g., by treating the protein with an enzyme known to cleave proteins at sites defined by particular amino acid residues, or by digesting the DNA with suitable restriction enzymes and isolating the desired
20 fragment. Yet another suitable technique involves isolating and amplifying a DNA fragment encoding a desired polypeptide fragment, by polymerase chain reaction (PCR). Oligonucleotides that define the desired termini of the DNA fragment are employed at the 5' and 3' primers in the PCR. Preferably, PRO polypeptide fragments share at least one biological and/or immunological activity with the native PRO polypeptide disclosed herein.

In particular embodiments, conservative substitutions of interest are shown in Table 6 under the heading
25 of preferred substitutions. If such substitutions result in a change in biological activity, then more substantial changes, denominated exemplary substitutions in Table 6, or as further described below in reference to amino acid classes, are introduced and the products screened.

Table 6

	<u>Original Residue</u>	<u>Exemplary Substitutions</u>	<u>Preferred Substitutions</u>
5	Ala (A)	val; leu; ile	val
	Arg (R)	lys; gln; asn	lys
	Asn (N)	gln; his; lys; arg	gln
	Asp (D)	glu	glu
	Cys (C)	ser	ser
10	Gln (Q)	asn	asn
	Glu (E)	asp	asp
	Gly (G)	pro; ala	ala
	His (H)	asn; gln; lys; arg	arg
	Ile (I)	leu; val; met; ala; phe;	
15		norleucine	leu
	Leu (L)	norleucine; ile; val;	
		met; ala; phe	ile
	Lys (K)	arg; gln; asn	arg
	Met (M)	leu; phe; ile	leu
20	Phe (F)	leu; val; ile; ala; tyr	leu
	Pro (P)	ala	ala
	Ser (S)	thr	thr
	Thr (T)	ser	ser
	Trp (W)	tyr; phe	tyr
25	Tyr (Y)	trp; phe; thr; ser	phe
	Val (V)	ile; leu; met; phe;	
		ala; norleucine	leu

30 Substantial modifications in function or immunological identity of the PRO polypeptide are accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues are divided into groups based on common side-chain properties:

- 35 (1) hydrophobic: norleucine, met, ala, val, leu, ile;
 (2) neutral hydrophilic: cys, ser, thr;
 (3) acidic: asp, glu;
 (4) basic: asn, gln, his, lys, arg;
 (5) residues that influence chain orientation: gly, pro; and
 40 (6) aromatic: trp, tyr, phe.

 Non-conservative substitutions will entail exchanging a member of one of these classes for another class. Such substituted residues also may be introduced into the conservative substitution sites or, more preferably, into the remaining (non-conserved) sites.

45 The variations can be made using methods known in the art such as oligonucleotide-mediated (site-directed) mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis [Carter et al., Nucl. Acids Res., 13:4331 (1986); Zoller et al., Nucl. Acids Res., 10:6487 (1987)], cassette mutagenesis [Wells et al.,

Gene, 34:315 (1985)], restriction selection mutagenesis [Wells et al., Philos. Trans. R. Soc. London SerA, 317:415 (1986)] or other known techniques can be performed on the cloned DNA to produce the PRO variant DNA.

Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence. Among the preferred scanning amino acids are relatively small, neutral amino acids. Such amino acids include alanine, glycine, serine, and cysteine. Alanine is typically a preferred scanning amino acid among this group because it eliminates the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant [Cunningham and Wells, Science, 244: 1081-1085 (1989)]. Alanine is also typically preferred because it is the most common amino acid. Further, it is frequently found in both buried and exposed positions [Creighton, The Proteins, (W.H. Freeman & Co., N.Y.); Chothia, J. Mol. Biol., 150:1 (1976)]. If alanine substitution does not yield adequate amounts of variant, an isoteric amino acid can be used.

C. Modifications of PRO

Covalent modifications of PRO are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a PRO polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C- terminal residues of the PRO. Derivatization with bifunctional agents is useful, for instance, for crosslinking PRO to a water-insoluble support matrix or surface for use in the method for purifying anti-PRO antibodies, and vice-versa. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propioimide.

Other modifications include deamidation of glutamyl and asparaginy residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α -amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the PRO polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence PRO (either by removing the underlying glycosylation site or by deleting the glycosylation by chemical and/or enzymatic means), and/or adding one or more glycosylation sites that are not present in the native sequence PRO. In addition, the phrase includes qualitative changes in the glycosylation of the native proteins, involving a change in the nature and proportions of the various carbohydrate moieties present.

Addition of glycosylation sites to the PRO polypeptide may be accomplished by altering the amino acid sequence. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence PRO (for O-linked glycosylation sites). The PRO amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding

the PRO polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the PRO polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, CRC Crit. Rev. Biochem., pp. 259-306 (1981).

Removal of carbohydrate moieties present on the PRO polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., Arch. Biochem. Biophys., 259:52 (1987) and by Edge et al., Anal. Biochem., 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura et al., Meth. Enzymol., 138:350 (1987).

Another type of covalent modification of PRO comprises linking the PRO polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol (PEG), polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

The PRO of the present invention may also be modified in a way to form a chimeric molecule comprising PRO fused to another, heterologous polypeptide or amino acid sequence.

In one embodiment, such a chimeric molecule comprises a fusion of the PRO with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl- terminus of the PRO. The presence of such epitope-tagged forms of the PRO can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the PRO to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., Mol. Cell. Biol., 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., Molecular and Cellular Biology, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., Protein Engineering, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., BioTechnology, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., Science, 255:192-194 (1992)]; an α -tubulin epitope peptide [Skinner et al., J. Biol. Chem., 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-6397 (1990)].

In an alternative embodiment, the chimeric molecule may comprise a fusion of the PRO with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule (also referred to as an "immunoadhesin"), such a fusion could be to the Fc region of an IgG molecule. The Ig fusions preferably include the substitution of a soluble (transmembrane domain deleted or inactivated) form of a PRO polypeptide in place of at least one variable region within an Ig molecule. In a particularly preferred embodiment, the immunoglobulin fusion includes the hinge, CH2 and CH3, or the hinge, CH1, CH2 and CH3 regions of an IgG1 molecule. For the production of immunoglobulin fusions see also US Patent No. 5,428,130 issued June 27,

1995.

D. Preparation of PRO

The description below relates primarily to production of PRO by culturing cells transformed or transfected with a vector containing PRO nucleic acid. It is, of course, contemplated that alternative methods, which are well known in the art, may be employed to prepare PRO. For instance, the PRO sequence, or portions thereof, may be produced by direct peptide synthesis using solid-phase techniques [see, e.g., Stewart et al., Solid-Phase Peptide Synthesis, W.H. Freeman Co., San Francisco, CA (1969); Merrifield, J. Am. Chem. Soc., 85:2149-2154 (1963)]. *In vitro* protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be accomplished, for instance, using an Applied Biosystems Peptide Synthesizer (Foster City, CA) using manufacturer's instructions. Various portions of the PRO may be chemically synthesized separately and combined using chemical or enzymatic methods to produce the full-length PRO.

1. Isolation of DNA Encoding PRO

DNA encoding PRO may be obtained from a cDNA library prepared from tissue believed to possess the PRO mRNA and to express it at a detectable level. Accordingly, human PRO DNA can be conveniently obtained from a cDNA library prepared from human tissue, such as described in the Examples. The PRO-encoding gene may also be obtained from a genomic library or by known synthetic procedures (e.g., automated nucleic acid synthesis).

Libraries can be screened with probes (such as antibodies to the PRO or oligonucleotides of at least about 20-80 bases) designed to identify the gene of interest or the protein encoded by it. Screening the cDNA or genomic library with the selected probe may be conducted using standard procedures, such as described in Sambrook et al., Molecular Cloning: A Laboratory Manual (New York: Cold Spring Harbor Laboratory Press, 1989). An alternative means to isolate the gene encoding PRO is to use PCR methodology [Sambrook et al., supra; Dieffenbach et al., PCR Primer: A Laboratory Manual (Cold Spring Harbor Laboratory Press, 1995)].

The Examples below describe techniques for screening a cDNA library. The oligonucleotide sequences selected as probes should be of sufficient length and sufficiently unambiguous that false positives are minimized. The oligonucleotide is preferably labeled such that it can be detected upon hybridization to DNA in the library being screened. Methods of labeling are well known in the art, and include the use of radiolabels like ³²P-labeled ATP, biotinylation or enzyme labeling. Hybridization conditions, including moderate stringency and high stringency, are provided in Sambrook et al., supra.

Sequences identified in such library screening methods can be compared and aligned to other known sequences deposited and available in public databases such as GenBank or other private sequence databases. Sequence identity (at either the amino acid or nucleotide level) within defined regions of the molecule or across the full-length sequence can be determined using methods known in the art and as described herein.

Nucleic acid having protein coding sequence may be obtained by screening selected cDNA or genomic libraries using the deduced amino acid sequence disclosed herein for the first time, and, if necessary, using conventional primer extension procedures as described in Sambrook et al., supra, to detect precursors and

processing intermediates of mRNA that may not have been reverse-transcribed into cDNA.

2. Selection and Transformation of Host Cells

Host cells are transfected or transformed with expression or cloning vectors described herein for PRO production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. The culture conditions, such as media, temperature, pH and the like, can be selected by the skilled artisan without undue experimentation. In general, principles, protocols, and practical techniques for maximizing the productivity of cell cultures can be found in Mammalian Cell Biotechnology: a Practical Approach, M. Butler, ed. (IRL Press, 1991) and Sambrook et al., supra.

Methods of eukaryotic cell transfection and prokaryotic cell transformation are known to the ordinarily skilled artisan, for example, CaCl_2 , CaPO_4 , liposome-mediated and electroporation. Depending on the host cell used, transformation is performed using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in Sambrook et al., supra, or electroporation is generally used for prokaryotes. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw et al., Gene, 23:315 (1983) and WO 89/05859 published 29 June 1989. For mammalian cells without such cell walls, the calcium phosphate precipitation method of Graham and van der Eb, Virology, 52:456-457 (1978) can be employed. General aspects of mammalian cell host system transfections have been described in U.S. Patent No. 4,399,216. Transformations into yeast are typically carried out according to the method of Van Solingen et al., J. Bact., 130:946 (1977) and Hsiao et al., Proc. Natl. Acad. Sci. (USA), 76:3829 (1979). However, other methods for introducing DNA into cells, such as by nuclear microinjection, electroporation, bacterial protoplast fusion with intact cells, or polycations, e.g., polybrene, polyornithine, may also be used. For various techniques for transforming mammalian cells, see Keown et al., Methods in Enzymology, 185:527-537 (1990) and Mansour et al., Nature, 336:348-352 (1988).

Suitable host cells for cloning or expressing the DNA in the vectors herein include prokaryote, yeast, or higher eukaryote cells. Suitable prokaryotes include but are not limited to eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as *E. coli*. Various *E. coli* strains are publicly available, such as *E. coli* K12 strain MM294 (ATCC 31,446); *E. coli* X1776 (ATCC 31,537); *E. coli* strain W3110 (ATCC 27,325) and K5 772 (ATCC 53,635). Other suitable prokaryotic host cells include Enterobacteriaceae such as *Escherichia*, e.g., *E. coli*, *Enterobacter*, *Erwinia*, *Klebsiella*, *Proteus*, *Salmonella*, e.g., *Salmonella typhimurium*, *Serratia*, e.g., *Serratia marcescans*, and *Shigella*, as well as *Bacilli* such as *B. subtilis* and *B. licheniformis* (e.g., *B. licheniformis* 41P disclosed in DD 266,710 published 12 April 1989), *Pseudomonas* such as *P. aeruginosa*, and *Streptomyces*. These examples are illustrative rather than limiting. Strain W3110 is one particularly preferred host or parent host because it is a common host strain for recombinant DNA product fermentations. Preferably, the host cell secretes minimal amounts of proteolytic enzymes. For example, strain W3110 may be modified to effect a genetic mutation in the genes encoding proteins endogenous to the host, with examples of such hosts including *E. coli* W3110 strain 1A2, which has the complete genotype *tonA*; *E. coli* W3110 strain 9E4, which has the complete genotype *tonA ptr3*; *E. coli* W3110 strain 27C7 (ATCC

55,244), which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT kan^r*; *E. coli* W3110 strain 37D6, which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT rbs7 ilvG kan^r*; *E. coli* W3110 strain 40B4, which is strain 37D6 with a non-kanamycin resistant *degP* deletion mutation; and an *E. coli* strain having mutant periplasmic protease disclosed in U.S. Patent No. 4,946,783 issued 7 August 1990. Alternatively, *in vitro* methods of cloning, e.g., PCR or other nucleic acid polymerase reactions, are suitable.

5 In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for PRO-encoding vectors. *Saccharomyces cerevisiae* is a commonly used lower eukaryotic host microorganism. Others include *Schizosaccharomyces pombe* (Beach and Nurse, Nature, 290: 140 [1981]; EP 139,383 published 2 May 1985); *Kluyveromyces* hosts (U.S. Patent No. 4,943,529; Fleer et al., Bio/Technology, 9:968-975 (1991)) such as, e.g., *K. lactis* (MW98-8C, CBS683, CBS4574; Louvencourt et al.,
10 J. Bacteriol., 154(2):737-742 [1983]), *K. fragilis* (ATCC 12,424), *K. bulgaricus* (ATCC 16,045), *K. wickerhamii* (ATCC 24,178), *K. waltii* (ATCC 56,500), *K. drosophilum* (ATCC 36,906; Van den Berg et al., Bio/Technology, 8:135 (1990)), *K. thermotolerans*, and *K. marxianus*; *yarrowia* (EP 402,226); *Pichia pastoris* (EP 183,070; Sreekrishna et al., J. Basic Microbiol., 28:265-278 [1988]); *Candida*; *Trichoderma reesia* (EP 244,234); *Neurospora crassa* (Case et al., Proc. Natl. Acad. Sci. USA, 76:5259-5263 [1979]); *Schwanniomyces*
15 such as *Schwanniomyces occidentalis* (EP 394,538 published 31 October 1990); and filamentous fungi such as, e.g., *Neurospora*, *Penicillium*, *Tolypocladium* (WO 91/00357 published 10 January 1991), and *Aspergillus* hosts such as *A. nidulans* (Ballance et al., Biochem. Biophys. Res. Commun., 112:284-289 [1983]; Tilburn et al., Gene, 26:205-221 [1983]; Yelton et al., Proc. Natl. Acad. Sci. USA, 81: 1470-1474 [1984]) and *A. niger* (Kelly and Hynes, EMBO J., 4:475-479 [1985]). Methylophilic yeasts are suitable herein and include, but are not
20 limited to, yeast capable of growth on methanol selected from the genera consisting of *Hansenula*, *Candida*, *Kloeckera*, *Pichia*, *Saccharomyces*, *Torulopsis*, and *Rhodotorula*. A list of specific species that are exemplary of this class of yeasts may be found in C. Anthony, The Biochemistry of Methylophilic Yeasts, 269 (1982).

Suitable host cells for the expression of glycosylated PRO are derived from multicellular organisms. Examples of invertebrate cells include insect cells such as *Drosophila* S2 and *Spodoptera* Sf9, as well as plant
25 cells. Examples of useful mammalian host cell lines include Chinese hamster ovary (CHO) and COS cells. More specific examples include monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al., J. Gen. Virol., 36:59 (1977)); Chinese hamster ovary cells/-DHFR (CHO, Urlaub and Chasin, Proc. Natl. Acad. Sci. USA, 77:4216 (1980)); mouse sertoli cells (TM4, Mather, Biol. Reprod., 23:243-251 (1980)); human lung cells (W138,
30 ATCC CCL 75); human liver cells (Hep G2, HB 8065); and mouse mammary tumor (MMT 060562, ATCC CCL51). The selection of the appropriate host cell is deemed to be within the skill in the art.

3. Selection and Use of a Replicable Vector

35 The nucleic acid (e.g., cDNA or genomic DNA) encoding PRO may be inserted into a replicable vector for cloning (amplification of the DNA) or for expression. Various vectors are publicly available. The vector may, for example, be in the form of a plasmid, cosmid, viral particle, or phage. The appropriate nucleic acid sequence may be inserted into the vector by a variety of procedures. In general, DNA is inserted into an

appropriate restriction endonuclease site(s) using techniques known in the art. Vector components generally include, but are not limited to, one or more of a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence. Construction of suitable vectors containing one or more of these components employs standard ligation techniques which are known to the skilled artisan.

5 The PRO may be produced recombinantly not only directly, but also as a fusion polypeptide with a heterologous polypeptide, which may be a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or polypeptide. In general, the signal sequence may be a component of the vector, or it may be a part of the PRO-encoding DNA that is inserted into the vector. The signal sequence may be a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase, penicillinase, lpp, or heat-stable enterotoxin II leaders. For yeast secretion the signal sequence may be, e.g., the yeast invertase leader, alpha factor leader (including *Saccharomyces* and *Kluyveromyces* α -factor leaders, the latter described in U.S. Patent No. 5,010,182), or acid phosphatase leader, the *C. albicans* glucoamylase leader (EP 362,179 published 4 April 1990), or the signal described in WO 90/13646 published 15 November 1990. In mammalian cell expression, mammalian signal sequences may be used to direct secretion of the protein, such as signal sequences from secreted polypeptides of the same or related species, as well as viral secretory leaders.

15 Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Such sequences are well known for a variety of bacteria, yeast, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria, the 2 μ plasmid origin is suitable for yeast, and various viral origins (SV40, polyoma, adenovirus, VSV or BPV) are useful for cloning vectors in mammalian cells.

20 Expression and cloning vectors will typically contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, e.g., the gene encoding D-alanine racemase for *Bacilli*.

25 An example of suitable selectable markers for mammalian cells are those that enable the identification of cells competent to take up the PRO-encoding nucleic acid, such as DHFR or thymidine kinase. An appropriate host cell when wild-type DHFR is employed is the CHO cell line deficient in DHFR activity, prepared and propagated as described by Urlaub et al., Proc. Natl. Acad. Sci. USA, 77:4216 (1980). A suitable selection gene for use in yeast is the *trp1* gene present in the yeast plasmid YRp7 [Stinchcomb et al., Nature, 282:39 (1979); Kingsman et al., Gene, 7:141 (1979); Tschemper et al., Gene, 10:157 (1980)]. The *trp1* gene provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example, ATCC No. 44076 or PEP4-1 [Jones, Genetics, 85:12 (1977)].

30 Expression and cloning vectors usually contain a promoter operably linked to the PRO-encoding nucleic acid sequence to direct mRNA synthesis. Promoters recognized by a variety of potential host cells are well known. Promoters suitable for use with prokaryotic hosts include the β -lactamase and lactose promoter systems [Chang et al., Nature, 275:615 (1978); Goeddel et al., Nature, 281:544 (1979)], alkaline phosphatase, a tryptophan (*trp*) promoter system [Goeddel, Nucleic Acids Res., 8:4057 (1980); EP 36,776], and hybrid

promoters such as the tac promoter [deBoer et al., Proc. Natl. Acad. Sci. USA, 80:21-25 (1983)]. Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding PRO.

Examples of suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase [Hitzeman et al., J. Biol. Chem., 255:2073 (1980)] or other glycolytic enzymes [Hess et al., J. Adv. Enzyme Reg., 7:149 (1968); Holland, Biochemistry, 17:4900 (1978)], such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

Other yeast promoters, which are inducible promoters having the additional advantage of transcription controlled by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in EP 73,657.

PRO transcription from vectors in mammalian host cells is controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published 5 July 1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and Simian Virus 40 (SV40), from heterologous mammalian promoters, e.g., the actin promoter or an immunoglobulin promoter, and from heat-shock promoters, provided such promoters are compatible with the host cell systems.

Transcription of a DNA encoding the PRO by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp, that act on a promoter to increase its transcription. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin, α -fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. The enhancer may be spliced into the vector at a position 5' or 3' to the PRO coding sequence, but is preferably located at a site 5' from the promoter.

Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding PRO.

Still other methods, vectors, and host cells suitable for adaptation to the synthesis of PRO in recombinant vertebrate cell culture are described in Gething et al., Nature, 293:620-625 (1981); Mantei et al., Nature, 281:40-46 (1979); EP 117,060; and EP 117,058.

4. Detecting Gene Amplification/Expression

Gene amplification and/or expression may be measured in a sample directly, for example, by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA [Thomas, Proc. Natl. Acad. Sci. USA, 77:5201-5205 (1980)], dot blotting (DNA analysis), or *in situ* hybridization, using an appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. The antibodies in turn may be labeled and the assay may be carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

Gene expression, alternatively, may be measured by immunological methods, such as immunohistochemical staining of cells or tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. Antibodies useful for immunohistochemical staining and/or assay of sample fluids may be either monoclonal or polyclonal, and may be prepared in any mammal. Conveniently, the antibodies may be prepared against a native sequence PRO polypeptide or against a synthetic peptide based on the DNA sequences provided herein or against exogenous sequence fused to PRO DNA and encoding a specific antibody epitope.

5. Purification of Polypeptide

Forms of PRO may be recovered from culture medium or from host cell lysates. If membrane-bound, it can be released from the membrane using a suitable detergent solution (e.g. Triton-X 100) or by enzymatic cleavage. Cells employed in expression of PRO can be disrupted by various physical or chemical means, such as freeze-thaw cycling, sonication, mechanical disruption, or cell lysing agents.

It may be desired to purify PRO from recombinant cell proteins or polypeptides. The following procedures are exemplary of suitable purification procedures: by fractionation on an ion-exchange column; ethanol precipitation; reverse phase HPLC; chromatography on silica or on a cation-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75; protein A Sepharose columns to remove contaminants such as IgG; and metal chelating columns to bind epitope-tagged forms of the PRO. Various methods of protein purification may be employed and such methods are known in the art and described for example in Deutscher, Methods in Enzymology, 182 (1990); Scopes, Protein Purification: Principles and Practice, Springer-Verlag, New York (1982). The purification step(s) selected will depend, for example, on the nature of the production process used and the particular PRO produced.

E. Uses for PRO

Nucleotide sequences (or their complement) encoding PRO have various applications in the art of molecular biology, including uses as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. PRO nucleic acid will also be useful for the preparation of PRO polypeptides by the recombinant techniques described herein.

The full-length native sequence PRO gene, or portions thereof, may be used as hybridization probes for a cDNA library to isolate the full-length PRO cDNA or to isolate still other cDNAs (for instance, those encoding

naturally-occurring variants of PRO or PRO from other species) which have a desired sequence identity to the native PRO sequence disclosed herein. Optionally, the length of the probes will be about 20 to about 50 bases. The hybridization probes may be derived from at least partially novel regions of the full length native nucleotide sequence wherein those regions may be determined without undue experimentation or from genomic sequences including promoters, enhancer elements and introns of native sequence PRO. By way of example, a screening method will comprise isolating the coding region of the PRO gene using the known DNA sequence to synthesize a selected probe of about 40 bases. Hybridization probes may be labeled by a variety of labels, including radionucleotides such as ^{32}P or ^{35}S , or enzymatic labels such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems. Labeled probes having a sequence complementary to that of the PRO gene of the present invention can be used to screen libraries of human cDNA, genomic DNA or mRNA to determine which members of such libraries the probe hybridizes to. Hybridization techniques are described in further detail in the Examples below.

Any EST sequences disclosed in the present application may similarly be employed as probes, using the methods disclosed herein.

Other useful fragments of the PRO nucleic acids include antisense or sense oligonucleotides comprising a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target PRO mRNA (sense) or PRO DNA (antisense) sequences. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment of the coding region of PRO DNA. Such a fragment generally comprises at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (Cancer Res. 48:2659, 1988) and van der Krol et al. (BioTechniques 6:958, 1988).

Binding of antisense or sense oligonucleotides to target nucleic acid sequences results in the formation of duplexes that block transcription or translation of the target sequence by one of several means, including enhanced degradation of the duplexes, premature termination of transcription or translation, or by other means. The antisense oligonucleotides thus may be used to block expression of PRO proteins. Antisense or sense oligonucleotides further comprise oligonucleotides having modified sugar-phosphodiester backbones (or other sugar linkages, such as those described in WO 91/06629) and wherein such sugar linkages are resistant to endogenous nucleases. Such oligonucleotides with resistant sugar linkages are stable *in vivo* (i.e., capable of resisting enzymatic degradation) but retain sequence specificity to be able to bind to target nucleotide sequences.

Other examples of sense or antisense oligonucleotides include those oligonucleotides which are covalently linked to organic moieties, such as those described in WO 90/10048, and other moieties that increases affinity of the oligonucleotide for a target nucleic acid sequence, such as poly-(L-lysine). Further still, intercalating agents, such as ellipticine, and alkylating agents or metal complexes may be attached to sense or antisense oligonucleotides to modify binding specificities of the antisense or sense oligonucleotide for the target nucleotide sequence.

Antisense or sense oligonucleotides may be introduced into a cell containing the target nucleic acid sequence by any gene transfer method, including, for example, CaPO_4 -mediated DNA transfection, electroporation, or by using gene transfer vectors such as Epstein-Barr virus. In a preferred procedure, an

antisense or sense oligonucleotide is inserted into a suitable retroviral vector. A cell containing the target nucleic acid sequence is contacted with the recombinant retroviral vector, either *in vivo* or *ex vivo*. Suitable retroviral vectors include, but are not limited to, those derived from the murine retrovirus M-MuLV, N2 (a retrovirus derived from M-MuLV), or the double copy vectors designated DCT5A, DCT5B and DCT5C (see WO 90/13641).

5 Sense or antisense oligonucleotides also may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or
10 receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell.

Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex, as described in WO 90/10448. The sense or antisense oligonucleotide-lipid complex is preferably dissociated within the cell by an endogenous lipase.

15 Antisense or sense RNA or DNA molecules are generally at least about 5 bases in length, about 10 bases in length, about 15 bases in length, about 20 bases in length, about 25 bases in length, about 30 bases in length, about 35 bases in length, about 40 bases in length, about 45 bases in length, about 50 bases in length, about 55 bases in length, about 60 bases in length, about 65 bases in length, about 70 bases in length, about 75 bases in length, about 80 bases in length, about 85 bases in length, about 90 bases in length, about 95 bases in length, about 100 bases in length, or more.

20 The probes may also be employed in PCR techniques to generate a pool of sequences for identification of closely related PRO coding sequences.

Nucleotide sequences encoding a PRO can also be used to construct hybridization probes for mapping the gene which encodes that PRO and for the genetic analysis of individuals with genetic disorders. The nucleotide sequences provided herein may be mapped to a chromosome and specific regions of a chromosome
25 using known techniques, such as *in situ* hybridization, linkage analysis against known chromosomal markers, and hybridization screening with libraries.

When the coding sequences for PRO encode a protein which binds to another protein (example, where the PRO is a receptor), the PRO can be used in assays to identify the other proteins or molecules involved in the binding interaction. By such methods, inhibitors of the receptor/ligand binding interaction can be identified.
30 Proteins involved in such binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction. Also, the receptor PRO can be used to isolate correlative ligand(s). Screening assays can be designed to find lead compounds that mimic the biological activity of a native PRO or a receptor for PRO. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates. Small molecules
35 contemplated include synthetic organic or inorganic compounds. The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays and cell based assays, which are well characterized in the art.

Nucleic acids which encode PRO or its modified forms can also be used to generate either transgenic animals or "knock out" animals which, in turn, are useful in the development and screening of therapeutically useful reagents. A transgenic animal (e.g., a mouse or rat) is an animal having cells that contain a transgene, which transgene was introduced into the animal or an ancestor of the animal at a prenatal, e.g., an embryonic stage. A transgene is a DNA which is integrated into the genome of a cell from which a transgenic animal develops. In one embodiment, cDNA encoding PRO can be used to clone genomic DNA encoding PRO in accordance with established techniques and the genomic sequences used to generate transgenic animals that contain cells which express DNA encoding PRO. Methods for generating transgenic animals, particularly animals such as mice or rats, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009. Typically, particular cells would be targeted for PRO transgene incorporation with tissue-specific enhancers. Transgenic animals that include a copy of a transgene encoding PRO introduced into the germ line of the animal at an embryonic stage can be used to examine the effect of increased expression of DNA encoding PRO. Such animals can be used as tester animals for reagents thought to confer protection from, for example, pathological conditions associated with its overexpression. In accordance with this facet of the invention, an animal is treated with the reagent and a reduced incidence of the pathological condition, compared to untreated animals bearing the transgene, would indicate a potential therapeutic intervention for the pathological condition.

Alternatively, non-human homologues of PRO can be used to construct a PRO "knock out" animal which has a defective or altered gene encoding PRO as a result of homologous recombination between the endogenous gene encoding PRO and altered genomic DNA encoding PRO introduced into an embryonic stem cell of the animal. For example, cDNA encoding PRO can be used to clone genomic DNA encoding PRO in accordance with established techniques. A portion of the genomic DNA encoding PRO can be deleted or replaced with another gene, such as a gene encoding a selectable marker which can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector [see e.g., Thomas and Capecchi, Cell, 51:503 (1987) for a description of homologous recombination vectors]. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced DNA has homologously recombined with the endogenous DNA are selected [see e.g., Li et al., Cell, 69:915 (1992)]. The selected cells are then injected into a blastocyst of an animal (e.g., a mouse or rat) to form aggregation chimeras [see e.g., Bradley, in *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, E. J. Robertson, ed. (IRL, Oxford, 1987), pp. 113-152]. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term to create a "knock out" animal. Progeny harboring the homologously recombined DNA in their germ cells can be identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knockout animals can be characterized for instance, for their ability to defend against certain pathological conditions and for their development of pathological conditions due to absence of the PRO polypeptide.

Nucleic acid encoding the PRO polypeptides may also be used in gene therapy. In gene therapy applications, genes are introduced into cells in order to achieve *in vivo* synthesis of a therapeutically effective genetic product, for example for replacement of a defective gene. "Gene therapy" includes both conventional

gene therapy where a lasting effect is achieved by a single treatment, and the administration of gene therapeutic agents, which involves the one time or repeated administration of a therapeutically effective DNA or mRNA. Antisense RNAs and DNAs can be used as therapeutic agents for blocking the expression of certain genes *in vivo*. It has already been shown that short antisense oligonucleotides can be imported into cells where they act as inhibitors, despite their low intracellular concentrations caused by their restricted uptake by the cell membrane.

5 (Zamecnik *et al.*, Proc. Natl. Acad. Sci. USA 83:4143-4146 [1986]). The oligonucleotides can be modified to enhance their uptake, e.g. by substituting their negatively charged phosphodiester groups by uncharged groups.

There are a variety of techniques available for introducing nucleic acids into viable cells. The techniques vary depending upon whether the nucleic acid is transferred into cultured cells *in vitro*, or *in vivo* in the cells of the intended host. Techniques suitable for the transfer of nucleic acid into mammalian cells *in vitro* include the use of liposomes, electroporation, microinjection, cell fusion, DEAE-dextran, the calcium phosphate precipitation method, etc. The currently preferred *in vivo* gene transfer techniques include transfection with viral (typically retroviral) vectors and viral coat protein-liposome mediated transfection (Dzau *et al.*, Trends in Biotechnology 11, 205-210 [1993]). In some situations it is desirable to provide the nucleic acid source with an agent that targets the target cells, such as an antibody specific for a cell surface membrane protein or the target cell, a ligand for a receptor on the target cell, etc. Where liposomes are employed, proteins which bind to a cell surface membrane protein associated with endocytosis may be used for targeting and/or to facilitate uptake, e.g. capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins which undergo internalization in cycling, proteins that target intracellular localization and enhance intracellular half-life. The technique of receptor-mediated endocytosis is described, for example, by Wu *et al.*, J. Biol. Chem. 262, 4429-4432 (1987); and Wagner

10 15 20 *et al.*, Proc. Natl. Acad. Sci. USA 87, 3410-3414 (1990). For review of gene marking and gene therapy protocols see Anderson *et al.*, Science 256, 808-813 (1992).

The PRO polypeptides described herein may also be employed as molecular weight markers for protein electrophoresis purposes and the isolated nucleic acid sequences may be used for recombinantly expressing those markers.

25 The nucleic acid molecules encoding the PRO polypeptides or fragments thereof described herein are useful for chromosome identification. In this regard, there exists an ongoing need to identify new chromosome markers, since relatively few chromosome marking reagents, based upon actual sequence data are presently available. Each PRO nucleic acid molecule of the present invention can be used as a chromosome marker.

The PRO polypeptides and nucleic acid molecules of the present invention may also be used

30 diagnostically for tissue typing, wherein the PRO polypeptides of the present invention may be differentially expressed in one tissue as compared to another, preferably in a diseased tissue as compared to a normal tissue of the same tissue type. PRO nucleic acid molecules will find use for generating probes for PCR, Northern analysis, Southern analysis and Western analysis.

The PRO polypeptides described herein may also be employed as therapeutic agents. The PRO

35 polypeptides of the present invention can be formulated according to known methods to prepare pharmaceutically useful compositions, whereby the PRO product hereof is combined in admixture with a pharmaceutically acceptable carrier vehicle. Therapeutic formulations are prepared for storage by mixing the active ingredient

having the desired degree of purity with optional physiologically acceptable carriers, excipients or stabilizers (Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed. (1980)), in the form of lyophilized formulations or aqueous solutions. Acceptable carriers, excipients or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum
5 albumin, gelatin or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone, amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides and other carbohydrates including glucose, mannose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN™, PLURONICS™ or PEG.

10 The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes, prior to or following lyophilization and reconstitution.

Therapeutic compositions herein generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

The route of administration is in accord with known methods, e.g. injection or infusion by intravenous,
15 intraperitoneal, intracerebral, intramuscular, intraocular, intraarterial or intralesional routes, topical administration, or by sustained release systems.

Dosages and desired drug concentrations of pharmaceutical compositions of the present invention may vary depending on the particular use envisioned. The determination of the appropriate dosage or route of administration is well within the skill of an ordinary physician. Animal experiments provide reliable guidance
20 for the determination of effective doses for human therapy. Interspecies scaling of effective doses can be performed following the principles laid down by Mordenti, J. and Chappell, W. "The use of interspecies scaling in toxicokinetics" In *Toxicokinetics and New Drug Development*, Yacobi et al., Eds., Pergamon Press, New York 1989, pp. 42-96.

When *in vivo* administration of a PRO polypeptide or agonist or antagonist thereof is employed, normal
25 dosage amounts may vary from about 10 ng/kg to up to 100 mg/kg of mammal body weight or more per day, preferably about 1 µg/kg/day to 10 mg/kg/day, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature; see, for example, U.S. Pat. Nos. 4,657,760; 5,206,344; or 5,225,212. It is anticipated that different formulations will be effective for different treatment compounds and different disorders, that administration targeting one organ or tissue, for example, may
30 necessitate delivery in a manner different from that to another organ or tissue.

Where sustained-release administration of a PRO polypeptide is desired in a formulation with release characteristics suitable for the treatment of any disease or disorder requiring administration of the PRO polypeptide, microencapsulation of the PRO polypeptide is contemplated. Microencapsulation of recombinant proteins for sustained release has been successfully performed with human growth hormone (rhGH), interferon-
35 (rhIFN-), interleukin-2, and MN rgp120. Johnson et al., Nat. Med., 2:795-799 (1996); Yasuda, Biomed. Ther., 27:1221-1223 (1993); Hora et al., Bio/Technology, 8:755-758 (1990); Cleland, "Design and Production of Single Immunization Vaccines Using Polylactide Polyglycolide Microsphere Systems," in Vaccine Design: The Subunit

and Adjuvant Approach, Powell and Newman, eds, (Plenum Press: New York, 1995), pp. 439-462; WO 97/03692, WO 96/40072, WO 96/07399; and U.S. Pat. No. 5,654,010.

The sustained-release formulations of these proteins were developed using poly-lactic-coglycolic acid (PLGA) polymer due to its biocompatibility and wide range of biodegradable properties. The degradation products of PLGA; lactic and glycolic acids, can be cleared quickly within the human body. Moreover, the degradability of this polymer can be adjusted from months to years depending on its molecular weight and composition. Lewis, "Controlled release of bioactive agents from lactide/glycolide polymer," in: M. Chasin and R. Langer (Eds.), Biodegradable Polymers as Drug Delivery Systems (Marcel Dekker: New York, 1990), pp. 1-41.

This invention encompasses methods of screening compounds to identify those that mimic the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (antagonists). Screening assays for antagonist drug candidates are designed to identify compounds that bind or complex with the PRO polypeptides encoded by the genes identified herein, or otherwise interfere with the interaction of the encoded polypeptides with other cellular proteins. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates.

The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays, and cell-based assays, which are well characterized in the art.

All assays for antagonists are common in that they call for contacting the drug candidate with a PRO polypeptide encoded by a nucleic acid identified herein under conditions and for a time sufficient to allow these two components to interact.

In binding assays, the interaction is binding and the complex formed can be isolated or detected in the reaction mixture. In a particular embodiment, the PRO polypeptide encoded by the gene identified herein or the drug candidate is immobilized on a solid phase, e.g., on a microtiter plate, by covalent or non-covalent attachments. Non-covalent attachment generally is accomplished by coating the solid surface with a solution of the PRO polypeptide and drying. Alternatively, an immobilized antibody, e.g., a monoclonal antibody, specific for the PRO polypeptide to be immobilized can be used to anchor it to a solid surface. The assay is performed by adding the non-immobilized component, which may be labeled by a detectable label, to the immobilized component, e.g., the coated surface containing the anchored component. When the reaction is complete, the non-reacted components are removed, e.g., by washing, and complexes anchored on the solid surface are detected. When the originally non-immobilized component carries a detectable label, the detection of label immobilized on the surface indicates that complexing occurred. Where the originally non-immobilized component does not carry a label, complexing can be detected, for example, by using a labeled antibody specifically binding the immobilized complex.

If the candidate compound interacts with but does not bind to a particular PRO polypeptide encoded by a gene identified herein, its interaction with that polypeptide can be assayed by methods well known for detecting protein-protein interactions. Such assays include traditional approaches, such as, e.g., cross-linking, co-immunoprecipitation, and co-purification through gradients or chromatographic columns. In addition, protein-protein interactions can be monitored by using a yeast-based genetic system described by Fields and co-workers (Fields and Song, Nature (London), 340:245-246 (1989); Chien et al., Proc. Natl. Acad. Sci. USA, 88:9578-9582

(1991)) as disclosed by Chevray and Nathans, Proc. Natl. Acad. Sci. USA, 89: 5789-5793 (1991). Many transcriptional activators, such as yeast GAL4, consist of two physically discrete modular domains, one acting as the DNA-binding domain, the other one functioning as the transcription-activation domain. The yeast expression system described in the foregoing publications (generally referred to as the "two-hybrid system") takes advantage of this property, and employs two hybrid proteins, one in which the target protein is fused to the DNA-binding domain of GAL4, and another, in which candidate activating proteins are fused to the activation domain. The expression of a GAL1-*lacZ* reporter gene under control of a GAL4-activated promoter depends on reconstitution of GAL4 activity via protein-protein interaction. Colonies containing interacting polypeptides are detected with a chromogenic substrate for β -galactosidase. A complete kit (MATCHMAKER™) for identifying protein-protein interactions between two specific proteins using the two-hybrid technique is commercially available from Clontech. This system can also be extended to map protein domains involved in specific protein interactions as well as to pinpoint amino acid residues that are crucial for these interactions.

Compounds that interfere with the interaction of a gene encoding a PRO polypeptide identified herein and other intra- or extracellular components can be tested as follows: usually a reaction mixture is prepared containing the product of the gene and the intra- or extracellular component under conditions and for a time allowing for the interaction and binding of the two products. To test the ability of a candidate compound to inhibit binding, the reaction is run in the absence and in the presence of the test compound. In addition, a placebo may be added to a third reaction mixture, to serve as positive control. The binding (complex formation) between the test compound and the intra- or extracellular component present in the mixture is monitored as described hereinabove. The formation of a complex in the control reaction(s) but not in the reaction mixture containing the test compound indicates that the test compound interferes with the interaction of the test compound and its reaction partner.

To assay for antagonists, the PRO polypeptide may be added to a cell along with the compound to be screened for a particular activity and the ability of the compound to inhibit the activity of interest in the presence of the PRO polypeptide indicates that the compound is an antagonist to the PRO polypeptide. Alternatively, antagonists may be detected by combining the PRO polypeptide and a potential antagonist with membrane-bound PRO polypeptide receptors or recombinant receptors under appropriate conditions for a competitive inhibition assay. The PRO polypeptide can be labeled, such as by radioactivity, such that the number of PRO polypeptide molecules bound to the receptor can be used to determine the effectiveness of the potential antagonist. The gene encoding the receptor can be identified by numerous methods known to those of skill in the art, for example, ligand panning and FACS sorting. Coligan et al., Current Protocols in Immun., 1(2): Chapter 5 (1991). Preferably, expression cloning is employed wherein polyadenylated RNA is prepared from a cell responsive to the PRO polypeptide and a cDNA library created from this RNA is divided into pools and used to transfect COS cells or other cells that are not responsive to the PRO polypeptide. Transfected cells that are grown on glass slides are exposed to labeled PRO polypeptide. The PRO polypeptide can be labeled by a variety of means including iodination or inclusion of a recognition site for a site-specific protein kinase. Following fixation and incubation, the slides are subjected to autoradiographic analysis. Positive pools are identified and sub-pools are prepared and re-transfected using an interactive sub-pooling and re-screening process, eventually yielding a single,

clone that encodes the putative receptor.

As an alternative approach for receptor identification, labeled PRO polypeptide can be photoaffinity-linked with cell membrane or extract preparations that express the receptor molecule. Cross-linked material is resolved by PAGE and exposed to X-ray film. The labeled complex containing the receptor can be excised, resolved into peptide fragments, and subjected to protein micro-sequencing. The amino acid sequence obtained from micro-sequencing would be used to design a set of degenerate oligonucleotide probes to screen a cDNA library to identify the gene encoding the putative receptor.

In another assay for antagonists, mammalian cells or a membrane preparation expressing the receptor would be incubated with labeled PRO polypeptide in the presence of the candidate compound. The ability of the compound to enhance or block this interaction could then be measured.

More specific examples of potential antagonists include an oligonucleotide that binds to the fusions of immunoglobulin with PRO polypeptide, and, in particular, antibodies including, without limitation, poly- and monoclonal antibodies and antibody fragments, single-chain antibodies, anti-idiotypic antibodies, and chimeric or humanized versions of such antibodies or fragments, as well as human antibodies and antibody fragments. Alternatively, a potential antagonist may be a closely related protein, for example, a mutated form of the PRO polypeptide that recognizes the receptor but imparts no effect, thereby competitively inhibiting the action of the PRO polypeptide.

Another potential PRO polypeptide antagonist is an antisense RNA or DNA construct prepared using antisense technology, where, e.g., an antisense RNA or DNA molecule acts to block directly the translation of mRNA by hybridizing to targeted mRNA and preventing protein translation. Antisense technology can be used to control gene expression through triple-helix formation or antisense DNA or RNA, both of which methods are based on binding of a polynucleotide to DNA or RNA. For example, the 5' coding portion of the polynucleotide sequence, which encodes the mature PRO polypeptides herein, is used to design an antisense RNA oligonucleotide of from about 10 to 40 base pairs in length. A DNA oligonucleotide is designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res., 6:3073 (1979); Cooney et al., Science, 241: 456 (1988); Dervan et al., Science, 251:1360 (1991)), thereby preventing transcription and the production of the PRO polypeptide. The antisense RNA oligonucleotide hybridizes to the mRNA *in vivo* and blocks translation of the mRNA molecule into the PRO polypeptide (antisense - Okano, Neurochem., 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression (CRC Press: Boca Raton, FL, 1988). The oligonucleotides described above can also be delivered to cells such that the antisense RNA or DNA may be expressed *in vivo* to inhibit production of the PRO polypeptide. When antisense DNA is used, oligodeoxyribonucleotides derived from the translation-initiation site, e.g., between about -10 and +10 positions of the target gene nucleotide sequence, are preferred.

Potential antagonists include small molecules that bind to the active site, the receptor binding site, or growth factor or other relevant binding site of the PRO polypeptide, thereby blocking the normal biological activity of the PRO polypeptide. Examples of small molecules include, but are not limited to, small peptides or peptide-like molecules, preferably soluble peptides, and synthetic non-peptidyl organic or inorganic compounds.

Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA.

Ribozymes act by sequence-specific hybridization to the complementary target RNA, followed by endonucleolytic cleavage. Specific ribozyme cleavage sites within a potential RNA target can be identified by known techniques. For further details see, e.g., Rossi, Current Biology, 4:469-471 (1994), and PCT publication No. WO 97/33551 (published September 18, 1997).

5 Nucleic acid molecules in triple-helix formation used to inhibit transcription should be single-stranded and composed of deoxynucleotides. The base composition of these oligonucleotides is designed such that it promotes triple-helix formation via Hoogsteen base-pairing rules, which generally require sizeable stretches of purines or pyrimidines on one strand of a duplex. For further details see, e.g., PCT publication No. WO 97/33551, *supra*.

10 These small molecules can be identified by any one or more of the screening assays discussed hereinabove and/or by any other screening techniques well known for those skilled in the art.

Diagnostic and therapeutic uses of the herein disclosed molecules may also be based upon the positive functional assay hits disclosed and described below.

F. Anti-PRO Antibodies

15 The present invention further provides anti-PRO antibodies. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies.

1. Polyclonal Antibodies

20 The anti-PRO antibodies may comprise polyclonal antibodies. Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the PRO polypeptide or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate).
25 The immunization protocol may be selected by one skilled in the art without undue experimentation.

30 2. Monoclonal Antibodies

The anti-PRO antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*.
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The immunizing agent will typically include the PRO polypeptide or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or

lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies [Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63].

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against PRO. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980).

After the desired hybridoma cells are identified, the clones may be subcloned by limiting dilution procedures and grown by standard methods [Goding, supra]. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells may be grown *in vivo* as ascites in a mammal.

The monoclonal antibodies secreted by the subclones may be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies may also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal antibodies in the recombinant host cells. The DNA also may be modified, for example, by substituting the coding

sequence for human heavy and light chain constant domains in place of the homologous murine sequences [U.S. Patent No. 4,816,567; Morrison et al., *supra*] or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

5 The antibodies may be monovalent antibodies. Methods for preparing monovalent antibodies are well known in the art. For example, one method involves recombinant expression of immunoglobulin light chain and modified heavy chain. The heavy chain is truncated generally at any point in the Fc region so as to prevent heavy chain crosslinking. Alternatively, the relevant cysteine residues are substituted with another amino acid residue or are deleted so as to prevent crosslinking.

10 *In vitro* methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly, Fab fragments, can be accomplished using routine techniques known in the art.

3. Human and Humanized Antibodies

15 The anti-PRO antibodies of the invention may further comprise humanized antibodies or human antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a
20 complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially
25 all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., *Nature*, 321:522-525 (1986); Riechmann et al., *Nature*, 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.*,
30 2:593-596 (1992)].

 Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed following the method of Winter and co-workers
35 [Jones et al., *Nature*, 321:522-525 (1986); Riechmann et al., *Nature*, 332:323-327 (1988); Verhoeven et al., *Science*, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Patent No.

4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, *J. Mol. Biol.*, 227:381 (1991); Marks et al., *J. Mol. Biol.*, 222:581 (1991)]. The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, p. 77 (1985) and Boerner et al., *J. Immunol.*, 147(1):86-95 (1991)]. Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks *et al.*, *Bio/Technology* 10, 779-783 (1992); Lonberg *et al.*, *Nature* 368 856-859 (1994); Morrison, *Nature* 368, 812-13 (1994); Fishwild *et al.*, *Nature Biotechnology* 14, 845-51 (1996); Neuberger, *Nature Biotechnology* 14, 826 (1996); Lonberg and Huszar, *Intern. Rev. Immunol.* 13 65-93 (1995).

The antibodies may also be affinity matured using known selection and/or mutagenesis methods as described above. Preferred affinity matured antibodies have an affinity which is five times, more preferably 10 times, even more preferably 20 or 30 times greater than the starting antibody (generally murine, humanized or human) from which the matured antibody is prepared.

4. Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for the PRO, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities [Milstein and Cuello, *Nature*, 305:537-539 (1983)]. Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker et al., *EMBO J.*, 10:3655-3659 (1991).

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least

one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

5 According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large
10 amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. F(ab')₂ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared using chemical
15 linkage. Brennan *et al.*, Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate F(ab')₂ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar
20 amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Fab' fragments may be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby *et al.*, J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')₂ molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to
25 directed chemical coupling *in vitro* to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various technique for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers.
30 Kostelny *et al.*, J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger *et al.*, Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for
35 making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (V_H) connected to a light-chain variable domain (V_L) by a linker which is too short to allow pairing between the two domains on the same chain. Accordingly, the V_H and V_L domains of one fragment are forced to pair with the complementary

V_L and V_H domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber *et al.*, J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt *et al.*, J. Immunol. 147:60 (1991).

- 5 Exemplary bispecific antibodies may bind to two different epitopes on a given PRO polypeptide herein. Alternatively, an anti-PRO polypeptide arm may be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular PRO polypeptide. Bispecific antibodies may also be used to localize cytotoxic agents to cells which express a particular PRO polypeptide. These antibodies possess a PRO-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the PRO polypeptide and further binds tissue factor (TF).
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5. Heteroconjugate Antibodies

- 15 Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells [U.S. Patent No. 4,676,980], and for treatment of HIV infection [WO 91/00360; WO 92/200373; EP 03089]. It is contemplated that the antibodies may be prepared *in vitro* using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.
- 20

6. Effector Function Engineering

- 25 It may be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, *e.g.*, the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) may be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated may have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron *et al.*, J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity may also be prepared using heterobifunctional cross-linkers as described in Wolff *et al.* Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and may thereby have enhanced complement lysis and ADCC capabilities. See Stevenson *et al.*, Anti-Cancer Drug Design, 3: 219-230 (1989).
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7. Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent

such as a chemotherapeutic agent, toxin (e.g., an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (i.e., a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, *Aleurites fordii* proteins, dianthin proteins, *Phytolaca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include ^{212}Bi , ^{131}I , ^{131}In , ^{90}Y , and ^{186}Re .

Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutaraldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta *et al.*, Science, **238**: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody may be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (e.g., avidin) that is conjugated to a cytotoxic agent (e.g., a radionucleotide).

8. Immunoliposomes

The antibodies disclosed herein may also be formulated as immunoliposomes. Liposomes containing the antibody are prepared by methods known in the art, such as described in Epstein *et al.*, Proc. Natl. Acad. Sci. USA, **82**: 3688 (1985); Hwang *et al.*, Proc. Natl. Acad. Sci. USA, **77**: 4030 (1980); and U.S. Pat. Nos. 4,485,045 and 4,544,545. Liposomes with enhanced circulation time are disclosed in U.S. Patent No. 5,013,556.

Particularly useful liposomes can be generated by the reverse-phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol, and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter. Fab' fragments of the antibody of the present invention can be conjugated to the liposomes as described in Martin *et al.*, J. Biol. Chem., **257**: 286-288 (1982) via a disulfide-interchange reaction. A chemotherapeutic agent (such as Doxorubicin) is optionally contained within the liposome. See Gabizon *et al.*, J. National Cancer Inst., **81**(19): 1484 (1989).

9. Pharmaceutical Compositions of Antibodies

Antibodies specifically binding a PRO polypeptide identified herein, as well as other molecules identified

by the screening assays disclosed hereinbefore, can be administered for the treatment of various disorders in the form of pharmaceutical compositions.

If the PRO polypeptide is intracellular and whole antibodies are used as inhibitors, internalizing antibodies are preferred. However, lipofections or liposomes can also be used to deliver the antibody, or an antibody fragment, into cells. Where antibody fragments are used, the smallest inhibitory fragment that specifically binds to the binding domain of the target protein is preferred. For example, based upon the variable-region sequences of an antibody, peptide molecules can be designed that retain the ability to bind the target protein sequence. Such peptides can be synthesized chemically and/or produced by recombinant DNA technology. See, *e.g.*, Marasco *et al.*, Proc. Natl. Acad. Sci. USA, 90: 7889-7893 (1993). The formulation herein may also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. Alternatively, or in addition, the composition may comprise an agent that enhances its function, such as, for example, a cytotoxic agent, cytokine, chemotherapeutic agent, or growth-inhibitory agent. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

The active ingredients may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methacrylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles, and nanocapsules) or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences, *supra*.

The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes.

Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, *e.g.*, films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and γ ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOTTM (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods. When encapsulated antibodies remain in the body for a long time, they may denature or aggregate as a result of exposure to moisture at 37°C, resulting in a loss of biological activity and possible changes in immunogenicity. Rational strategies can be devised for stabilization depending on the mechanism involved. For example, if the aggregation mechanism is discovered to be intermolecular S-S bond formation through thio-disulfide interchange, stabilization may be achieved by modifying sulfhydryl residues, lyophilizing from acidic solutions, controlling moisture content, using appropriate additives, and developing specific polymer matrix compositions.

G. Uses for anti-PRO Antibodies

The anti-PRO antibodies of the invention have various utilities. For example, anti-PRO antibodies may be used in diagnostic assays for PRO, *e.g.*, detecting its expression (and in some cases, differential expression) in specific cells, tissues, or serum. Various diagnostic assay techniques known in the art may be used, such as competitive binding assays, direct or indirect sandwich assays and immunoprecipitation assays conducted in either heterogeneous or homogeneous phases [Zola, Monoclonal Antibodies: A Manual of Techniques, CRC Press, Inc. (1987) pp. 147-158]. The antibodies used in the diagnostic assays can be labeled with a detectable moiety. The detectable moiety should be capable of producing, either directly or indirectly, a detectable signal. For example, the detectable moiety may be a radioisotope, such as ^3H , ^{14}C , ^{32}P , ^{35}S , or ^{125}I , a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the detectable moiety may be employed, including those methods described by Hunter et al., Nature, 144:945 (1962); David et al., Biochemistry, 13:1014 (1974); Pain et al., J. Immunol. Meth., 40:219 (1981); and Nygren, J. Histochem. and Cytochem., 30:407 (1982).

Anti-PRO antibodies also are useful for the affinity purification of PRO from recombinant cell culture or natural sources. In this process, the antibodies against PRO are immobilized on a suitable support, such as Sephadex resin or filter paper, using methods well known in the art. The immobilized antibody then is contacted with a sample containing the PRO to be purified, and thereafter the support is washed with a suitable solvent that will remove substantially all the material in the sample except the PRO, which is bound to the immobilized antibody. Finally, the support is washed with another suitable solvent that will release the PRO from the antibody.

The following examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

All patent and literature references cited in the present specification are hereby incorporated by reference in their entirety.

EXAMPLES

Commercially available reagents referred to in the examples were used according to manufacturer's instructions unless otherwise indicated. The source of those cells identified in the following examples, and throughout the specification, by ATCC accession numbers is the American Type Culture Collection, Manassas, VA.

EXAMPLE 1: Extracellular Domain Homology Screening to Identify Novel Polypeptides and cDNA Encoding Therefor

The extracellular domain (ECD) sequences (including the secretion signal sequence, if any) from about 950 known secreted proteins from the Swiss-Prot public database were used to search EST databases. The EST databases included public databases (*e.g.*, Dayhoff, GenBank), and proprietary databases (*e.g.* LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, CA). The search was performed using the computer program BLAST or

BLAST-2 (Altschul *et al.*, Methods in Enzymology, 266:460-480 (1996)) as a comparison of the ECD protein sequences to a 6 frame translation of the EST sequences. Those comparisons with a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into consensus DNA sequences with the program "phrap" (Phil Green, University of Washington, Seattle, WA).

Using this extracellular domain homology screen, consensus DNA sequences were assembled relative to the other identified EST sequences using phrap. In addition, the consensus DNA sequences obtained were often (but not always) extended using repeated cycles of BLAST or BLAST-2 and phrap to extend the consensus sequence as far as possible using the sources of EST sequences discussed above.

Based upon the consensus sequences obtained as described above, oligonucleotides were then synthesized and used to identify by PCR a cDNA library that contained the sequence of interest and for use as probes to isolate a clone of the full-length coding sequence for a PRO polypeptide. Forward and reverse PCR primers generally range from 20 to 30 nucleotides and are often designed to give a PCR product of about 100-1000 bp in length. The probe sequences are typically 40-55 bp in length. In some cases, additional oligonucleotides are synthesized when the consensus sequence is greater than about 1-1.5kbp. In order to screen several libraries for a full-length clone, DNA from the libraries was screened by PCR amplification, as per Ausubel *et al.*, Current Protocols in Molecular Biology, with the PCR primer pair. A positive library was then used to isolate clones encoding the gene of interest using the probe oligonucleotide and one of the primer pairs.

The cDNA libraries used to isolate the cDNA clones were constructed by standard methods using commercially available reagents such as those from Invitrogen, San Diego, CA. The cDNA was primed with oligo dT containing a NotI site, linked with blunt to SalI hemikinased adaptors, cleaved with NotI, sized appropriately by gel electrophoresis, and cloned in a defined orientation into a suitable cloning vector (such as pRKB or pRKD; pRK5B is a precursor of pRK5D that does not contain the SfiI site; *see*, Holmes *et al.*, Science, 253:1278-1280 (1991)) in the unique XhoI and NotI sites.

EXAMPLE 2: Isolation of cDNA clones by Amylase Screening

1. Preparation of oligo dT primed cDNA library

mRNA was isolated from a human tissue of interest using reagents and protocols from Invitrogen, San Diego, CA (Fast Track 2). This RNA was used to generate an oligo dT primed cDNA library in the vector pRK5D using reagents and protocols from Life Technologies, Gaithersburg, MD (Super Script Plasmid System). In this procedure, the double stranded cDNA was sized to greater than 1000 bp and the SalI/NotI linkered cDNA was cloned into XhoI/NotI cleaved vector. pRK5D is a cloning vector that has an sp6 transcription initiation site followed by an SfiI restriction enzyme site preceding the XhoI/NotI cDNA cloning sites.

2. Preparation of random primed cDNA library

A secondary cDNA library was generated in order to preferentially represent the 5' ends of the primary cDNA clones. Sp6 RNA was generated from the primary library (described above), and this RNA was used to generate a random primed cDNA library in the vector pSST-AMY.0 using reagents and protocols from Life Technologies (Super Script Plasmid System, referenced above). In this procedure the double stranded cDNA was

sized to 500-1000 bp, linked with blunt to NotI adaptors, cleaved with SfiI, and cloned into SfiI/NotI cleaved vector. pSST-AMY.0 is a cloning vector that has a yeast alcohol dehydrogenase promoter preceding the cDNA cloning sites and the mouse amylase sequence (the mature sequence without the secretion signal) followed by the yeast alcohol dehydrogenase terminator, after the cloning sites. Thus, cDNAs cloned into this vector that are fused in frame with amylase sequence will lead to the secretion of amylase from appropriately transfected yeast colonies.

3. Transformation and Detection

DNA from the library described in paragraph 2 above was chilled on ice to which was added electrocompetent DH10B bacteria (Life Technologies, 20 ml). The bacteria and vector mixture was then electroporated as recommended by the manufacturer. Subsequently, SOC media (Life Technologies, 1 ml) was added and the mixture was incubated at 37°C for 30 minutes. The transformants were then plated onto 20 standard 150 mm LB plates containing ampicillin and incubated for 16 hours (37°C). Positive colonies were scraped off the plates and the DNA was isolated from the bacterial pellet using standard protocols, *e.g.* CsCl-gradient. The purified DNA was then carried on to the yeast protocols below.

The yeast methods were divided into three categories: (1) Transformation of yeast with the plasmid/cDNA combined vector; (2) Detection and isolation of yeast clones secreting amylase; and (3) PCR amplification of the insert directly from the yeast colony and purification of the DNA for sequencing and further analysis.

The yeast strain used was HD56-5A (ATCC-90785). This strain has the following genotype: MAT alpha, *ura3-52*, *leu2-3*, *leu2-112*, *his3-11*, *his3-15*, *MAL*⁺, *SUC*⁺, *GAL*⁺. Preferably, yeast mutants can be employed that have deficient post-translational pathways. Such mutants may have translocation deficient alleles in *sec71*, *sec72*, *sec62*, with truncated *sec71* being most preferred. Alternatively, antagonists (including antisense nucleotides and/or ligands) which interfere with the normal operation of these genes, other proteins implicated in this post translation pathway (*e.g.*, SEC61p, SEC72p, SEC62p, SEC63p, TDJ1p or SSA1p-4p) or the complex formation of these proteins may also be preferably employed in combination with the amylase-expressing yeast.

Transformation was performed based on the protocol outlined by Gietz *et al.*, Nucl. Acid. Res., 20:1425 (1992). Transformed cells were then inoculated from agar into YEPD complex media broth (100 ml) and grown overnight at 30°C. The YEPD broth was prepared as described in Kaiser *et al.*, Methods in Yeast Genetics, Cold Spring Harbor Press, Cold Spring Harbor, NY, p. 207 (1994). The overnight culture was then diluted to about 2×10^6 cells/ml (approx. OD₆₀₀=0.1) into fresh YEPD broth (500 ml) and regrown to 1×10^7 cells/ml (approx. OD₆₀₀=0.4-0.5).

The cells were then harvested and prepared for transformation by transfer into GS3 rotor bottles in a Sorval GS3 rotor at 5,000 rpm for 5 minutes, the supernatant discarded, and then resuspended into sterile water, and centrifuged again in 50 ml falcon tubes at 3,500 rpm in a Beckman GS-6KR centrifuge. The supernatant was discarded and the cells were subsequently washed with LiAc/TE (10 ml, 10 mM Tris-HCl, 1 mM EDTA pH 7.5, 100 mM Li₂OOCCH₃), and resuspended into LiAc/TE (2.5 ml).

Transformation took place by mixing the prepared cells (100 µl) with freshly denatured single stranded

salmon testes DNA (Lofstrand Labs, Gaithersburg, MD) and transforming DNA (1 μ g, vol. < 10 μ l) in microfuge tubes. The mixture was mixed briefly by vortexing, then 40% PEG/TE (600 μ l, 40% polyethylene glycol-4000, 10 mM Tris-HCl, 1 mM EDTA, 100 mM Li₂OOCCH₃, pH 7.5) was added. This mixture was gently mixed and incubated at 30°C while agitating for 30 minutes. The cells were then heat shocked at 42°C for 15 minutes, and the reaction vessel centrifuged in a microfuge at 12,000 rpm for 5-10 seconds, decanted and resuspended into TE (500 μ l, 10 mM Tris-HCl, 1 mM EDTA pH 7.5) followed by recentrifugation. The cells were then diluted into TE (1 ml) and aliquots (200 μ l) were spread onto the selective media previously prepared in 150 mm growth plates (VWR).

Alternatively, instead of multiple small reactions, the transformation was performed using a single, large scale reaction, wherein reagent amounts were scaled up accordingly.

The selective media used was a synthetic complete dextrose agar lacking uracil (SCD-Ura) prepared as described in Kaiser *et al.*, Methods in Yeast Genetics, Cold Spring Harbor Press, Cold Spring Harbor, NY, p. 208-210 (1994). Transformants were grown at 30°C for 2-3 days.

The detection of colonies secreting amylase was performed by including red starch in the selective growth media. Starch was coupled to the red dye (Reactive Red-120, Sigma) as per the procedure described by Biely *et al.*, Anal. Biochem., 172:176-179 (1988). The coupled starch was incorporated into the SCD-Ura agar plates at a final concentration of 0.15% (w/v), and was buffered with potassium phosphate to a pH of 7.0 (50-100 mM final concentration).

The positive colonies were picked and streaked across fresh selective media (onto 150 mm plates) in order to obtain well isolated and identifiable single colonies. Well isolated single colonies positive for amylase secretion were detected by direct incorporation of red starch into buffered SCD-Ura agar. Positive colonies were determined by their ability to break down starch resulting in a clear halo around the positive colony visualized directly.

4. Isolation of DNA by PCR Amplification

When a positive colony was isolated, a portion of it was picked by a toothpick and diluted into sterile water (30 μ l) in a 96 well plate. At this time, the positive colonies were either frozen and stored for subsequent analysis or immediately amplified. An aliquot of cells (5 μ l) was used as a template for the PCR reaction in a 25 μ l volume containing: 0.5 μ l KlenTaq (Clontech, Palo Alto, CA); 4.0 μ l 10 mM dNTP's (Perkin Elmer-Cetus); 2.5 μ l KlenTaq buffer (Clontech); 0.25 μ l forward oligo 1; 0.25 μ l reverse oligo 2; 12.5 μ l distilled water. The sequence of the forward oligonucleotide 1 was:

5'-TGTAACACGACGGCCAGTTAAATAGACCTGCAATTATTAATCT-3' (SEQ ID NO:611)

The sequence of reverse oligonucleotide 2 was:

5'-CAGGAAACAGCTATGACCACCTGCACACCTGCAAATCCATT-3' (SEQ ID NO:612)

PCR was then performed as follows:

- | | | |
|----|--------------|------------------|
| a. | Denature | 92°C, 5 minutes |
| b. | 3 cycles of: | |
| | Denature | 92°C, 30 seconds |
| | Anneal | 59°C, 30 seconds |

		Extend	72°C, 60 seconds
5	c.	3 cycles of:	
		Denature	92°C, 30 seconds
		Anneal	57°C, 30 seconds
		Extend	72°C, 60 seconds
	d.	25 cycles of:	
		Denature	92°C, 30 seconds
		Anneal	55°C, 30 seconds
		Extend	72°C, 60 seconds
10	e.	Hold	4°C

The underlined regions of the oligonucleotides annealed to the ADH promoter region and the amylase region, respectively, and amplified a 307 bp region from vector pSST-AMY.0 when no insert was present. Typically, the first 18 nucleotides of the 5' end of these oligonucleotides contained annealing sites for the sequencing primers. Thus, the total product of the PCR reaction from an empty vector was 343 bp. However, signal sequence-fused cDNA resulted in considerably longer nucleotide sequences.

Following the PCR, an aliquot of the reaction (5 µl) was examined by agarose gel electrophoresis in a 1% agarose gel using a Tris-Borate-EDTA (TBE) buffering system as described by Sambrook *et al.*, *supra*. Clones resulting in a single strong PCR product larger than 400 bp were further analyzed by DNA sequencing after purification with a 96 Qiaquick PCR clean-up column (Qiagen Inc., Chatsworth, CA).

EXAMPLE 3: Isolation of cDNA Clones Using Signal Algorithm Analysis

Various polypeptide-encoding nucleic acid sequences were identified by applying a proprietary signal sequence finding algorithm developed by Genentech, Inc. (South San Francisco, CA) upon ESTs as well as clustered and assembled EST fragments from public (*e.g.*, GenBank) and/or private (LIFESEQ®, Incyte Pharmaceuticals, Inc., Palo Alto, CA) databases. The signal sequence algorithm computes a secretion signal score based on the character of the DNA nucleotides surrounding the first and optionally the second methionine codon(s) (ATG) at the 5'-end of the sequence or sequence fragment under consideration. The nucleotides following the first ATG must code for at least 35 unambiguous amino acids without any stop codons. If the first ATG has the required amino acids, the second is not examined. If neither meets the requirement, the candidate sequence is not scored. In order to determine whether the EST sequence contains an authentic signal sequence, the DNA and corresponding amino acid sequences surrounding the ATG codon are scored using a set of seven sensors (evaluation parameters) known to be associated with secretion signals. Use of this algorithm resulted in the identification of numerous polypeptide-encoding nucleic acid sequences.

EXAMPLE 4: Isolation of cDNA clones Encoding Human PRO Polypeptides

Using the techniques described in Examples 1 to 3 above, numerous full-length cDNA clones were identified as encoding PRO polypeptides as disclosed herein. These cDNAs were then deposited under the terms of the Budapest Treaty with the American Type Culture Collection, 10801 University Blvd., Manassas, VA 20110-2209, USA (ATCC) as shown in Table 7 below.

Table 7

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA16435-1208	209930	June 2, 1998
	DNA23318-1211	209787	April 21, 1998
	DNA23322-1393	203400	October 27, 1998
5	DNA23334-1392	209918	June 2, 1998
	DNA26843-1389	203099	August 4, 1998
	DNA 26844-1394	209926	June 2, 1998
	DNA30867-1335	209807	April 28, 1998
	DNA33470-1175	209398	October 17, 1997
10	DNA34436-1238	209523	December 10, 1997
	DNA35557-1137	209255	September 16, 1997
	DNA35599-1168	209373	October 16, 1997
	DNA35668-1171	209371	October 16, 1997
	DNA36992-1168	209382	October 16, 1997
15	DNA39423-1182	209387	October 17, 1997
	DNA39427-1179	209395	October 17, 1997
	DNA39510-1181	209392	October 17, 1997
	DNA39518-1247	209529	December 10, 1997
	DNA39975-1210	209783	April 21, 1998
20	DNA39976-1215	209524	December 10, 1997
	DNA39979-1213	209789	April 21, 1998
	DNA40594-1233	209617	February 5, 1998
	DNA40603-1232	209486	November 21, 1997
	DNA40604-1187	209394	October 17, 1997
25	DNA40625-1189	209788	April 21, 1998
	DNA41225-1217	209491	November 21, 1997
	DNA41379-1236	209488	November 21, 1997
	DNA41386-1316	209703	March 26, 1998
	DNA44161-1434	209907	May 27, 1998
30	DNA44179-1362	209851	May 6, 1998
	DNA44192-1246	209531	December 10, 1997
	DNA44694-1500	203114	August 11, 1998
	DNA45234-1277	209654	March 5, 1998
	DNA45409-2511	203579	January 12, 1999
35	DNA45415-1318	209810	April 28, 1998
	DNA45417-1432	209910	May 27, 1998
	DNA45493-1349	209805	April 28, 1998

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA46776-1284	209721	March 31, 1998
	DNA48296-1292	209668	March 11, 1998
	DNA48306-1291	209911	May 27, 1998
5	DNA48328-1355	209843	May 6, 1998
	DNA48329-1290	209785	April 21, 1998
	DNA48334-1435	209924	June 2, 1998
	DNA49141-1431	203003	June 23, 1998
	DNA49624-1279	209655	March 5, 1998
10	DNA49647-1398	209919	June 2, 1998
	DNA49819-1439	209931	June 2, 1998
	DNA50911-1288	209714	March 31, 1998
	DNA50914-1289	209722	March 31, 1998
	DNA50919-1361	209848	May 6, 1998
15	DNA50980-1286	209717	March 31, 1998
	DNA52185-1370	209861	May 14, 1998
	DNA53906-1368	209747	April 7, 1998
	DNA53912-1457	209870	May 14, 1998
	DNA53913-1490	203162	August 25, 1998
20	DNA53977-1371	209862	May 14, 1998
	DNA53978-1443	209983	June 16, 1998
	DNA53996-1442	209921	June 2, 1998
	DNA54002-1367	209754	April 7, 1998
	DNA55737-1345	209753	April 7, 1998
25	DNA56050-1455	203011	June 23, 1998
	DNA56052-1454	203026	June 23, 1998
	DNA56107-1415	203405	October 27, 1998
	DNA56110-1437	203113	August 11, 1998
	DNA56406-1704	203478	November 17, 1998
30	DNA56409-1377	209882	May 20, 1998
	DNA56410-1414	209923	June 2, 1998
	DNA56436-1448	209902	May 27, 1998
	DNA56529-1647	203293	September 29, 1998
	DNA56855-1447	203004	June 23, 1998
35	DNA56859-1445	203019	June 23, 1998
	DNA56860-1510	209952	June 9, 1998
	DNA56865-1491	203022	June 23, 1998

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA56868-1478	203024	June 23, 1998
	DNA56869-1545	203161	August 25, 1998
	DNA56870-1492	209925	June 2, 1998
5	DNA57039-1402	209777	April 14, 1998
	DNA57253-1382	209867	May 14, 1998
	DNA57254-1477	203289	September 29, 1998
	DNA57699-1412	203020	June 23, 1998
	DNA57704-1452	209953	June 9, 1998
10	DNA57710-1451	203048	July 1, 1998
	DNA57827-1493	203045	July 1, 1998
	DNA57844-1410	203010	June 23, 1998
	DNA58723-1588	203133	August 18, 1998
	DNA58727-1474	203171	September 1, 1998
15	DNA58730-1607	203221	September 15, 1998
	DNA58732-1650	203290	September 29, 1998
	DNA58737-1473	203136	August 18, 1998
	DNA58743-1609	203154	August 25, 1998
	DNA58747-1384	209868	May 14, 1998
20	DNA58828-1519	203172	September 1, 1998
	DNA58846-1409	209957	June 9, 1998
	DNA58848-1472	209955	June 9, 1998
	DNA58849-1494	209958	June 9, 1998
	DNA58850-1495	209956	June 9, 1998
25	DNA58852-1637	203271	September 22, 1998
	DNA58853-1423	203016	June 23, 1998
	DNA58855-1422	203018	June 23, 1998
	DNA59211-1450	209960	June 9, 1998
	DNA59212-1627	203245	September 9, 1998
30	DNA59213-1487	209959	June 9, 1998
	DNA59219-1613	203220	September 15, 1998
	DNA59497-1496	209941	June 4, 1998
	DNA59602-1436	203051	July 1, 1998
	DNA59603-1419	209944	June 9, 1998
35	DNA59605-1418	203005	June 23, 1998
	DNA59607-1497	209946	June 9, 1998
	DNA59610-1556	209990	June 16, 1998

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA59612-1466	209947	June 9, 1998
	DNA59613-1417	203007	June 23, 1998
	DNA59616-1465	209991	June 16, 1998
5	DNA59619-1464	203041	July 1, 1998
	DNA59625-1498	209992	June 16, 1998
	DNA59817-1703	203470	November 17, 1998
	DNA59827-1426	203089	August 4, 1998
	DNA59828-1608	203158	August 25, 1998
10	DNA59837-2545	203658	February 9, 1999
	DNA59844-2542	203650	February 9, 1999
	DNA59853-1505	209985	June 16, 1998
	DNA59854-1459	209974	June 16, 1998
	DNA59855-1485	209987	June 16, 1998
15	DNA60278-1530	203170	September 1, 1998
	DNA60283-1484	203043	July 1, 1998
	DNA60608-1577	203126	August 18, 1998
	DNA60611-1524	203175	September 1, 1998
	DNA60619-1482	209993	June 16, 1998
20	DNA60625-1507	209975	June 16, 1998
	DNA60629-1481	209979	June 16, 1998
	DNA60740-1615	203456	November 3, 1998
	DNA61608-1606	203239	September 9, 1998
	DNA61755-1554	203112	August 11, 1998
25	DNA62809-1531	203237	September 9, 1998
	DNA62812-1594	203248	September 9, 1998
	DNA62813-2544	203655	February 9, 1999
	DNA62845-1684	203361	October 20, 1998
	DNA64849-1604	203468	November 17, 1998
30	DNA64852-1589	203127	August 18, 1998
	DNA64863-1573	203251	September 9, 1998
	DNA64881-1602	203240	September 9, 1998
	DNA64902-1667	203317	October 6, 1998
	DNA64952-1568	203222	September 15, 1998
35	DNA65403-1565	203230	September 15, 1998
	DNA65413-1534	203234	September 15, 1998
	DNA65423-1595	203227	September 15, 1998

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA66304-1546	203321	October 6, 1998
	DNA66308-1537	203159	August 25, 1998
	DNA66511-1563	203228	September 15, 1998
5	DNA66512-1564	203218	September 15, 1998
	DNA66519-1535	203236	September 15, 1998
	DNA66521-1583	203225	September 15, 1998
	DNA66658-1584	203229	September 15, 1998
	DNA66660-1585	203279	September 22, 1998
10	DNA66669-1597	203272	September 22, 1998
	DNA66674-1599	203281	September 22, 1998
	DNA68836-1656	203455	November 3, 1998
	DNA68862-2546	203652	February 9, 1999
	DNA68866-1644	203283	September 22, 1998
15	DNA68869-1610	203164	August 25, 1998
	DNA68871-1638	203280	September 22, 1998
	DNA68879-1631	203274	September 22, 1998
	DNA68880-1676	203319	October 6, 1998
	DNA68882-1677	203318	October 6, 1998
20	DNA68883-1691	203535	December 15, 1998
	DNA68885-1678	203311	October 6, 1998
	DNA71180-1655	203403	October 27, 1998
	DNA71184-1634	203266	September 22, 1998
	DNA71213-1659	203401	October 27, 1998
25	DNA71234-1651	203402	October 27, 1998
	DNA71269-1621	203284	September 22, 1998
	DNA71277-1636	203285	September 22, 1998
	DNA71286-1687	203357	October 20, 1998
	DNA71883-1660	203475	November 17, 1998
30	DNA73401-1633	203273	September 22, 1998
	DNA73492-1671	203324	October 6, 1998
	DNA73730-1679	203320	October 6, 1998
	DNA73734-1680	203363	October 20, 1998
	DNA73735-1681	203356	October 20, 1998
35	DNA73742-1662	203316	October 6, 1998
	DNA73746-1654	203411	October 27, 1998
	DNA73760-1672	203314	October 6, 1998

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA76393-1664	203323	October 6, 1998
	DNA76398-1699	203474	November 17, 1998
	DNA76399-1700	203472	November 17, 1998
5	DNA76522-2500	203469	November 17, 1998
	DNA76533-1689	203410	October 27, 1998
	DNA77303-2502	203479	November 17, 1998
	DNA77626-1705	203536	December 15, 1998
	DNA77648-1688	203408	October 27, 1998
10	DNA81754-2532	203542	December 15, 1998
	DNA81757-2512	203543	December 15, 1998
	DNA82302-2529	203534	December 15, 1998
	DNA82340-2530	203547	December 22, 1998
	DNA87991-2540	203656	February 9, 1999
15	DNA92238-2539	203602	January 20, 1999
	DNA115291-2681	PTA-202	June 8, 1999
	DNA23336-2861	PTA-1673	April 11, 2000
	DNA30862-1396	209920	June 2, 1998
	DNA30871-1157	209380	October 16, 1997
20	DNA32279-1131	209259	September 16, 1997
	DNA33206-1165	209372	October 16, 1997
	DNA35673-1201	209418	October 28, 1997
	DNA47361-1154-2	209431	November 7, 1997
	DNA49631-1328	209806	April 28, 1998
25	DNA52594-1270	209679	March 17, 1998
	DNA55800-1263	209680	March 17, 1998
	DNA56531-1648	203286	September 29, 1998
	DNA56965-1356	209842	May 6, 1998
	DNA57037-1444	209903	May 27, 1998
30	DNA57695-1340	203006	June 23, 1998
	DNA57834-1339	209954	June 9, 1998
	DNA57841-1522	203458	November 3, 1998
	DNA58847-1383	209879	May 20, 1998
	DNA59493-1420	203050	July 1, 1998
35	DNA59586-1520	203288	September 29, 1998
	DNA59608-2577	203870	March 23, 1999
	DNA59849-1504	209986	June 16, 1998

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA60292-1506	203540	December 15, 1998
	DNA62377-1381-1	203552	December 22, 1998
	DNA62880-1513	203097	August 4, 1998
5	DNA66672-1586	203265	September 22, 1998
	DNA67962-1649	203291	September 29, 1998
	DNA69555-2867	PTA-1632	April 4, 2000
	DNA71162-2764	PTA-860	October 19, 1999
	DNA71290-1630	203275	September 22, 1998
10	DNA76401-1683	203360	October 20, 1998
	DNA76541-1675	203409	October 27, 1998
	DNA76788-2526	203551	December 22, 1998
	DNA77623-2524	203546	December 22, 1998
	DNA80136-2503	203541	December 15, 1998
15	DNA83568-2692	PTA-386	July 20, 1999
	DNA84210-2576	203818	March 2, 1999
	DNA86576-2595	203868	March 23, 1999
	DNA87976-2593	203888	March 30, 1999
	DNA92256-2596	203891	March 30, 1999
20	DNA92289-2598	PTA-131	May 25, 1999
	DNA96850-2705	PTA-479	August 3, 1999
	DNA96855-2629	PTA-18	May 4, 1999
	DNA96857-2636	PTA-17	May 4, 1999
	DNA96860-2700	PTA-478	August 3, 1999
25	DNA96861-2844	PTA-1436	March 2, 2000
	DNA96866-2698	PTA-491	August 3, 1999
	DNA96870-2676	PTA-254	June 22, 1999
	DNA96872-2674	PTA-550	August 17, 1999
	DNA96878-2626	PTA-23	May 4, 1999
30	DNA96879-2619	203967	April 27, 1999
	DNA96889-2641	PTA-119	May 25, 1999
	DNA96893-2621	PTA-12	May 4, 1999
	DNA96897-2688	PTA-379	July 20, 1999
	DNA98564-2643	PTA-125	May 25, 1999
35	DNA107443-2718	PTA-490	August 3, 1999
	DNA107786-2723	PTA-474	August 3, 1999
	DNA108682-2712	PTA-486	August 3, 1999

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA108684-2761	PTA-653	September 14, 1999
	DNA108701-2749	PTA-554	August 17, 1999
	DNA108720-2717	PTA-511	August 10, 1999
5	DNA108726-2729	PTA-514	August 10, 1999
	DNA108728-2760	PTA-654	September 14, 1999
	DNA108738-2767	PTA-862	October 19, 1999
	DNA108743-2722	PTA-508	August 10, 1999
	DNA108758-2759	PTA-655	September 14, 1999
10	DNA108765-2758	PTA-657	September 14, 1999
	DNA108783-2747	PTA-616	August 31, 1999
	DNA108789-2748	PTA-547	August 17, 1999
	DNA108806-2724	PTA-610	August 31, 1999
	DNA108936-2719	PTA-519	August 10, 1999
15	DNA119510-2771	PTA-947	November 9, 1999
	DNA119517-2778	PTA-951	November 16, 1999
	DNA119535-2756	PTA-613	August 31, 1999
	DNA119537-2777	PTA-956	November 16, 1999
	DNA119714-2851	PTA-1537	March 21, 2000
20	DNA125170-2780	PTA-953	November 16, 1999
	DNA129594-2841	PTA-1481	March 14, 2000
	DNA129793-2857	PTA-1733	April 18, 2000
	DNA130809-2769	PTA-949	November 9, 1999
	DNA131639-2874	PTA-1784	April 25, 2000
25	DNA131649-2855	PTA-1482	March 14, 2000
	DNA131652-2876	PTA-1628	April 4, 2000
	DNA131658-2875	PTA-1671	April 11, 2000
	DNA132162-2770	PTA-950	November 9, 1999
	DNA136110-2763	PTA-652	September 14, 1999
30	DNA139592-2866	PTA-1587	March 28, 2000
	DNA139608-2856	PTA-1581	March 28, 2000
	DNA143292-2848	PTA-1778	April 25, 2000
	DNA144844-2843	PTA-1536	March 21, 2000
	DNA144857-2845	PTA-1589	March 28, 2000
35	DNA145841-2868	PTA-1678	April 11, 2000
	DNA148004-2882	PTA-1779	April 25, 2000
	DNA149893-2873	PTA-1672	April 11, 2000

Table 7 (cont')

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA149930-2884	PTA-1668	April 11, 2000
	DNA150157-2898	PTA-1777	April 25, 2000
	DNA150163-2842	PTA-1533	March 21, 2000
5	DNA153579-2894	PTA-1729	April 18, 2000
	DNA164625-2890	PTA-1535	March 21, 2000
	DNA57838-1337	203014	June 23, 1998
	DNA59777-1480	203111	August 11, 1998
	DNA66675-1587	203282	September 22, 1998
10	DNA76532-1702	203473	November 17, 1998
	DNA105849-2704	PTA-473	August 3, 1999
	DNA83500-2506	203391	October 29, 1998

These deposits were made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure and the Regulations thereunder (Budapest Treaty). This assures maintenance of a viable culture of the deposit for 30 years from the date of deposit. The deposits will be made available by ATCC under the terms of the Budapest Treaty, and subject to an agreement between Genentech, Inc. and ATCC, which assures permanent and unrestricted availability of the progeny of the culture of the deposit to the public upon issuance of the pertinent U.S. patent or upon laying open to the public of any U.S. or foreign patent application, whichever comes first, and assures availability of the progeny to one determined by the U.S. Commissioner of Patents and Trademarks to be entitled thereto according to 35 USC § 122 and the Commissioner's rules pursuant thereto (including 37 CFR § 1.14 with particular reference to 886 OG 638).

The assignee of the present application has agreed that if a culture of the materials on deposit should die or be lost or destroyed when cultivated under suitable conditions, the materials will be promptly replaced on notification with another of the same. Availability of the deposited material is not to be construed as a license to practice the invention in contravention of the rights granted under the authority of any government in accordance with its patent laws.

30 EXAMPLE 5: Use of PRO as a hybridization probe

The following method describes use of a nucleotide sequence encoding PRO as a hybridization probe.

DNA comprising the coding sequence of full-length or mature PRO as disclosed herein is employed as a probe to screen for homologous DNAs (such as those encoding naturally-occurring variants of PRO) in human tissue cDNA libraries or human tissue genomic libraries.

35 Hybridization and washing of filters containing either library DNAs is performed under the following high stringency conditions. Hybridization of radiolabeled PRO-derived probe to the filters is performed in a solution of 50% formamide, 5x SSC, 0.1% SDS, 0.1% sodium pyrophosphate, 50 mM sodium phosphate, pH

6.8, 2x Denhardt's solution, and 10% dextran sulfate at 42°C for 20 hours. Washing of the filters is performed in an aqueous solution of 0.1x SSC and 0.1% SDS at 42°C.

DNAs having a desired sequence identity with the DNA encoding full-length native sequence PRO can then be identified using standard techniques known in the art.

5 EXAMPLE 6: Expression of PRO in *E. coli*

This example illustrates preparation of an unglycosylated form of PRO by recombinant expression in *E. coli*.

The DNA sequence encoding PRO is initially amplified using selected PCR primers. The primers should contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector. A variety of expression vectors may be employed. An example of a suitable vector is pBR322 (derived from *E. coli*; see Bolivar et al., Gene, 2:95 (1977)) which contains genes for ampicillin and tetracycline resistance. The vector is digested with restriction enzyme and dephosphorylated. The PCR amplified sequences are then ligated into the vector. The vector will preferably include sequences which encode for an antibiotic resistance gene, a trp promoter, a polyhis leader (including the first six STII codons, polyhis sequence, and enterokinase cleavage site), the PRO coding region, lambda transcriptional terminator, and an argU gene.

The ligation mixture is then used to transform a selected *E. coli* strain using the methods described in Sambrook et al., supra. Transformants are identified by their ability to grow on LB plates and antibiotic resistant colonies are then selected. Plasmid DNA can be isolated and confirmed by restriction analysis and DNA sequencing.

Selected clones can be grown overnight in liquid culture medium such as LB broth supplemented with antibiotics. The overnight culture may subsequently be used to inoculate a larger scale culture. The cells are then grown to a desired optical density, during which the expression promoter is turned on.

After culturing the cells for several more hours, the cells can be harvested by centrifugation. The cell pellet obtained by the centrifugation can be solubilized using various agents known in the art, and the solubilized PRO protein can then be purified using a metal chelating column under conditions that allow tight binding of the protein.

PRO may be expressed in *E. coli* in a poly-His tagged form, using the following procedure. The DNA encoding PRO is initially amplified using selected PCR primers. The primers will contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector, and other useful sequences providing for efficient and reliable translation initiation, rapid purification on a metal chelation column, and proteolytic removal with enterokinase. The PCR-amplified, poly-His tagged sequences are then ligated into an expression vector, which is used to transform an *E. coli* host based on strain 52 (W3110 fuhA(tonA) lon galE rpoHts(htpRts) clpP(lacIq). Transformants are first grown in LB containing 50 mg/ml carbenicillin at 30°C with shaking until an O.D.600 of 3-5 is reached. Cultures are then diluted 50-100 fold into CRAP media (prepared by mixing 3.57 g (NH₄)₂SO₄, 0.71 g sodium citrate•2H₂O, 1.07 g KCl, 5.36 g Difco yeast extract, 5.36 g Sheffield hycase SF in 500 mL water, as well as 110 mM MPOS, pH 7.3, 0.55% (w/v) glucose and 7 mM MgSO₄) and grown for approximately 20-30 hours at 30°C with shaking. Samples are removed to verify

expression by SDS-PAGE analysis, and the bulk culture is centrifuged to pellet the cells. Cell pellets are frozen until purification and refolding.

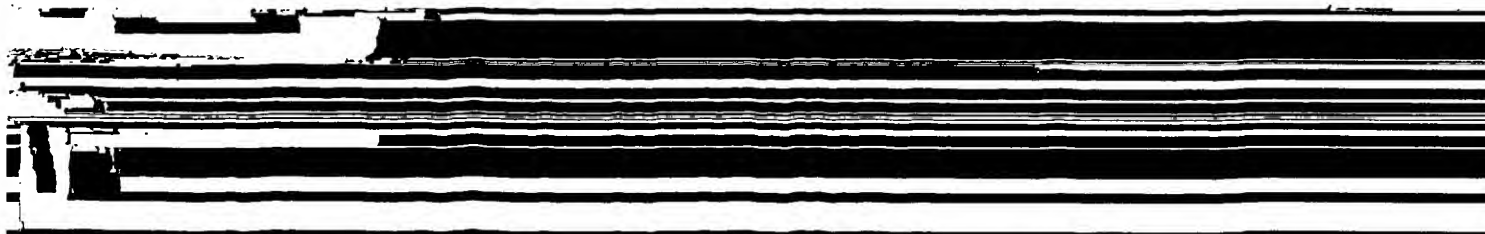
5 *E. coli* paste from 0.5 to 1 L fermentations (6-10 g pellets) is resuspended in 10 volumes (w/v) in 7 M guanidine, 20 mM Tris, pH 8 buffer. Solid sodium sulfite and sodium tetrathionate is added to make final concentrations of 0.1M and 0.02 M, respectively, and the solution is stirred overnight at 4°C. This step results
10 in a denatured protein with all cysteine residues blocked by sulfitolization. The solution is centrifuged at 40,000 rpm in a Beckman Ultracentrifuge for 30 min. The supernatant is diluted with 3-5 volumes of metal chelate column buffer (6 M guanidine, 20 mM Tris, pH 7.4) and filtered through 0.22 micron filters to clarify. The clarified extract is loaded onto a 5 ml Qiagen Ni-NTA metal chelate column equilibrated in the metal chelate column buffer. The column is washed with additional buffer containing 50 mM imidazole (Calbiochem, Utrol grade), pH 7.4. The protein is eluted with buffer containing 250 mM imidazole. Fractions containing the desired protein are pooled and stored at 4°C. Protein concentration is estimated by its absorbance at 280 nm using the calculated extinction coefficient based on its amino acid sequence.

15 The proteins are refolded by diluting the sample slowly into freshly prepared refolding buffer consisting of: 20 mM Tris, pH 8.6, 0.3 M NaCl, 2.5 M urea, 5 mM cysteine, 20 mM glycine and 1 mM EDTA. Refolding volumes are chosen so that the final protein concentration is between 50 to 100 micrograms/ml. The refolding solution is stirred gently at 4°C for 12-36 hours. The refolding reaction is quenched by the addition of TFA to a final concentration of 0.4% (pH of approximately 3). Before further purification of the protein, the solution is filtered through a 0.22 micron filter and acetonitrile is added to 2-10% final concentration. The refolded protein is chromatographed on a Poros R1/H reversed phase column using a mobile buffer of 0.1% TFA with
20 elution with a gradient of acetonitrile from 10 to 80%. Aliquots of fractions with A280 absorbance are analyzed on SDS polyacrylamide gels and fractions containing homogeneous refolded protein are pooled. Generally, the properly refolded species of most proteins are eluted at the lowest concentrations of acetonitrile since those species are the most compact with their hydrophobic interiors shielded from interaction with the reversed phase resin. Aggregated species are usually eluted at higher acetonitrile concentrations. In addition to resolving misfolded
25 forms of proteins from the desired form, the reversed phase step also removes endotoxin from the samples.

Fractions containing the desired folded PRO polypeptide are pooled and the acetonitrile removed using a gentle stream of nitrogen directed at the solution. Proteins are formulated into 20 mM Hepes, pH 6.8 with 0.14 M sodium chloride and 4% mannitol by dialysis or by gel filtration using G25 Superfine (Pharmacia) resins equilibrated in the formulation buffer and sterile filtered.

30 Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

EXAMPLE 7: Expression of PRO in mammalian cells



PRO.

In one embodiment, the selected host cells may be 293 cells. Human 293 cells (ATCC CCL 1573) are grown to confluence in tissue culture plates in medium such as DMEM supplemented with fetal calf serum and optionally, nutrient components and/or antibiotics. About 10 μ g pRK5-PRO DNA is mixed with about 1 μ g DNA encoding the VA RNA gene [Thimmappaya et al., *Cell*, 31:543 (1982)] and dissolved in 500 μ l of 1 mM Tris-HCl, 0.1 mM EDTA, 0.227 M CaCl_2 . To this mixture is added, dropwise, 500 μ l of 50 mM HEPES (pH 7.35), 280 mM NaCl, 1.5 mM NaPO_4 , and a precipitate is allowed to form for 10 minutes at 25°C. The precipitate is suspended and added to the 293 cells and allowed to settle for about four hours at 37°C. The culture medium is aspirated off and 2 ml of 20% glycerol in PBS is added for 30 seconds. The 293 cells are then washed with serum free medium, fresh medium is added and the cells are incubated for about 5 days.

Approximately 24 hours after the transfections, the culture medium is removed and replaced with culture medium (alone) or culture medium containing 200 μ Ci/ml ^{35}S -cysteine and 200 μ Ci/ml ^{35}S -methionine. After a 12 hour incubation, the conditioned medium is collected, concentrated on a spin filter, and loaded onto a 15% SDS gel. The processed gel may be dried and exposed to film for a selected period of time to reveal the presence of PRO polypeptide. The cultures containing transfected cells may undergo further incubation (in serum free medium) and the medium is tested in selected bioassays.

In an alternative technique, PRO may be introduced into 293 cells transiently using the dextran sulfate method described by Sompayrac et al., *Proc. Natl. Acad. Sci.*, 12:7575 (1981). 293 cells are grown to maximal density in a spinner flask and 700 μ g pRK5-PRO DNA is added. The cells are first concentrated from the spinner flask by centrifugation and washed with PBS. The DNA-dextran precipitate is incubated on the cell pellet for four hours. The cells are treated with 20% glycerol for 90 seconds, washed with tissue culture medium, and re-introduced into the spinner flask containing tissue culture medium, 5 μ g/ml bovine insulin and 0.1 μ g/ml bovine transferrin. After about four days, the conditioned media is centrifuged and filtered to remove cells and debris. The sample containing expressed PRO can then be concentrated and purified by any selected method, such as dialysis and/or column chromatography.

In another embodiment, PRO can be expressed in CHO cells. The pRK5-PRO can be transfected into CHO cells using known reagents such as CaPO_4 or DEAE-dextran. As described above, the cell cultures can be incubated, and the medium replaced with culture medium (alone) or medium containing a radiolabel such as ^{35}S -methionine. After determining the presence of PRO polypeptide, the culture medium may be replaced with serum free medium. Preferably, the cultures are incubated for about 6 days, and then the conditioned medium is harvested. The medium containing the expressed PRO can then be concentrated and purified by any selected method.

Epitope-tagged PRO may also be expressed in host CHO cells. The PRO may be subcloned out of the pRK5 vector. The subclone insert can undergo PCR to fuse in frame with a selected epitope tag such as a poly-his tag into a Baculovirus expression vector. The poly-his tagged PRO insert can then be subcloned into a SV40 driven vector containing a selection marker such as DHFR for selection of stable clones. Finally, the CHO cells can be transfected (as described above) with the SV40 driven vector. Labeling may be performed, as described above, to verify expression. The culture medium containing the expressed poly-His tagged PRO can then be

concentrated and purified by any selected method, such as by Ni^{2+} -chelate affinity chromatography.

PRO may also be expressed in CHO and/or COS cells by a transient expression procedure or in CHO cells by another stable expression procedure.

Stable expression in CHO cells is performed using the following procedure. The proteins are expressed as an IgG construct (immunoadhesin), in which the coding sequences for the soluble forms (e.g. extracellular domains) of the respective proteins are fused to an IgG1 constant region sequence containing the hinge, CH2 and CH2 domains and/or is a poly-His tagged form.

Following PCR amplification, the respective DNAs are subcloned in a CHO expression vector using standard techniques as described in Ausubel et al., Current Protocols of Molecular Biology, Unit 3.16, John Wiley and Sons (1997). CHO expression vectors are constructed to have compatible restriction sites 5' and 3' of the DNA of interest to allow the convenient shuttling of cDNA's. The vector used expression in CHO cells is as described in Lucas et al., Nucl. Acids Res. 24:9 (1774-1779 (1996), and uses the SV40 early promoter/enhancer to drive expression of the cDNA of interest and dihydrofolate reductase (DHFR). DHFR expression permits selection for stable maintenance of the plasmid following transfection.

Twelve micrograms of the desired plasmid DNA is introduced into approximately 10 million CHO cells using commercially available transfection reagents Superfect[®] (Qiagen), Dosper[®] or Fugene[®] (Boehringer Mannheim). The cells are grown as described in Lucas et al., supra. Approximately 3×10^7 cells are frozen in an ampule for further growth and production as described below.

The ampules containing the plasmid DNA are thawed by placement into water bath and mixed by vortexing. The contents are pipetted into a centrifuge tube containing 10 mLs of media and centrifuged at 1000 rpm for 5 minutes. The supernatant is aspirated and the cells are resuspended in 10 mL of selective media (0.2 μm filtered PS20 with 5% 0.2 μm diafiltered fetal bovine serum). The cells are then aliquoted into a 100 mL spinner containing 90 mL of selective media. After 1-2 days, the cells are transferred into a 250 mL spinner filled with 150 mL selective growth medium and incubated at 37°C. After another 2-3 days, 250 mL, 500 mL and 2000 mL spinners are seeded with 3×10^5 cells/mL. The cell media is exchanged with fresh media by centrifugation and resuspension in production medium. Although any suitable CHO media may be employed, a production medium described in U.S. Patent No. 5,122,469, issued June 16, 1992 may actually be used. A 3L production spinner is seeded at 1.2×10^6 cells/mL. On day 0, the cell number pH is determined. On day 1, the spinner is sampled and sparging with filtered air is commenced. On day 2, the spinner is sampled, the temperature shifted to 33°C, and 30 mL of 500 g/L glucose and 0.6 mL of 10% antifoam (e.g., 35% polydimethylsiloxane emulsion, Dow Corning 365 Medical Grade Emulsion) taken. Throughout the production, the pH is adjusted as necessary to keep it at around 7.2. After 10 days, or until the viability dropped below 70%, the cell culture is harvested by centrifugation and filtering through a 0.22 μm filter. The filtrate was either stored at 4°C or immediately loaded onto columns for purification.

For the poly-His tagged constructs, the proteins are purified using a Ni-NTA column (Qiagen). Before purification, imidazole is added to the conditioned media to a concentration of 5 mM. The conditioned media is pumped onto a 6 ml Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 ml/min. at 4°C. After loading, the column is washed with additional

equilibration buffer and the protein eluted with equilibration buffer containing 0.25 M imidazole. The highly purified protein is subsequently desalted into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 ml G25 Superfine (Pharmacia) column and stored at -80°C.

Immunoadhesin (Fc-containing) constructs are purified from the conditioned media as follows. The conditioned medium is pumped onto a 5 ml Protein A column (Pharmacia) which had been equilibrated in 20 mM Na phosphate buffer, pH 6.8. After loading, the column is washed extensively with equilibration buffer before elution with 100 mM citric acid, pH 3.5. The eluted protein is immediately neutralized by collecting 1 ml fractions into tubes containing 275 μ L of 1 M Tris buffer, pH 9. The highly purified protein is subsequently desalted into storage buffer as described above for the poly-His tagged proteins. The homogeneity is assessed by SDS polyacrylamide gels and by N-terminal amino acid sequencing by Edman degradation.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

EXAMPLE 8: Expression of PRO in Yeast

The following method describes recombinant expression of PRO in yeast.

First, yeast expression vectors are constructed for intracellular production or secretion of PRO from the ADH2/GAPDH promoter. DNA encoding PRO and the promoter is inserted into suitable restriction enzyme sites in the selected plasmid to direct intracellular expression of PRO. For secretion, DNA encoding PRO can be cloned into the selected plasmid, together with DNA encoding the ADH2/GAPDH promoter, a native PRO signal peptide or other mammalian signal peptide, or, for example, a yeast alpha-factor or invertase secretory signal/leader sequence, and linker sequences (if needed) for expression of PRO.

Yeast cells, such as yeast strain AB110, can then be transformed with the expression plasmids described above and cultured in selected fermentation media. The transformed yeast supernatants can be analyzed by precipitation with 10% trichloroacetic acid and separation by SDS-PAGE, followed by staining of the gels with Coomassie Blue stain.

Recombinant PRO can subsequently be isolated and purified by removing the yeast cells from the fermentation medium by centrifugation and then concentrating the medium using selected cartridge filters. The concentrate containing PRO may further be purified using selected column chromatography resins.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

EXAMPLE 9: Expression of PRO in Baculovirus-Infected Insect Cells

The following method describes recombinant expression of PRO in Baculovirus-infected insect cells.

The sequence coding for PRO is fused upstream of an epitope tag contained within a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG). A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the sequence encoding PRO or the desired portion of the coding sequence of PRO such as the sequence encoding the extracellular domain of a transmembrane protein or the sequence encoding the mature protein if the protein is extracellular is amplified by PCR with primers complementary to the 5' and 3' regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then

digested with those selected restriction enzymes and subcloned into the expression vector.

Recombinant baculovirus is generated by co-transfecting the above plasmid and BaculoGold™ virus DNA (Pharmingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using lipofectin (commercially available from GIBCO-BRL). After 4 - 5 days of incubation at 28°C, the released viruses are harvested and used for further amplifications. Viral infection and protein expression are performed as described by O'Reilley et al.,
5 Baculovirus expression vectors: A Laboratory Manual, Oxford: Oxford University Press (1994).

Expressed poly-his tagged PRO can then be purified, for example, by Ni²⁺-chelate affinity chromatography as follows. Extracts are prepared from recombinant virus-infected Sf9 cells as described by Rupert et al., Nature, 362:175-179 (1993). Briefly, Sf9 cells are washed, resuspended in sonication buffer (25 mL Hepes, pH 7.9; 12.5 mM MgCl₂; 0.1 mM EDTA; 10% glycerol; 0.1% NP-40; 0.4 M KCl), and sonicated
10 twice for 20 seconds on ice. The sonicates are cleared by centrifugation, and the supernatant is diluted 50-fold in loading buffer (50 mM phosphate, 300 mM NaCl, 10% glycerol, pH 7.8) and filtered through a 0.45 μm filter. A Ni²⁺-NTA agarose column (commercially available from Qiagen) is prepared with a bed volume of 5 mL, washed with 25 mL of water and equilibrated with 25 mL of loading buffer. The filtered cell extract is loaded onto the column at 0.5 mL per minute. The column is washed to baseline A₂₈₀ with loading buffer, at which point
15 fraction collection is started. Next, the column is washed with a secondary wash buffer (50 mM phosphate; 300 mM NaCl, 10% glycerol, pH 6.0), which elutes nonspecifically bound protein. After reaching A₂₈₀ baseline again, the column is developed with a 0 to 500 mM Imidazole gradient in the secondary wash buffer. One mL fractions are collected and analyzed by SDS-PAGE and silver staining or Western blot with Ni²⁺-NTA-conjugated to alkaline phosphatase (Qiagen). Fractions containing the eluted His₁₀-tagged PRO are pooled and dialyzed
20 against loading buffer.

Alternatively, purification of the IgG tagged (or Fc tagged) PRO can be performed using known chromatography techniques, including for instance, Protein A or protein G column chromatography.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

25 EXAMPLE 10: Preparation of Antibodies that Bind PRO

This example illustrates preparation of monoclonal antibodies which can specifically bind PRO.

Techniques for producing the monoclonal antibodies are known in the art and are described, for instance, in Goding, supra. Immunogens that may be employed include purified PRO, fusion proteins containing PRO, and cells expressing recombinant PRO on the cell surface. Selection of the immunogen can be made by the skilled
30 artisan without undue experimentation.

Mice, such as Balb/c, are immunized with the PRO immunogen emulsified in complete Freund's adjuvant and injected subcutaneously or intraperitoneally in an amount from 1-100 micrograms. Alternatively, the immunogen is emulsified in MPL-TDM adjuvant (Ribi Immunochemical Research, Hamilton, MT) and injected into the animal's hind foot pads. The immunized mice are then boosted 10 to 12 days later with additional
35 immunogen emulsified in the selected adjuvant. Thereafter, for several weeks, the mice may also be boosted with additional immunization injections. Serum samples may be periodically obtained from the mice by retro-orbital bleeding for testing in ELISA assays to detect anti-PRO antibodies.

After a suitable antibody titer has been detected, the animals "positive" for antibodies can be injected

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are harvested. The spleen cells are then fused (using 35 % polyethylene glycol) to a selected murine myeloma line such as P3X63AgU.1, available from ATCC, No. CRL 1597. The fusions generate hybridoma cells which can then be plated in 96 well tissue culture plates containing HAT (hypoxanthine, aminopterin, and thymine) medium to inhibit proliferation of non-fused cells, myeloma hybrids, and spleen cell hybrids.

The hybridoma cells will be screened in an ELISA for reactivity against PRO. Determination of "positive" hybridoma cells secreting the desired monoclonal antibodies against PRO is within the skill of one of ordinary skill in the art.

The positive hybridoma cells can be injected intraperitoneally into syngeneic Balb/c mice to produce ascites containing the anti-PRO monoclonal antibodies. Alternatively, the hybridoma cells can be grown in culture flasks or roller bottles. Purification of the monoclonal antibodies produced in the ascites can be accomplished using ammonium sulfate precipitation, followed by gel exclusion chromatography. Alternatively, affinity chromatography based upon binding of antibody to protein A or protein G can be employed.

EXAMPLE 11: Purification of PRO Polypeptides Using Specific Antibodies

Native or recombinant PRO polypeptides may be purified by a variety of standard techniques in the art of protein purification. For example, pro-PRO polypeptide, mature PRO polypeptide, or pre-PRO polypeptide is purified by immunoaffinity chromatography using antibodies specific for the PRO polypeptide of interest. In general, an immunoaffinity column is constructed by covalently coupling the anti-PRO polypeptide antibody to an activated chromatographic resin.

Polyclonal immunoglobulins are prepared from immune sera either by precipitation with ammonium sulfate or by purification on immobilized Protein A (Pharmacia LKB Biotechnology, Piscataway, N.J.). Likewise, monoclonal antibodies are prepared from mouse ascites fluid by ammonium sulfate precipitation.

EXAMPLE 12: Drug Screening

This invention is particularly useful for screening compounds by using PRO polypeptides or binding fragment thereof in any of a variety of drug screening techniques. The PRO polypeptide or fragment employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the PRO polypeptide or fragment. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between PRO polypeptide or a fragment and the agent being tested. Alternatively, one can examine the diminution in complex formation between the PRO polypeptide and its target cell or target receptors caused by the agent being tested.

Thus, the present invention provides methods of screening for drugs or any other agents which can affect a PRO polypeptide-associated disease or disorder. These methods comprise contacting such an agent with an PRO polypeptide or fragment thereof and assaying (i) for the presence of a complex between the agent and the PRO polypeptide or fragment, or (ii) for the presence of a complex between the PRO polypeptide or fragment and the cell, by methods well known in the art. In such competitive binding assays, the PRO polypeptide or fragment is typically labeled. After suitable incubation, free PRO polypeptide or fragment is separated from that present in bound form, and the amount of free or uncomplexed label is a measure of the ability of the particular agent to bind to PRO polypeptide or to interfere with the PRO polypeptide/cell complex.

Another technique for drug screening provides high throughput screening for compounds having suitable binding affinity to a polypeptide and is described in detail in WO 84/03564, published on September 13, 1984. Briefly stated, large numbers of different small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. As applied to a PRO polypeptide, the peptide test compounds are reacted with PRO polypeptide and washed. Bound PRO polypeptide is detected by methods well known in the art. Purified PRO polypeptide can also be coated directly onto plates for use in the aforementioned drug screening techniques. In addition, non-neutralizing antibodies can be used to capture the peptide and immobilize it on the solid support.

This invention also contemplates the use of competitive drug screening assays in which neutralizing antibodies capable of binding PRO polypeptide specifically compete with a test compound for binding to PRO polypeptide or fragments thereof. In this manner, the antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with PRO polypeptide.

EXAMPLE 13: Rational Drug Design

The goal of rational drug design is to produce structural analogs of biologically active polypeptide of interest (*i.e.*, a PRO polypeptide) or of small molecules with which they interact, *e.g.*, agonists, antagonists, or inhibitors. Any of these examples can be used to fashion drugs which are more active or stable forms of the PRO polypeptide or which enhance or interfere with the function of the PRO polypeptide *in vivo* (*c.f.*, Hodgson, Bio/Technology, 9: 19-21 (1991)).

In one approach, the three-dimensional structure of the PRO polypeptide, or of an PRO

polypeptide-inhibitor complex, is determined by x-ray crystallography, by computer modeling or, most typically, by a combination of the two approaches. Both the shape and charges of the PRO polypeptide must be ascertained to elucidate the structure and to determine active site(s) of the molecule. Less often, useful information regarding the structure of the PRO polypeptide may be gained by modeling based on the structure of homologous proteins. In both cases, relevant structural information is used to design analogous PRO polypeptide-like molecules or to identify efficient inhibitors. Useful examples of rational drug design may include molecules which have improved activity or stability as shown by Braxton and Wells, *Biochemistry*, **31**:7796-7801 (1992) or which act as inhibitors, agonists, or antagonists of native peptides as shown by Athauda *et al.*, *J. Biochem.*, **113**:742-746 (1993).

It is also possible to isolate a target-specific antibody, selected by functional assay, as described above, and then to solve its crystal structure. This approach, in principle, yields a pharmacore upon which subsequent drug design can be based. It is possible to bypass protein crystallography altogether by generating anti-idiotypic antibodies (anti-ids) to a functional, pharmacologically active antibody. As a mirror image of a mirror image, the binding site of the anti-ids would be expected to be an analog of the original receptor. The anti-id could then be used to identify and isolate peptides from banks of chemically or biologically produced peptides. The isolated peptides would then act as the pharmacore.

By virtue of the present invention, sufficient amounts of the PRO polypeptide may be made available to perform such analytical studies as X-ray crystallography. In addition, knowledge of the PRO polypeptide amino acid sequence provided herein will provide guidance to those employing computer modeling techniques in place of or in addition to x-ray crystallography.

EXAMPLE 14: Identification of PRO Polypeptides That Stimulate TNF- α Release In Human Blood (Assay 128)

This assay shows that certain PRO polypeptides of the present invention act to stimulate the release of TNF- α in human blood. PRO polypeptides testing positive in this assay are useful for, among other things, research purposes where stimulation of the release of TNF- α would be desired and for the therapeutic treatment of conditions wherein enhanced TNF- α release would be beneficial. Specifically, 200 μ l of human blood supplemented with 50mM Hepes buffer (pH 7.2) is aliquoted per well in a 96 well test plate. To each well is then added 300 μ l of either the test PRO polypeptide in 50 mM Hepes buffer (at various concentrations) or 50 mM Hepes buffer alone (negative control) and the plates are incubated at 37°C for 6 hours. The samples are then centrifuged and 50 μ l of plasma is collected from each well and tested for the presence of TNF- α by ELISA assay. A positive in the assay is a higher amount of TNF- α in the PRO polypeptide treated samples as compared to the negative control samples.

The following PRO polypeptides tested positive in this assay:

PRO1079, PRO827, PRO791, PRO1131, PRO1316, PRO1183, PRO1343, PRO1760, PRO1567, and PRO4333.

EXAMPLE 15: Promotion of Chondrocyte Redifferentiation (Assay 129)

This assay is designed to determine whether PRO polypeptides of the present invention show the ability to induce the proliferation and/or redifferentiation of chondrocytes in culture. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of various bone and/or cartilage

disorders such as, for example, sports injuries and arthritis.

Porcine chondrocytes are isolated by overnight collagenase digestion of articular cartilage of the metacarpophalangeal joint of 4-6 month old female pigs. The isolated cells are then seeded at 25,000 cells/cm² in Ham F-12 containing 10% FBS and 4 µg/ml gentamycin. The culture media is changed every third day. On day 12, the cells are seeded in 96 well plates at 5,000 cells/well in 100 µl of the same media without serum and 100 µl of either serum-free medium (negative control), staurosporin (final concentration of 5 nM; positive control) or the test PRO polypeptide are added to give a final volume of 200 µl/well. After 5 days at 37°C, 22 µl of media containing 100 µg/ml Hoechst 33342 and 50 µg/ml 5-CFDA is added to each well and incubated for an additional 10 minutes at 37°C. A picture of the green fluorescence is taken for each well and the differentiation state of the chondrocytes is calculated by morphometric analysis. A positive result in the assay is obtained when the >50% of the PRO polypeptide treated cells are differentiated (compared to the background obtained by the negative control).

PRO6029 polypeptide tested positive in this assay.

EXAMPLE 16: Microarray Analysis to Detect Overexpression of PRO Polypeptides in Cancerous Tumors

Nucleic acid microarrays, often containing thousands of gene sequences, are useful for identifying differentially expressed genes in diseased tissues as compared to their normal counterparts. Using nucleic acid microarrays, test and control mRNA samples from test and control tissue samples are reverse transcribed and labeled to generate cDNA probes. The cDNA probes are then hybridized to an array of nucleic acids immobilized on a solid support. The array is configured such that the sequence and position of each member of the array is known. For example, a selection of genes known to be expressed in certain disease states may be arrayed on a solid support. Hybridization of a labeled probe with a particular array member indicates that the sample from which the probe was derived expresses that gene. If the hybridization signal of a probe from a test (disease tissue) sample is greater than hybridization signal of a probe from a control (normal tissue) sample, the gene or genes overexpressed in the disease tissue are identified. The implication of this result is that an overexpressed protein in a diseased tissue is useful not only as a diagnostic marker for the presence of the disease condition, but also as a therapeutic target for treatment of the disease condition.

The methodology of hybridization of nucleic acids and microarray technology is well known in the art. In the present example, the specific preparation of nucleic acids for hybridization and probes, slides, and hybridization conditions are all detailed in U.S. Provisional Patent Application Serial No. 60/193,767, filed on March 31, 2000 and which is herein incorporated by reference.

In the present example, cancerous tumors derived from various human tissues were studied for PRO polypeptide-encoding gene expression relative to non-cancerous human tissue in an attempt to identify those PRO polypeptides which are overexpressed in cancerous tumors. Two sets of experimental data were generated. In one set, cancerous human colon tumor tissue and matched non-cancerous human colon tumor tissue from the same patient ("matched colon control") were obtained and analyzed for PRO polypeptide expression using the above described microarray technology. In the second set of data, cancerous human tumor tissue from any of a variety of different human tumors was obtained and compared to a "universal" epithelial control sample which was

prepared by pooling non-cancerous human tissues of epithelial origin, including liver, kidney, and lung. mRNA isolated from the pooled tissues represents a mixture of expressed gene products from these different tissues. Microarray hybridization experiments using the pooled control samples generated a linear plot in a 2-color analysis. The slope of the line generated in a 2-color analysis was then used to normalize the ratios of (test:control detection) within each experiment. The normalized ratios from various experiments were then compared and used to identify clustering of gene expression. Thus, the pooled "universal control" sample not only allowed effective relative gene expression determinations in a simple 2-sample comparison, it also allowed multi-sample comparisons across several experiments.

In the present experiments, nucleic acid probes derived from the herein described PRO polypeptide-encoding nucleic acid sequences were used in the creation of the microarray and RNA from the tumor tissues

above this cutoff ratio were determined to be , demonstrating that various PRO polypeptides s human tumor tissues as compared to a non-demonstrate that the PRO polypeptides of the e presence of one or more cancerous tumors, nors.

was designated as a "cutoff ratio". Only values that were at significant. Table 8 below shows the results of these experiments, of the preent invention are significantly overexpressed in variou cancerous human tissue control. As described above, these data present invention are useful not only as diagnostic markers for th but also serve as therapeutic targets for the treatment of those tun

Table 8

<u>as compared to:</u>	<u>Molecule</u>	<u>is overexpressed in:</u>
universal normal control	PRO276	lung tumor
universal normal control	PRO284	colon tumor
universal normal control	PRO284	lung tumor
universal normal control	PRO284	breast tumor
universal normal control	PRO193	colon tumor
universal normal control	PRO193	lung tumor
universal normal control	PRO193	breast tumor
universal normal control	PRO193	prostate tumor

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO234	colon tumor	universal normal control
	PRO234	lung tumor	universal normal control
	PRO234	breast tumor	universal normal control
5	PRO234	liver tumor	universal normal control
	PRO236	colon tumor	universal normal control
	PRO236	lung tumor	universal normal control
	PRO236	breast tumor	universal normal control
	PRO244	colon tumor	universal normal control
10	PRO244	lung tumor	universal normal control
	PRO262	colon tumor	universal normal control
	PRO262	lung tumor	universal normal control
	PRO262	breast tumor	universal normal control
	PRO271	colon tumor	universal normal control
15	PRO271	lung tumor	universal normal control
	PRO268	colon tumor	universal normal control
	PRO268	lung tumor	universal normal control
	PRO268	breast tumor	universal normal control
	PRO270	colon tumor	universal normal control
20	PRO270	lung tumor	universal normal control
	PRO270	breast tumor	universal normal control
	PRO270	liver tumor	universal normal control
	PRO355	lung tumor	universal normal control
	PRO355	breast tumor	universal normal control
25	PRO355	prostate tumor	universal normal control
	PRO298	colon tumor	universal normal control
	PRO298	lung tumor	universal normal control
	PRO298	breast tumor	universal normal control
	PRO299	colon tumor	universal normal control
30	PRO299	lung tumor	universal normal control
	PRO299	breast tumor	universal normal control
	PRO296	colon tumor	universal normal control
	PRO296	breast tumor	universal normal control
	PRO329	colon tumor	universal normal control
35	PRO329	lung tumor	universal normal control
	PRO329	breast tumor	universal normal control
	PRO330	colon tumor	universal normal control
	PRO330	lung tumor	universal normal control
	PRO294	lung tumor	universal normal control
40	PRO294	breast tumor	universal normal control
	PRO300	colon tumor	universal normal control
	PRO300	lung tumor	universal normal control
	PRO300	breast tumor	universal normal control
	PRO307	lung tumor	universal normal control
45	PRO334	colon tumor	universal normal control
	PRO334	lung tumor	universal normal control
	PRO334	breast tumor	universal normal control
	PRO334	prostate tumor	universal normal control
	PRO352	colon tumor	universal normal control
50	PRO352	lung tumor	universal normal control
	PRO352	breast tumor	universal normal control
	PRO352	liver tumor	universal normal control
	PRO710	breast tumor	universal normal control
	PRO873	colon tumor	universal normal control
55	PRO873	lung tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO873	breast tumor	universal normal control
	PRO873	prostate tumor	universal normal control
	PRO354	colon tumor	universal normal control
5	PRO354	lung tumor	universal normal control
	PRO354	breast tumor	universal normal control
	PRO1151	lung tumor	universal normal control
	PRO1151	breast tumor	universal normal control
	PRO382	colon tumor	universal normal control
10	PRO382	lung tumor	universal normal control
	PRO382	breast tumor	universal normal control
	PRO1864	lung tumor	universal normal control
	PRO1864	breast tumor	universal normal control
	PRO1864	liver tumor	universal normal control
15	PRO386	colon tumor	universal normal control
	PRO386	lung tumor	universal normal control
	PRO386	prostate tumor	universal normal control
	PRO541	colon tumor	universal normal control
	PRO541	lung tumor	universal normal control
20	PRO541	breast tumor	universal normal control
	PRO852	breast tumor	universal normal control
	PRO700	colon tumor	universal normal control
	PRO700	lung tumor	universal normal control
	PRO700	breast tumor	universal normal control
25	PRO700	rectal tumor	universal normal control
	PRO708	colon tumor	universal normal control
	PRO708	lung tumor	universal normal control
	PRO708	breast tumor	universal normal control
	PRO707	colon tumor	universal normal control
30	PRO707	lung tumor	universal normal control
	PRO864	colon tumor	universal normal control
	PRO864	lung tumor	universal normal control
	PRO864	breast tumor	universal normal control
	PRO706	colon tumor	universal normal control
35	PRO706	lung tumor	universal normal control
	PRO706	breast tumor	universal normal control
	PRO706	liver tumor	universal normal control
	PRO732	lung tumor	universal normal control
	PRO732	breast tumor	universal normal control
40	PRO732	cervical tumor	universal normal control
	PRO537	colon tumor	universal normal control
	PRO537	lung tumor	universal normal control
	PRO537	breast tumor	universal normal control
	PRO545	lung tumor	universal normal control
45	PRO545	breast tumor	universal normal control
	PRO718	lung tumor	universal normal control
	PRO718	breast tumor	universal normal control
	PRO872	lung tumor	universal normal control
	PRO872	breast tumor	universal normal control
50	PRO872	liver tumor	universal normal control
	PRO704	colon tumor	universal normal control
	PRO704	lung tumor	universal normal control
	PRO704	breast tumor	universal normal control
	PRO705	lung tumor	universal normal control
55	PRO705	breast tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO871	lung tumor	universal normal control
	PRO871	breast tumor	universal normal control
	PRO871	liver tumor	universal normal control
5	PRO702	lung tumor	universal normal control
	PRO944	colon tumor	universal normal control
	PRO944	lung tumor	universal normal control
	PRO944	rectal tumor	universal normal control
	PRO739	lung tumor	universal normal control
10	PRO739	breast tumor	universal normal control
	PRO739	prostate tumor	universal normal control
	PRO941	colon tumor	universal normal control
	PRO941	lung tumor	universal normal control
	PRO941	breast tumor	universal normal control
15	PRO941	rectal tumor	universal normal control
	PRO1082	lung tumor	universal normal control
	PRO1082	breast tumor	universal normal control
	PRO1133	colon tumor	universal normal control
	PRO1133	lung tumor	universal normal control
20	PRO983	colon tumor	universal normal control
	PRO983	lung tumor	universal normal control
	PRO983	breast tumor	universal normal control
	PRO784	colon tumor	universal normal control
	PRO784	lung tumor	universal normal control
25	PRO784	breast tumor	universal normal control
	PRO784	prostate tumor	universal normal control
	PRO783	colon tumor	universal normal control
	PRO783	lung tumor	universal normal control
	PRO783	breast tumor	universal normal control
30	PRO783	liver tumor	universal normal control
	PRO940	colon tumor	universal normal control
	PRO940	lung tumor	universal normal control
	PRO940	breast tumor	universal normal control
	PRO768	colon tumor	universal normal control
35	PRO768	lung tumor	universal normal control
	PRO768	breast tumor	universal normal control
	PRO1079	colon tumor	universal normal control
	PRO1079	lung tumor	universal normal control
	PRO1079	breast tumor	universal normal control
40	PRO1079	rectal tumor	universal normal control
	PRO1078	colon tumor	universal normal control
	PRO1078	lung tumor	universal normal control
	PRO1018	colon tumor	universal normal control
	PRO1018	lung tumor	universal normal control
45	PRO1018	breast tumor	universal normal control
	PRO793	colon tumor	universal normal control
	PRO793	lung tumor	universal normal control
	PRO793	breast tumor	universal normal control
	PRO793	rectal tumor	universal normal control
50	PRO1773	colon tumor	universal normal control
	PRO1773	lung tumor	universal normal control
	PRO1773	prostate tumor	universal normal control
	PRO1014	lung tumor	universal normal control
	PRO1014	breast tumor	universal normal control
55	PRO1013	colon tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO1013	lung tumor	universal normal control
	PRO1013	breast tumor	universal normal control
	PRO1013	liver tumor	universal normal control
5	PRO937	colon tumor	universal normal control
	PRO937	lung tumor	universal normal control
	PRO937	breast tumor	universal normal control
	PRO937	cervical tumor	universal normal control
	PRO937	rectal tumor	universal normal control
10	PRO1477	lung tumor	universal normal control
	PRO1477	breast tumor	universal normal control
	PRO1477	rectal tumor	universal normal control
	PRO842	colon tumor	universal normal control
	PRO842	lung tumor	universal normal control
15	PRO842	breast tumor	universal normal control
	PRO839	colon tumor	universal normal control
	PRO1180	colon tumor	universal normal control
	PRO1180	lung tumor	universal normal control
	PRO1180	liver tumor	universal normal control
20	PRO1134	lung tumor	universal normal control
	PRO1134	breast tumor	universal normal control
	PRO1134	prostate tumor	universal normal control
	PRO1115	colon tumor	universal normal control
	PRO1115	lung tumor	universal normal control
25	PRO1115	breast tumor	universal normal control
	PRO1277	colon tumor	universal normal control
	PRO1277	lung tumor	universal normal control
	PRO1135	lung tumor	universal normal control
	PRO1135	breast tumor	universal normal control
30	PRO1135	cervical tumor	universal normal control
	PRO827	colon tumor	universal normal control
	PRO827	lung tumor	universal normal control
	PRO827	prostate tumor	universal normal control
	PRO827	cervical tumor	universal normal control
35	PRO1057	lung tumor	universal normal control
	PRO1057	breast tumor	universal normal control
	PRO1113	colon tumor	universal normal control
	PRO1113	lung tumor	universal normal control
	PRO1006	colon tumor	universal normal control
40	PRO1006	lung tumor	universal normal control
	PRO1006	breast tumor	universal normal control
	PRO1006	rectal tumor	universal normal control
	PRO1074	lung tumor	universal normal control
	PRO1074	rectal tumor	universal normal control
45	PRO1073	lung tumor	universal normal control
	PRO1073	breast tumor	universal normal control
	PRO1136	colon tumor	universal normal control
	PRO1136	lung tumor	universal normal control
	PRO1136	breast tumor	universal normal control
50	PRO1004	lung tumor	universal normal control
	PRO1344	colon tumor	universal normal control
	PRO1344	lung tumor	universal normal control
	PRO1344	breast tumor	universal normal control
	PRO1344	rectal tumor	universal normal control
55	PRO1110	colon tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO1110	lung tumor	universal normal control
	PRO1110	breast tumor	universal normal control
	PRO1378	colon tumor	universal normal control
5	PRO1378	lung tumor	universal normal control
	PRO1378	prostate tumor	universal normal control
	PRO1378	cervical tumor	universal normal control
	PRO1481	colon tumor	universal normal control
	PRO1481	lung tumor	universal normal control
10	PRO1109	lung tumor	universal normal control
	PRO1109	breast tumor	universal normal control
	PRO1383	colon tumor	universal normal control
	PRO1383	lung tumor	universal normal control
	PRO1383	breast tumor	universal normal control
15	PRO1072	lung tumor	universal normal control
	PRO1189	colon tumor	universal normal control
	PRO1189	lung tumor	universal normal control
	PRO1189	breast tumor	universal normal control
	PRO1189	prostate tumor	universal normal control
20	PRO1003	colon tumor	universal normal control
	PRO1003	lung tumor	universal normal control
	PRO1003	breast tumor	universal normal control
	PRO1003	liver tumor	universal normal control
	PRO1003	rectal tumor	universal normal control
25	PRO1108	colon tumor	universal normal control
	PRO1108	lung tumor	universal normal control
	PRO1108	breast tumor	universal normal control
	PRO1137	colon tumor	universal normal control
	PRO1137	lung tumor	universal normal control
30	PRO1137	breast tumor	universal normal control
	PRO1138	colon tumor	universal normal control
	PRO1138	lung tumor	universal normal control
	PRO1138	breast tumor	universal normal control
	PRO1415	colon tumor	universal normal control
35	PRO1415	lung tumor	universal normal control
	PRO1415	prostate tumor	universal normal control
	PRO1054	lung tumor	universal normal control
	PRO1054	breast tumor	universal normal control
40	PRO994	colon tumor	universal normal control
	PRO994	lung tumor	universal normal control
	PRO994	rectal tumor	universal normal control
	PRO1069	lung tumor	universal normal control
	PRO1069	breast tumor	universal normal control
	PRO1411	colon tumor	universal normal control
45	PRO1411	lung tumor	universal normal control
	PRO1129	lung tumor	universal normal control
	PRO1129	rectal tumor	universal normal control
	PRO1359	colon tumor	universal normal control
	PRO1359	lung tumor	universal normal control
50	PRO1359	breast tumor	universal normal control
	PRO1359	prostate tumor	universal normal control
	PRO1139	lung tumor	universal normal control
	PRO1065	lung tumor	universal normal control
	PRO1028	colon tumor	universal normal control
55	PRO1028	lung tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO1028	breast tumor	universal normal control
	PRO1028	cervical tumor	universal normal control
	PRO1027	colon tumor	universal normal control
5	PRO1027	lung tumor	universal normal control
	PRO1027	breast tumor	universal normal control
	PRO1140	colon tumor	universal normal control
	PRO1140	breast tumor	universal normal control
	PRO1291	colon tumor	universal normal control
10	PRO1291	breast tumor	universal normal control
	PRO1105	colon tumor	universal normal control
	PRO1105	lung tumor	universal normal control
	PRO1026	lung tumor	universal normal control
	PRO1026	prostate tumor	universal normal control
15	PRO1104	colon tumor	universal normal control
	PRO1104	lung tumor	universal normal control
	PRO1104	breast tumor	universal normal control
	PRO1100	colon tumor	universal normal control
	PRO1100	lung tumor	universal normal control
20	PRO1100	breast tumor	universal normal control
	PRO1100	rectal tumor	universal normal control
	PRO1141	lung tumor	universal normal control
	PRO1772	colon tumor	universal normal control
	PRO1772	lung tumor	universal normal control
25	PRO1772	breast tumor	universal normal control
	PRO1772	cervical tumor	universal normal control
	PRO1064	colon tumor	universal normal control
	PRO1064	lung tumor	universal normal control
	PRO1379	colon tumor	universal normal control
30	PRO1379	lung tumor	universal normal control
	PRO1379	cervical tumor	universal normal control
	PRO3573	lung tumor	universal normal control
	PRO3573	breast tumor	universal normal control
	PRO3566	colon tumor	universal normal control
35	PRO3566	lung tumor	universal normal control
	PRO1156	lung tumor	universal normal control
	PRO1156	breast tumor	universal normal control
	PRO1156	prostate tumor	universal normal control
	PRO1098	colon tumor	universal normal control
40	PRO1098	lung tumor	universal normal control
	PRO1098	rectal tumor	universal normal control
	PRO1128	colon tumor	universal normal control
	PRO1128	lung tumor	universal normal control
	PRO1128	breast tumor	universal normal control
45	PRO1248	lung tumor	universal normal control
	PRO1248	breast tumor	universal normal control
	PRO1127	colon tumor	universal normal control
	PRO1127	lung tumor	universal normal control
	PRO1127	breast tumor	universal normal control
50	PRO1316	colon tumor	universal normal control
	PRO1316	lung tumor	universal normal control
	PRO1316	breast tumor	universal normal control
	PRO1197	colon tumor	universal normal control
	PRO1197	lung tumor	universal normal control
55	PRO1197	breast tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO1125	lung tumor	universal normal control
	PRO1158	breast tumor	universal normal control
	PRO1124	colon tumor	universal normal control
5	PRO1124	lung tumor	universal normal control
	PRO1380	colon tumor	universal normal control
	PRO1380	lung tumor	universal normal control
	PRO1380	breast tumor	universal normal control
	PRO1380	liver tumor	universal normal control
10	PRO1377	colon tumor	universal normal control
	PRO1377	lung tumor	universal normal control
	PRO1287	lung tumor	universal normal control
	PRO1287	breast tumor	universal normal control
	PRO1249	lung tumor	universal normal control
15	PRO1249	breast tumor	universal normal control
	PRO1335	colon tumor	universal normal control
	PRO1335	lung tumor	universal normal control
	PRO1335	breast tumor	universal normal control
	PRO3572	lung tumor	universal normal control
20	PRO1599	colon tumor	universal normal control
	PRO1599	lung tumor	universal normal control
	PRO1599	breast tumor	universal normal control
	PRO1374	lung tumor	universal normal control
	PRO1374	breast tumor	universal normal control
25	PRO1345	lung tumor	universal normal control
	PRO1345	breast tumor	universal normal control
	PRO1311	lung tumor	universal normal control
	PRO1311	breast tumor	universal normal control
	PRO1357	colon tumor	universal normal control
30	PRO1357	lung tumor	universal normal control
	PRO1557	colon tumor	universal normal control
	PRO1557	lung tumor	universal normal control
	PRO1557	breast tumor	universal normal control
	PRO1305	colon tumor	universal normal control
35	PRO1305	lung tumor	universal normal control
	PRO1305	breast tumor	universal normal control
	PRO1302	colon tumor	universal normal control
	PRO1302	lung tumor	universal normal control
	PRO1302	breast tumor	universal normal control
40	PRO1302	rectal tumor	universal normal control
	PRO1266	colon tumor	universal normal control
	PRO1336	colon tumor	universal normal control
	PRO1336	lung tumor	universal normal control
	PRO1336	breast tumor	universal normal control
45	PRO1278	colon tumor	universal normal control
	PRO1278	lung tumor	universal normal control
	PRO1270	breast tumor	universal normal control
	PRO1298	colon tumor	universal normal control
	PRO1298	lung tumor	universal normal control
50	PRO1301	lung tumor	universal normal control
	PRO1301	breast tumor	universal normal control
	PRO1268	colon tumor	universal normal control
	PRO1268	breast tumor	universal normal control
	PRO1327	lung tumor	universal normal control
55	PRO1327	breast tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO1328	colon tumor	universal normal control
	PRO1328	lung tumor	universal normal control
	PRO1328	breast tumor	universal normal control
5	PRO1329	colon tumor	universal normal control
	PRO1329	lung tumor	universal normal control
	PRO1329	breast tumor	universal normal control
	PRO1339	colon tumor	universal normal control
	PRO1339	lung tumor	universal normal control
10	PRO1342	colon tumor	universal normal control
	PRO1342	lung tumor	universal normal control
	PRO1342	breast tumor	universal normal control
	PRO1342	rectal tumor	universal normal control
	PRO1487	colon tumor	universal normal control
15	PRO1487	breast tumor	universal normal control
	PRO3579	lung tumor	universal normal control
	PRO3579	breast tumor	universal normal control
	PRO1472	colon tumor	universal normal control
	PRO1472	lung tumor	universal normal control
20	PRO1385	lung tumor	universal normal control
	PRO1385	breast tumor	universal normal control
	PRO1461	colon tumor	universal normal control
	PRO1461	lung tumor	universal normal control
	PRO1461	breast tumor	universal normal control
25	PRO1429	colon tumor	universal normal control
	PRO1429	lung tumor	universal normal control
	PRO1429	breast tumor	universal normal control
	PRO1568	lung tumor	universal normal control
	PRO1568	breast tumor	universal normal control
30	PRO1569	colon tumor	universal normal control
	PRO1569	lung tumor	universal normal control
	PRO1569	breast tumor	universal normal control
	PRO1753	colon tumor	universal normal control
	PRO1753	lung tumor	universal normal control
35	PRO1570	colon tumor	universal normal control
	PRO1570	lung tumor	universal normal control
	PRO1570	breast tumor	universal normal control
	PRO1570	prostate tumor	universal normal control
	PRO1570	rectal tumor	universal normal control
40	PRO1559	colon tumor	universal normal control
	PRO1559	lung tumor	universal normal control
	PRO1559	breast tumor	universal normal control
	PRO1486	lung tumor	universal normal control
	PRO1486	breast tumor	universal normal control
45	PRO1433	colon tumor	universal normal control
	PRO1433	lung tumor	universal normal control
	PRO1433	breast tumor	universal normal control
	PRO1433	rectal tumor	universal normal control
	PRO1490	lung tumor	universal normal control
50	PRO1490	breast tumor	universal normal control
	PRO1482	lung tumor	universal normal control
	PRO1482	breast tumor	universal normal control
	PRO1409	colon tumor	universal normal control
	PRO1409	lung tumor	universal normal control
55	PRO1409	breast tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO1446	colon tumor	universal normal control
	PRO1446	lung tumor	universal normal control
	PRO1446	breast tumor	universal normal control
5	PRO1446	prostate tumor	universal normal control
	PRO1604	colon tumor	universal normal control
	PRO1604	lung tumor	universal normal control
	PRO1604	breast tumor	universal normal control
	PRO1491	colon tumor	universal normal control
10	PRO1491	lung tumor	universal normal control
	PRO1491	breast tumor	universal normal control
	PRO1431	colon tumor	universal normal control
	PRO1431	lung tumor	universal normal control
	PRO1563	colon tumor	universal normal control
15	PRO1563	lung tumor	universal normal control
	PRO1563	breast tumor	universal normal control
	PRO1571	colon tumor	universal normal control
	PRO1571	lung tumor	universal normal control
	PRO1571	breast tumor	universal normal control
20	PRO1572	lung tumor	universal normal control
	PRO1572	prostate tumor	universal normal control
	PRO1573	lung tumor	universal normal control
	PRO1573	breast tumor	universal normal control
	PRO1508	lung tumor	universal normal control
25	PRO1508	breast tumor	universal normal control
	PRO1485	colon tumor	universal normal control
	PRO1485	lung tumor	universal normal control
	PRO1564	colon tumor	universal normal control
	PRO1564	lung tumor	universal normal control
30	PRO1564	breast tumor	universal normal control
	PRO1550	colon tumor	universal normal control
	PRO1550	lung tumor	universal normal control
	PRO1550	breast tumor	universal normal control
	PRO1757	lung tumor	universal normal control
35	PRO1757	breast tumor	universal normal control
	PRO1757	prostate tumor	universal normal control
	PRO1758	lung tumor	universal normal control
	PRO1781	colon tumor	universal normal control
	PRO1781	lung tumor	universal normal control
40	PRO1781	breast tumor	universal normal control
	PRO1606	lung tumor	universal normal control
	PRO1606	breast tumor	universal normal control
	PRO1784	colon tumor	universal normal control
	PRO1784	lung tumor	universal normal control
45	PRO1784	breast tumor	universal normal control
	PRO1774	colon tumor	universal normal control
	PRO1774	lung tumor	universal normal control
	PRO1774	breast tumor	universal normal control
	PRO1605	colon tumor	universal normal control
50	PRO1605	lung tumor	universal normal control
	PRO1605	prostate tumor	universal normal control
	PRO1928	colon tumor	universal normal control
	PRO1928	lung tumor	universal normal control
	PRO1928	cervical tumor	universal normal control
55	PRO1865	lung tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO1865	liver tumor	universal normal control
	PRO1925	lung tumor	universal normal control
	PRO1926	liver tumor	universal normal control
5	PRO2630	colon tumor	universal normal control
	PRO2630	lung tumor	universal normal control
	PRO2630	breast tumor	universal normal control
	PRO2630	liver tumor	universal normal control
	PRO3443	colon tumor	universal normal control
10	PRO3443	lung tumor	universal normal control
	PRO3443	breast tumor	universal normal control
	PRO3301	colon tumor	universal normal control
	PRO3301	lung tumor	universal normal control
	PRO3301	breast tumor	universal normal control
15	PRO3301	rectal tumor	universal normal control
	PRO3442	colon tumor	universal normal control
	PRO3442	lung tumor	universal normal control
	PRO3442	rectal tumor	universal normal control
	PRO4978	colon tumor	universal normal control
20	PRO4978	lung tumor	universal normal control
	PRO4978	breast tumor	universal normal control
	PRO4978	rectal tumor	universal normal control
	PRO5801	colon tumor	universal normal control
	PRO5801	breast tumor	universal normal control
25	PRO19630	colon tumor	universal normal control
	PRO203	colon tumor	universal normal control
	PRO204	colon tumor	universal normal control
	PRO204	lung tumor	universal normal control
	PRO204	breast tumor	universal normal control
30	PRO204	prostate tumor	universal normal control
	PRO210	colon tumor	universal normal control
	PRO210	lung tumor	universal normal control
	PRO223	lung tumor	universal normal control
	PRO223	breast tumor	universal normal control
35	PRO247	colon tumor	universal normal control
	PRO247	lung tumor	universal normal control
	PRO247	breast	universal normal control
	PRO358	lung tumor	universal normal control
	PRO358	breast tumor	universal normal control
40	PRO358	prostate tumor	universal normal control
	PRO724	lung tumor	universal normal control
	PRO868	colon tumor	universal normal control
	PRO868	lung tumor	universal normal control
	PRO868	prostate tumor	universal normal control
45	PRO868	rectal tumor	universal normal control
	PRO740	colon tumor	universal normal control
	PRO1478	colon tumor	universal normal control
	PRO1478	lung tumor	universal normal control
	PRO162	colon tumor	universal normal control
50	PRO162	lung tumor	universal normal control
	PRO162	breast tumor	universal normal control
	PRO828	colon tumor	universal normal control
	PRO828	lung tumor	universal normal control
	PRO828	breast tumor	universal normal control
55	PRO828	cervical tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO828	liver tumor	universal normal control
	PRO819	lung tumor	universal normal control
	PRO819	breast tumor	universal normal control
5	PRO819	rectal tumor	universal normal control
	PRO813	colon tumor	universal normal control
	PRO813	lung tumor	universal normal control
	PRO813	breast tumor	universal normal control
	PRO813	prostate tumor	universal normal control
10	PRO1194	colon tumor	universal normal control
	PRO1194	lung tumor	universal normal control
	PRO1194	breast tumor	universal normal control
	PRO887	colon tumor	universal normal control
	PRO887	lung tumor	universal normal control
15	PRO887	rectal tumor	universal normal control
	PRO1071	colon tumor	universal normal control
	PRO1071	lung tumor	universal normal control
	PRO1071	breast tumor	universal normal control
	PRO1029	colon tumor	universal normal control
20	PRO1029	lung tumor	universal normal control
	PRO1029	breast tumor	universal normal control
	PRO1190	lung tumor	universal normal control
	PRO1190	breast tumor	universal normal control
	PRO4334	lung tumor	universal normal control
25	PRO1155	colon tumor	universal normal control
	PRO1155	lung tumor	universal normal control
	PRO1157	breast tumor	universal normal control
	PRO1157	cervical tumor	universal normal control
	PRO1122	lung tumor	universal normal control
30	PRO1122	breast tumor	universal normal control
	PRO1183	colon tumor	universal normal control
	PRO1183	lung tumor	universal normal control
	PRO1183	breast tumor	universal normal control
	PRO1337	colon tumor	universal normal control
35	PRO1337	lung tumor	universal normal control
	PRO1337	breast tumor	universal normal control
	PRO1480	colon tumor	universal normal control
	PRO1480	lung tumor	universal normal control
	PRO1480	breast tumor	universal normal control
40	PRO19645	colon tumor	universal normal control
	PRO9782	colon tumor	universal normal control
	PRO1419	colon tumor	universal normal control
	PRO1575	colon tumor	universal normal control
	PRO1575	lung tumor	universal normal control
45	PRO1567	colon tumor	universal normal control
	PRO1567	lung tumor	universal normal control
	PRO1567	breast tumor	universal normal control
	PRO1891	colon tumor	universal normal control
	PRO1889	colon tumor	universal normal control
50	PRO1889	lung tumor	universal normal control
	PRO1785	lung tumor	universal normal control
	PRO1785	prostate tumor	universal normal control
	PRO6003	colon tumor	universal normal control
	PRO4333	colon tumor	universal normal control
55	PRO4356	colon tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO4352	colon tumor	universal normal control
	PRO4354	colon tumor	universal normal control
	PRO4354	lung tumor	universal normal control
5	PRO4354	prostate tumor	universal normal control
	PRO4369	colon tumor	universal normal control
	PRO6030	colon tumor	universal normal control
	PRO4433	colon tumor	universal normal control
	PRO4424	colon tumor	universal normal control
10	PRO4424	breast tumor	universal normal control
	PRO6017	colon tumor	universal normal control
	PRO19563	colon tumor	universal normal control
	PRO6015	colon tumor	universal normal control
	PRO5779	colon tumor	universal normal control
15	PRO5776	colon tumor	universal normal control
	PRO4430	lung tumor	universal normal control
	PRO4421	colon tumor	universal normal control
	PRO4499	colon tumor	universal normal control
	PRO4423	colon tumor	universal normal control
20	PRO5998	colon tumor	universal normal control
	PRO5998	lung tumor	universal normal control
	PRO4501	colon tumor	universal normal control
	PRO6240	colon tumor	universal normal control
	PRO6245	colon tumor	universal normal control
25	PRO6175	colon tumor	universal normal control
	PRO9742	colon tumor	universal normal control
	PRO7179	colon tumor	universal normal control
	PRO6239	colon tumor	universal normal control
	PRO6493	colon tumor	universal normal control
30	PRO9741	colon tumor	universal normal control
	PRO9822	colon tumor	universal normal control
	PRO6244	colon tumor	universal normal control
	PRO9740	colon tumor	universal normal control
	PRO9739	colon tumor	universal normal control
35	PRO7177	colon tumor	universal normal control
	PRO7178	colon tumor	universal normal control
	PRO6246	colon tumor	universal normal control
	PRO6241	colon tumor	universal normal control
	PRO9835	colon tumor	universal normal control
40	PRO9857	colon tumor	universal normal control
	PRO7436	colon tumor	universal normal control
	PRO9856	colon tumor	universal normal control
	PRO19605	colon tumor	universal normal control
	PRO9859	colon tumor	universal normal control
45	PRO12970	colon tumor	universal normal control
	PRO19626	colon tumor	universal normal control
	PRO9883	colon tumor	universal normal control
	PRO19670	colon tumor	universal normal control
	PRO19624	colon tumor	universal normal control
50	PRO19680	colon tumor	universal normal control
	PRO19675	colon tumor	universal normal control
	PRO9834	colon tumor	universal normal control
	PRO9744	colon tumor	universal normal control
	PRO19644	colon tumor	universal normal control
55	PRO19625	colon tumor	universal normal control

Table 8 (cont')

	<u>Molecule</u>	<u>is overexpressed in:</u>	<u>as compared to:</u>
	PRO19597	colon tumor	universal normal control
	PRO16090	colon tumor	universal normal control
	PRO19576	colon tumor	universal normal control
5	PRO19646	colon tumor	universal normal control
	PRO19814	colon tumor	universal normal control
	PRO19669	colon tumor	universal normal control
	PRO19818	colon tumor	universal normal control
	PRO20088	colon tumor	universal normal control
10	PRO16089	colon tumor	universal normal control
	PRO20025	colon tumor	universal normal control
	PRO20040	colon tumor	universal normal control
	PRO1760	adrenal tumor	universal normal control
	PRO1760	breast tumor	universal normal control
15	PRO1760	cervical tumor	universal normal control
	PRO1760	colon tumor	universal normal control
	PRO1760	liver tumor	universal normal control
	PRO1760	lung tumor	universal normal control
	PRO1760	prostate tumor	universal normal control
20	PRO1760	rectal tumor	universal normal control
	PRO6029	adrenal tumor	universal normal control
	PRO6029	colon tumor	universal normal control
	PRO6029	prostate tumor	universal normal control
	PRO1801	colon tumor	universal normal control
25	PRO1801	lung tumor	universal normal control

WHAT IS CLAIMED IS:

1. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence that encodes an amino acid sequence selected from the group consisting of the amino acid sequence shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16),
5 Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54),
10 Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92),
15 Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure
20 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure
25 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), Figure 244 (SEQ ID NO:244), Figure 246 (SEQ ID NO:246), Figure 248 (SEQ ID NO:248), Figure 250 (SEQ ID NO:250), Figure 252 (SEQ ID NO:252), Figure 254 (SEQ ID

[illegible]

NO:520), Figure 522 (SEQ ID NO:522), Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ ID NO:528), Figure 530 (SEQ ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534 (SEQ ID NO:534), Figure 536 (SEQ ID NO:536), Figure 538 (SEQ ID NO:538), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ ID NO:542), Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 548 (SEQ ID NO:548), Figure 550 (SEQ ID NO:550), Figure 552 (SEQ ID NO:552), Figure 554 (SEQ ID NO:554), Figure 556 (SEQ ID NO:556), Figure 558 (SEQ ID NO:558), Figure 560 (SEQ ID NO:560), Figure 562 (SEQ ID NO:562), Figure 564 (SEQ ID NO:564), Figure 566 (SEQ ID NO:566), Figure 568 (SEQ ID NO:568), Figure 570 (SEQ ID NO:570), Figure 572 (SEQ ID NO:572), Figure 574 (SEQ ID NO:574), Figure 576 (SEQ ID NO:576), Figure 578 (SEQ ID NO:578), Figure 580 (SEQ ID NO:580), Figure 582 (SEQ ID NO:582), Figure 584 (SEQ ID NO:584), Figure 586 (SEQ ID NO:586), Figure 588 (SEQ ID NO:588), Figure 590 (SEQ ID NO:590), Figure 592 (SEQ ID NO:592), Figure 594 (SEQ ID NO:594), Figure 596 (SEQ ID NO:596), Figure 598 (SEQ ID NO:598), Figure 600 (SEQ ID NO:600), Figure 602 (SEQ ID NO:602), Figure 604 (SEQ ID NO:604), Figure 606 (SEQ ID NO:606), Figure 608 (SEQ ID NO:608), and Figure 610 (SEQ ID NO:610).

2. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of the nucleotide sequence shown in Figure 1 (SEQ ID NO:1), Figure 3 (SEQ ID NO:3), Figure 5 (SEQ ID NO:5), Figure 7 (SEQ ID NO:7), Figure 9 (SEQ ID NO:9), Figure 11 (SEQ ID NO:11), Figure 13 (SEQ ID NO:13), Figure 15 (SEQ ID NO:15), Figure 17 (SEQ ID NO:17), Figure 19 (SEQ ID NO:19), Figure 21 (SEQ ID NO:21), Figure 23 (SEQ ID NO:23), Figure 25 (SEQ ID NO:25), Figure 27 (SEQ ID NO:27), Figure 29 (SEQ ID NO:29), Figure 31 (SEQ ID NO:31), Figure 33 (SEQ ID NO:33), Figure 35 (SEQ ID NO:35), Figure 37 (SEQ ID NO:37), Figure 39 (SEQ ID NO:39), Figure 41 (SEQ ID NO:41), Figure 43 (SEQ ID NO:43), Figure 45 (SEQ ID NO:45), Figure 47 (SEQ ID NO:47), Figure 49 (SEQ ID NO:49), Figure 51 (SEQ ID NO:51), Figure 53 (SEQ ID NO:53), Figure 55 (SEQ ID NO:55), Figure 57 (SEQ ID NO:57), Figure 59 (SEQ ID NO:59), Figure 61 (SEQ ID NO:61), Figure 63 (SEQ ID NO:63), Figure 65 (SEQ ID NO:65), Figure 67 (SEQ ID NO:67), Figure 69 (SEQ ID NO:69), Figure 71 (SEQ ID NO:71), Figure 73 (SEQ ID NO:73), Figures 75A-75B (SEQ ID NO:75), Figure 77 (SEQ ID NO:77), Figure 79 (SEQ ID NO:79), Figure 81 (SEQ ID NO:81), Figure 83 (SEQ ID NO:83), Figure 85 (SEQ ID NO:85), Figure 87 (SEQ ID NO:87), Figure 89 (SEQ ID NO:89), Figure 91 (SEQ ID NO:91), Figure 93 (SEQ ID NO:93), Figure 95 (SEQ ID NO:95), Figure 97 (SEQ ID NO:97), Figure 99 (SEQ ID NO:99), Figure 101 (SEQ ID NO:101), Figure 103 (SEQ ID NO:103), Figure 105 (SEQ ID NO:105), Figure 107 (SEQ ID NO:107), Figure 109 (SEQ ID NO:109), Figure 111 (SEQ ID NO:111), Figure 113 (SEQ ID NO:113), Figure 115 (SEQ ID NO:115), Figure 117 (SEQ ID NO:117), Figure 119 (SEQ ID NO:119), Figure 121 (SEQ ID NO:121), Figure 123 (SEQ ID NO:123), Figure 125 (SEQ ID NO:125), Figure 127 (SEQ ID NO:127), Figure 129 (SEQ ID NO:129), Figure 131 (SEQ ID NO:131), Figure 133 (SEQ ID NO:133), Figure 135 (SEQ ID NO:135), Figure 137 (SEQ ID NO:137), Figure 139 (SEQ ID NO:139), Figure 141 (SEQ ID NO:141), Figure 143 (SEQ ID NO:143), Figure 145 (SEQ ID NO:145), Figure 147 (SEQ ID NO:147), Figure 149 (SEQ ID NO:149), Figure 151 (SEQ ID NO:151), Figure 153 (SEQ ID NO:153), Figure 155 (SEQ ID NO:155), Figure 157 (SEQ ID NO:157), Figure 159 (SEQ ID NO:159), Figure 161 (SEQ ID NO:161), Figure 163 (SEQ ID NO:163), Figure 165 (SEQ ID

NO:165), Figure 167 (SEQ ID NO:167), Figure 169 (SEQ ID NO:169), Figure 171 (SEQ ID NO:171), Figure 173 (SEQ ID NO:173), Figure 175 (SEQ ID NO:175), Figure 177 (SEQ ID NO:177), Figure 179 (SEQ ID NO:179), Figure 181 (SEQ ID NO:181), Figure 183 (SEQ ID NO:183), Figure 185 (SEQ ID NO:185), Figure 187 (SEQ ID NO:187), Figure 189 (SEQ ID NO:189), Figure 191 (SEQ ID NO:191), Figure 193 (SEQ ID NO:193), Figure 195 (SEQ ID NO:195), Figure 197 (SEQ ID NO:197), Figure 199 (SEQ ID NO:199), Figure 201 (SEQ ID NO:201), Figure 203 (SEQ ID NO:203), Figure 205 (SEQ ID NO:205), Figure 207 (SEQ ID NO:207), Figure 209 (SEQ ID NO:209), Figure 211 (SEQ ID NO:211), Figure 213 (SEQ ID NO:213), Figure 215 (SEQ ID NO:215), Figure 217 (SEQ ID NO:217), Figure 219 (SEQ ID NO:219), Figure 221 (SEQ ID NO:221), Figure 223 (SEQ ID NO:223), Figure 225 (SEQ ID NO:225), Figure 227 (SEQ ID NO:227), Figure 229 (SEQ ID NO:229), Figure 231 (SEQ ID NO:231), Figure 233 (SEQ ID NO:233), Figure 235 (SEQ ID NO:235), Figure 237 (SEQ ID NO:237), Figure 239 (SEQ ID NO:239), Figure 241 (SEQ ID NO:241), Figure 243 (SEQ ID NO:243), Figure 245 (SEQ ID NO:245), Figure 247 (SEQ ID NO:247), Figure 249 (SEQ ID NO:249), Figure 251 (SEQ ID NO:251), Figure 253 (SEQ ID NO:253), Figure 255 (SEQ ID NO:255), Figure 257 (SEQ ID NO:257), Figure 259 (SEQ ID NO:259), Figure 261 (SEQ ID NO:261), Figure 263 (SEQ ID NO:263), Figure 265 (SEQ ID NO:265), Figure 267 (SEQ ID NO:267), Figure 269 (SEQ ID NO:269), Figure 271 (SEQ ID NO:271), Figure 273 (SEQ ID NO:273), Figure 275 (SEQ ID NO:275), Figure 277 (SEQ ID NO:277), Figure 279 (SEQ ID NO:279), Figure 281 (SEQ ID NO:281), Figure 283 (SEQ ID NO:283), Figure 285 (SEQ ID NO:285), Figure 287 (SEQ ID NO:287), Figures 289A-289B (SEQ ID NO:289), Figure 291 (SEQ ID NO:291), Figure 293 (SEQ ID NO:293), Figure 295 (SEQ ID NO:295), Figure 297 (SEQ ID NO:297), Figure 299 (SEQ ID NO:299), Figure 301 (SEQ ID NO:301), Figure 303 (SEQ ID NO:303), Figure 305 (SEQ ID NO:305), Figure 307 (SEQ ID NO:307), Figure 309 (SEQ ID NO:309), Figures 311A-311B (SEQ ID NO:311), Figure 313 (SEQ ID NO:313), Figure 315 (SEQ ID NO:315), Figure 317 (SEQ ID NO:317), Figure 319 (SEQ ID NO:319), Figure 321 (SEQ ID NO:321), Figure 323 (SEQ ID NO:323), Figure 325 (SEQ ID NO:325), Figure 327 (SEQ ID NO:327), Figure 329 (SEQ ID NO:329), Figure 331 (SEQ ID NO:331), Figure 333 (SEQ ID NO:333), Figure 335 (SEQ ID NO:335), Figure 337 (SEQ ID NO:337), Figure 339 (SEQ ID NO:339), Figure 341 (SEQ ID NO:341), Figure 343 (SEQ ID NO:343), Figure 345 (SEQ ID NO:345), Figure 347 (SEQ ID NO:347), Figure 349 (SEQ ID NO:349), Figures 351A-351B (SEQ ID NO:351), Figure 353 (SEQ ID NO:353), Figure 355 (SEQ ID NO:355), Figure 357 (SEQ ID NO:357), Figure 359 (SEQ ID NO:359), Figure 361 (SEQ ID NO:361), Figure 363 (SEQ ID NO:363), Figure 365 (SEQ ID NO:365), Figure 367 (SEQ ID NO:367), Figure 369 (SEQ ID NO:369), Figure 371 (SEQ ID NO:371), Figure 373 (SEQ ID NO:373), Figure 375 (SEQ ID NO:375), Figure 377 (SEQ ID NO:377), Figure 379 (SEQ ID NO:379), Figure 381 (SEQ ID NO:381), Figure 383 (SEQ ID NO:383), Figure 385 (SEQ ID NO:385), Figure 387 (SEQ ID NO:387), Figure 389 (SEQ ID NO:389), Figure 391 (SEQ ID NO:391), Figure 393 (SEQ ID NO:393), Figure 395 (SEQ ID NO:395), Figure 397 (SEQ ID NO:397), Figure 399 (SEQ ID NO:399), Figure 401 (SEQ ID NO:401), Figure 403 (SEQ ID NO:403), Figure 405 (SEQ ID NO:405), Figure 407 (SEQ ID NO:407), Figure 409 (SEQ ID NO:409), Figure 411 (SEQ ID NO:411), Figure 413 (SEQ ID NO:413), Figure 415 (SEQ ID NO:415), Figure 417 (SEQ ID NO:417), Figure 419 (SEQ ID NO:419), Figure 421 (SEQ ID NO:421), Figure 423 (SEQ ID NO:423), Figure 425 (SEQ ID NO:425), Figure 427 (SEQ ID NO:427), Figure 429 (SEQ ID NO:429), Figure 431 (SEQ ID

NO:431), Figure 433 (SEQ ID NO:433), Figure 435 (SEQ ID NO:435), Figure 437 (SEQ ID NO:437), Figure 439 (SEQ ID NO:439), Figure 441 (SEQ ID NO:441), Figure 443 (SEQ ID NO:443), Figure 445 (SEQ ID NO:445), Figure 447 (SEQ ID NO:447), Figure 449 (SEQ ID NO:449), Figure 451 (SEQ ID NO:451), Figure 453 (SEQ ID NO:453), Figure 455 (SEQ ID NO:455), Figure 457 (SEQ ID NO:457), Figure 459 (SEQ ID NO:459), Figure 461 (SEQ ID NO:461), Figure 463 (SEQ ID NO:463), Figure 465 (SEQ ID NO:465), Figure 467 (SEQ ID NO:467), Figure 469 (SEQ ID NO:469), Figure 471 (SEQ ID NO:471), Figure 473 (SEQ ID NO:473), Figure 475 (SEQ ID NO:475), Figure 477 (SEQ ID NO:477), Figure 479 (SEQ ID NO:479), Figure 481 (SEQ ID NO:481), Figure 483 (SEQ ID NO:483), Figure 485 (SEQ ID NO:485), Figure 487 (SEQ ID NO:487), Figure 489 (SEQ ID NO:489), Figure 491 (SEQ ID NO:491), Figure 493 (SEQ ID NO:493), Figure 495 (SEQ ID NO:495), Figure 497 (SEQ ID NO:497), Figure 499 (SEQ ID NO:499), Figure 501 (SEQ ID NO:501), Figure 503 (SEQ ID NO:503), Figure 505 (SEQ ID NO:505), Figure 507 (SEQ ID NO:507), Figure 509 (SEQ ID NO:509), Figure 511 (SEQ ID NO:511), Figure 513 (SEQ ID NO:513), Figure 515 (SEQ ID NO:515), Figure 517 (SEQ ID NO:517), Figure 519 (SEQ ID NO:519), Figure 521 (SEQ ID NO:521), Figure 523 (SEQ ID NO:523), Figures 525A-525B (SEQ ID NO:525), Figure 527 (SEQ ID NO:527), Figure 529 (SEQ ID NO:529), Figure 531 (SEQ ID NO:531), Figure 533 (SEQ ID NO:533), Figure 535 (SEQ ID NO:535), Figure 537 (SEQ ID NO:537), Figure 539 (SEQ ID NO:539), Figure 541 (SEQ ID NO:541), Figure 543 (SEQ ID NO:543), Figure 545 (SEQ ID NO:545), Figure 547 (SEQ ID NO:547), Figure 549 (SEQ ID NO:549), Figure 551 (SEQ ID NO:551), Figure 553 (SEQ ID NO:553), Figure 555 (SEQ ID NO:555), Figure 557 (SEQ ID NO:557), Figure 559 (SEQ ID NO:559), Figure 561 (SEQ ID NO:561), Figure 563 (SEQ ID NO:563), Figure 565 (SEQ ID NO:565), Figure 567 (SEQ ID NO:567), Figure 569 (SEQ ID NO:569), Figure 571 (SEQ ID NO:571), Figure 573 (SEQ ID NO:573), Figure 575 (SEQ ID NO:575), Figure 577 (SEQ ID NO:577), Figure 579 (SEQ ID NO:579), Figure 581 (SEQ ID NO:581), Figure 583 (SEQ ID NO:583), Figure 585 (SEQ ID NO:585), Figure 587 (SEQ ID NO:587), Figure 589 (SEQ ID NO:589), Figure 591 (SEQ ID NO:591), Figure 593 (SEQ ID NO:593), Figure 595 (SEQ ID NO:595), Figure 597 (SEQ ID NO:597), Figure 599 (SEQ ID NO:599), Figure 601 (SEQ ID NO:601), Figure 603 (SEQ ID NO:603), Figure 605 (SEQ ID NO:605), Figure 607 (SEQ ID NO:607), and Figure 609 (SEQ ID NO:609).

3. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of the full-length coding sequence of the nucleotide sequence shown in Figure 1 (SEQ ID NO:1), Figure 3 (SEQ ID NO:3), Figure 5 (SEQ ID NO:5), Figure 7 (SEQ ID NO:7), Figure 9 (SEQ ID NO:9), Figure 11 (SEQ ID NO:11), Figure 13 (SEQ ID NO:13), Figure 15 (SEQ ID NO:15), Figure 17 (SEQ ID NO:17), Figure 19 (SEQ ID NO:19), Figure 21 (SEQ ID NO:21), Figure 23 (SEQ ID NO:23), Figure 25 (SEQ ID NO:25), Figure 27 (SEQ ID NO:27), Figure 29 (SEQ ID NO:29), Figure 31 (SEQ ID NO:31), Figure 33 (SEQ ID NO:33), Figure 35 (SEQ ID NO:35), Figure 37 (SEQ ID NO:37), Figure 39 (SEQ ID NO:39), Figure 41 (SEQ ID NO:41), Figure 43 (SEQ ID NO:43), Figure 45 (SEQ ID NO:45), Figure 47 (SEQ ID NO:47), Figure 49 (SEQ ID NO:49), Figure 51 (SEQ ID NO:51), Figure 53 (SEQ ID NO:53), Figure 55 (SEQ ID NO:55), Figure 57 (SEQ ID NO:57), Figure 59 (SEQ ID NO:59), Figure 61 (SEQ ID NO:61), Figure 63 (SEQ ID NO:63), Figure 65 (SEQ ID NO:65), Figure 67 (SEQ ID NO:67), Figure 69 (SEQ ID NO:69), Figure

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339 (SEQ ID NO:339), Figure 341 (SEQ ID NO:341), Figure 343 (SEQ ID NO:343), Figure 345 (SEQ ID NO:345), Figure 347 (SEQ ID NO:347), Figure 349 (SEQ ID NO:349), Figures 351A-351B (SEQ ID NO:351), Figure 353 (SEQ ID NO:353), Figure 355 (SEQ ID NO:355), Figure 357 (SEQ ID NO:357), Figure 359 (SEQ ID NO:359), Figure 361 (SEQ ID NO:361), Figure 363 (SEQ ID NO:363), Figure 365 (SEQ ID NO:365), Figure 367 (SEQ ID NO:367), Figure 369 (SEQ ID NO:369), Figure 371 (SEQ ID NO:371), Figure 373 (SEQ ID NO:373), Figure 375 (SEQ ID NO:375), Figure 377 (SEQ ID NO:377), Figure 379 (SEQ ID NO:379), Figure 381 (SEQ ID NO:381), Figure 383 (SEQ ID NO:383), Figure 385 (SEQ ID NO:385), Figure 387 (SEQ ID NO:387), Figure 389 (SEQ ID NO:389), Figure 391 (SEQ ID NO:391), Figure 393 (SEQ ID NO:393), Figure 395 (SEQ ID NO:395), Figure 397 (SEQ ID NO:397), Figure 399 (SEQ ID NO:399), Figure 401 (SEQ ID NO:401), Figure 403 (SEQ ID NO:403), Figure 405 (SEQ ID NO:405), Figure 407 (SEQ ID NO:407), Figure 409 (SEQ ID NO:409), Figure 411 (SEQ ID NO:411), Figure 413 (SEQ ID NO:413), Figure 415 (SEQ ID NO:415), Figure 417 (SEQ ID NO:417), Figure 419 (SEQ ID NO:419), Figure 421 (SEQ ID NO:421), Figure 423 (SEQ ID NO:423), Figure 425 (SEQ ID NO:425), Figure 427 (SEQ ID NO:427), Figure 429 (SEQ ID NO:429), Figure 431 (SEQ ID NO:431), Figure 433 (SEQ ID NO:433), Figure 435 (SEQ ID NO:435), Figure 437 (SEQ ID NO:437), Figure 439 (SEQ ID NO:439), Figure 441 (SEQ ID NO:441), Figure 443 (SEQ ID NO:443), Figure 445 (SEQ ID NO:445), Figure 447 (SEQ ID NO:447), Figure 449 (SEQ ID NO:449), Figure 451 (SEQ ID NO:451), Figure 453 (SEQ ID NO:453), Figure 455 (SEQ ID NO:455), Figure 457 (SEQ ID NO:457), Figure 459 (SEQ ID NO:459), Figure 461 (SEQ ID NO:461), Figure 463 (SEQ ID NO:463), Figure 465 (SEQ ID NO:465), Figure 467 (SEQ ID NO:467), Figure 469 (SEQ ID NO:469), Figure 471 (SEQ ID NO:471), Figure 473 (SEQ ID NO:473), Figure 475 (SEQ ID NO:475), Figure 477 (SEQ ID NO:477), Figure 479 (SEQ ID NO:479), Figure 481 (SEQ ID NO:481), Figure 483 (SEQ ID NO:483), Figure 485 (SEQ ID NO:485), Figure 487 (SEQ ID NO:487), Figure 489 (SEQ ID NO:489), Figure 491 (SEQ ID NO:491), Figure 493 (SEQ ID NO:493), Figure 495 (SEQ ID NO:495), Figure 497 (SEQ ID NO:497), Figure 499 (SEQ ID NO:499), Figure 501 (SEQ ID NO:501), Figure 503 (SEQ ID NO:503), Figure 505 (SEQ ID NO:505), Figure 507 (SEQ ID NO:507), Figure 509 (SEQ ID NO:509), Figure 511 (SEQ ID NO:511), Figure 513 (SEQ ID NO:513), Figure 515 (SEQ ID NO:515), Figure 517 (SEQ ID NO:517), Figure 519 (SEQ ID NO:519), Figure 521 (SEQ ID NO:521), Figure 523 (SEQ ID NO:523), Figures 525A-525B (SEQ ID NO:525), Figure 527 (SEQ ID NO:527), Figure 529 (SEQ ID NO:529), Figure 531 (SEQ ID NO:531), Figure 533 (SEQ ID NO:533), Figure 535 (SEQ ID NO:535), Figure 537 (SEQ ID NO:537), Figure 539 (SEQ ID NO:539), Figure 541 (SEQ ID NO:541), Figure 543 (SEQ ID NO:543), Figure 545 (SEQ ID NO:545), Figure 547 (SEQ ID NO:547), Figure 549 (SEQ ID NO:549), Figure 551 (SEQ ID NO:551), Figure 553 (SEQ ID NO:553), Figure 555 (SEQ ID NO:555), Figure 557 (SEQ ID NO:557), Figure 559 (SEQ ID NO:559), Figure 561 (SEQ ID NO:561), Figure 563 (SEQ ID NO:563), Figure 565 (SEQ ID NO:565), Figure 567 (SEQ ID NO:567), Figure 569 (SEQ ID NO:569), Figure 571 (SEQ ID NO:571), Figure 573 (SEQ ID NO:573), Figure 575 (SEQ ID NO:575), Figure 577 (SEQ ID NO:577), Figure 579 (SEQ ID NO:579), Figure 581 (SEQ ID NO:581), Figure 583 (SEQ ID NO:583), Figure 585 (SEQ ID NO:585), Figure 587 (SEQ ID NO:587), Figure 589 (SEQ ID NO:589), Figure 591 (SEQ ID NO:591), Figure 593 (SEQ ID NO:593), Figure 595 (SEQ ID NO:595), Figure 597 (SEQ ID NO:597), Figure 599 (SEQ ID NO:599), Figure 601 (SEQ ID NO:601), Figure 603 (SEQ ID NO:603), Figure

605 (SEQ ID NO:605), Figure 607 (SEQ ID NO:607), and Figure 609 (SEQ ID NO:609).

4. Isolated nucleic acid having at least 80% nucleic acid sequence identity to the full-length coding sequence of the DNA deposited under any ATCC accession number shown in Table 7.

5 5. A vector comprising the nucleic acid of Claim 1.

6. A host cell comprising the vector of Claim 5.

7. The host cell of Claim 6, wherein said cell is a CHO cell.

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8. The host cell of Claim 6, wherein said cell is an *E. coli*.

9. The host cell of Claim 6, wherein said cell is a yeast cell.

15 10. A process for producing a PRO polypeptide comprising culturing the host cell of Claim 6 under conditions suitable for expression of said PRO polypeptide and recovering said PRO polypeptide from the cell culture.

20 11. An isolated polypeptide having at least 80% amino acid sequence identity to an amino acid sequence selected from the group consisting of the amino acid sequence shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID

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NO:396), Figure 398 (SEQ ID NO:398), Figure 400 (SEQ ID NO:400), Figure 402 (SEQ ID NO:402), Figure 404 (SEQ ID NO:404), Figure 406 (SEQ ID NO:406), Figure 408 (SEQ ID NO:408), Figure 410 (SEQ ID NO:410), Figure 412 (SEQ ID NO:412), Figure 414 (SEQ ID NO:414), Figure 416 (SEQ ID NO:416), Figure 418 (SEQ ID NO:418), Figure 420 (SEQ ID NO:420), Figure 422 (SEQ ID NO:422), Figure 424 (SEQ ID NO:424), Figure 426 (SEQ ID NO:426), Figure 428 (SEQ ID NO:428), Figure 430 (SEQ ID NO:430), Figure 432 (SEQ ID NO:432), Figure 434 (SEQ ID NO:434), Figure 436 (SEQ ID NO:436), Figure 438 (SEQ ID NO:438), Figure 440 (SEQ ID NO:440), Figure 442 (SEQ ID NO:442), Figure 444 (SEQ ID NO:444), Figure 446 (SEQ ID NO:446), Figure 448 (SEQ ID NO:448), Figure 450 (SEQ ID NO:450), Figure 452 (SEQ ID NO:452), Figure 454 (SEQ ID NO:454), Figure 456 (SEQ ID NO:456), Figure 458 (SEQ ID NO:458), Figure 460 (SEQ ID NO:460), Figure 462 (SEQ ID NO:462), Figure 464 (SEQ ID NO:464), Figure 466 (SEQ ID NO:466), Figure 468 (SEQ ID NO:468), Figure 470 (SEQ ID NO:470), Figure 472 (SEQ ID NO:472), Figure 474 (SEQ ID NO:474), Figure 476 (SEQ ID NO:476), Figure 478 (SEQ ID NO:478), Figure 480 (SEQ ID NO:480), Figure 482 (SEQ ID NO:482), Figure 484 (SEQ ID NO:484), Figure 486 (SEQ ID NO:486), Figure 488 (SEQ ID NO:488), Figure 490 (SEQ ID NO:490), Figure 492 (SEQ ID NO:492), Figure 494 (SEQ ID NO:494), Figure 496 (SEQ ID NO:496), Figure 498 (SEQ ID NO:498), Figure 500 (SEQ ID NO:500), Figure 502 (SEQ ID NO:502), Figure 504 (SEQ ID NO:504), Figure 506 (SEQ ID NO:506), Figure 508 (SEQ ID NO:508), Figure 510 (SEQ ID NO:510), Figure 512 (SEQ ID NO:512), Figure 514 (SEQ ID NO:514), Figure 516 (SEQ ID NO:516), Figure 518 (SEQ ID NO:518), Figure 520 (SEQ ID NO:520), Figure 522 (SEQ ID NO:522), Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ ID NO:528), Figure 530 (SEQ ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534 (SEQ ID NO:534), Figure 536 (SEQ ID NO:536), Figure 538 (SEQ ID NO:538), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ ID NO:542), Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 548 (SEQ ID NO:548), Figure 550 (SEQ ID NO:550), Figure 552 (SEQ ID NO:552), Figure 554 (SEQ ID NO:554), Figure 556 (SEQ ID NO:556), Figure 558 (SEQ ID NO:558), Figure 560 (SEQ ID NO:560), Figure 562 (SEQ ID NO:562), Figure 564 (SEQ ID NO:564), Figure 566 (SEQ ID NO:566), Figure 568 (SEQ ID NO:568), Figure 570 (SEQ ID NO:570), Figure 572 (SEQ ID NO:572), Figure 574 (SEQ ID NO:574), Figure 576 (SEQ ID NO:576), Figure 578 (SEQ ID NO:578), Figure 580 (SEQ ID NO:580), Figure 582 (SEQ ID NO:582), Figure 584 (SEQ ID NO:584), Figure 586 (SEQ ID NO:586), Figure 588 (SEQ ID NO:588), Figure 590 (SEQ ID NO:590), Figure 592 (SEQ ID NO:592), Figure 594 (SEQ ID NO:594), Figure 596 (SEQ ID NO:596), Figure 598 (SEQ ID NO:598), Figure 600 (SEQ ID NO:600), Figure 602 (SEQ ID NO:602), Figure 604 (SEQ ID NO:604), Figure 606 (SEQ ID NO:606), Figure 608 (SEQ ID NO:608), and Figure 610 (SEQ ID NO:610).

12. An isolated polypeptide having at least 80% amino acid sequence identity to an amino acid sequence encoded by the full-length coding sequence of the DNA deposited under any ATCC accession number shown in Table 7.

13. A chimeric molecule comprising a polypeptide according to Claim 11 fused to a heterologous amino acid sequence.

14. The chimeric molecule of Claim 13, wherein said heterologous amino acid sequence is an epitope tag sequence.

15. The chimeric molecule of Claim 13, wherein said heterologous amino acid sequence is a Fc region of an immunoglobulin.

5

16. An antibody which specifically binds to a polypeptide according to Claim 11.

17. The antibody of Claim 16, wherein said antibody is a monoclonal antibody, a humanized antibody or a single-chain antibody.

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18. Isolated nucleic acid having at least 80% nucleic acid sequence identity to:

(a) a nucleotide sequence encoding the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure

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188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), Figure 244 (SEQ ID NO:244), Figure 246 (SEQ ID NO:246), Figure 248 (SEQ ID NO:248), Figure 250 (SEQ ID NO:250), Figure 252 (SEQ ID NO:252), Figure 254 (SEQ ID NO:254), Figure 256 (SEQ ID NO:256), Figure 258 (SEQ ID NO:258), Figure 260 (SEQ ID NO:260), Figure 262 (SEQ ID NO:262), Figure 264 (SEQ ID NO:264), Figure 266 (SEQ ID NO:266), Figure 268 (SEQ ID NO:268), Figure 270 (SEQ ID NO:270), Figure 272 (SEQ ID NO:272), Figure 274 (SEQ ID NO:274), Figure 276 (SEQ ID NO:276), Figure 278 (SEQ ID NO:278), Figure 280 (SEQ ID NO:280), Figure 282 (SEQ ID NO:282), Figure 284 (SEQ ID NO:284), Figure 286 (SEQ ID NO:286), Figure 288 (SEQ ID NO:288), Figure 290 (SEQ ID NO:290), Figure 292 (SEQ ID NO:292), Figure 294 (SEQ ID NO:294), Figure 296 (SEQ ID NO:296), Figure 298 (SEQ ID NO:298), Figure 300 (SEQ ID NO:300), Figure 302 (SEQ ID NO:302), Figure 304 (SEQ ID NO:304), Figure 306 (SEQ ID NO:306), Figure 308 (SEQ ID NO:308), Figure 310 (SEQ ID NO:310), Figure 312 (SEQ ID NO:312), Figure 314 (SEQ ID NO:314), Figure 316 (SEQ ID NO:316), Figure 318 (SEQ ID NO:318), Figure 320 (SEQ ID NO:320), Figure 322 (SEQ ID NO:322), Figure 324 (SEQ ID NO:324), Figure 326 (SEQ ID NO:326), Figure 328 (SEQ ID NO:328), Figure 330 (SEQ ID NO:330), Figure 332 (SEQ ID NO:332), Figure 334 (SEQ ID NO:334), Figure 336 (SEQ ID NO:336), Figure 338 (SEQ ID NO:338), Figure 340 (SEQ ID NO:340), Figure 342 (SEQ ID NO:342), Figure 344 (SEQ ID NO:344), Figure 346 (SEQ ID NO:346), Figure 348 (SEQ ID NO:348), Figure 350 (SEQ ID NO:350), Figure 352 (SEQ ID NO:352), Figure 354 (SEQ ID NO:354), Figure 356 (SEQ ID NO:356), Figure 358 (SEQ ID NO:358), Figure 360 (SEQ ID NO:360), Figure 362 (SEQ ID NO:362), Figure 364 (SEQ ID NO:364), Figure 366 (SEQ ID NO:366), Figure 368 (SEQ ID NO:368), Figure 370 (SEQ ID NO:370), Figure 372 (SEQ ID NO:372), Figure 374 (SEQ ID NO:374), Figure 376 (SEQ ID NO:376), Figure 378 (SEQ ID NO:378), Figure 380 (SEQ ID NO:380), Figure 382 (SEQ ID NO:382), Figure 384 (SEQ ID NO:384), Figure 386 (SEQ ID NO:386), Figure 388 (SEQ ID NO:388), Figure 390 (SEQ ID NO:390), Figure 392 (SEQ ID NO:392), Figure 394 (SEQ ID NO:394), Figure 396 (SEQ ID NO:396), Figure 398 (SEQ ID NO:398), Figure 400 (SEQ ID NO:400), Figure 402 (SEQ ID NO:402), Figure 404 (SEQ ID NO:404), Figure 406 (SEQ ID NO:406), Figure 408 (SEQ ID NO:408), Figure 410 (SEQ ID NO:410), Figure 412 (SEQ ID NO:412), Figure 414 (SEQ ID NO:414), Figure 416 (SEQ ID NO:416), Figure 418 (SEQ ID NO:418), Figure 420 (SEQ ID NO:420), Figure 422 (SEQ ID NO:422), Figure 424 (SEQ ID NO:424), Figure 426 (SEQ ID NO:426), Figure 428 (SEQ ID NO:428), Figure 430 (SEQ ID NO:430), Figure 432 (SEQ ID NO:432), Figure 434 (SEQ ID NO:434), Figure 436 (SEQ ID NO:436), Figure 438 (SEQ ID NO:438), Figure 440 (SEQ ID NO:440), Figure 442 (SEQ ID NO:442), Figure 444 (SEQ ID NO:444), Figure 446 (SEQ ID NO:446), Figure 448 (SEQ ID NO:448), Figure 450 (SEQ ID NO:450), Figure 452 (SEQ ID NO:452), Figure

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(b) a nucleotide sequence encoding an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ

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(c) a nucleotide sequence encoding an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18

(SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ ID NO:116), Figure 118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure 132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure 146 (SEQ ID NO:146), Figure 148 (SEQ ID NO:148), Figure 150 (SEQ ID NO:150), Figure 152 (SEQ ID NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure 160 (SEQ ID NO:160), Figure 162 (SEQ ID NO:162), Figure 164 (SEQ ID NO:164), Figure 166 (SEQ ID NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure 188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), Figure 244 (SEQ ID NO:244), Figure 246 (SEQ ID NO:246), Figure 248 (SEQ ID NO:248), Figure 250 (SEQ ID NO:250), Figure 252 (SEQ ID NO:252), Figure 254 (SEQ ID NO:254), Figure 256 (SEQ ID NO:256), Figure 258 (SEQ ID NO:258), Figure 260 (SEQ ID NO:260), Figure 262 (SEQ ID NO:262), Figure 264 (SEQ ID NO:264), Figure 266 (SEQ ID NO:266), Figure 268 (SEQ ID NO:268), Figure 270 (SEQ ID NO:270), Figure 272 (SEQ ID NO:272), Figure 274 (SEQ ID NO:274), Figure 276 (SEQ ID NO:276), Figure 278 (SEQ ID NO:278), Figure 280 (SEQ ID NO:280), Figure 282 (SEQ ID NO:282), Figure 284 (SEQ ID NO:284), Figure 286 (SEQ ID NO:286), Figure 288 (SEQ ID NO:288), Figure 290 (SEQ ID

NO:290), Figure 292 (SEQ ID NO:292), Figure 294 (SEQ ID NO:294), Figure 296 (SEQ ID NO:296), Figure 298 (SEQ ID NO:298), Figure 300 (SEQ ID NO:300), Figure 302 (SEQ ID NO:302), Figure 304 (SEQ ID NO:304), Figure 306 (SEQ ID NO:306), Figure 308 (SEQ ID NO:308), Figure 310 (SEQ ID NO:310), Figure 312 (SEQ ID NO:312), Figure 314 (SEQ ID NO:314), Figure 316 (SEQ ID NO:316), Figure 318 (SEQ ID NO:318), Figure 320 (SEQ ID NO:320), Figure 322 (SEQ ID NO:322), Figure 324 (SEQ ID NO:324), Figure 326 (SEQ ID NO:326), Figure 328 (SEQ ID NO:328), Figure 330 (SEQ ID NO:330), Figure 332 (SEQ ID NO:332), Figure 334 (SEQ ID NO:334), Figure 336 (SEQ ID NO:336), Figure 338 (SEQ ID NO:338), Figure 340 (SEQ ID NO:340), Figure 342 (SEQ ID NO:342), Figure 344 (SEQ ID NO:344), Figure 346 (SEQ ID NO:346), Figure 348 (SEQ ID NO:348), Figure 350 (SEQ ID NO:350), Figure 352 (SEQ ID NO:352), Figure 354 (SEQ ID NO:354), Figure 356 (SEQ ID NO:356), Figure 358 (SEQ ID NO:358), Figure 360 (SEQ ID NO:360), Figure 362 (SEQ ID NO:362), Figure 364 (SEQ ID NO:364), Figure 366 (SEQ ID NO:366), Figure 368 (SEQ ID NO:368), Figure 370 (SEQ ID NO:370), Figure 372 (SEQ ID NO:372), Figure 374 (SEQ ID NO:374), Figure 376 (SEQ ID NO:376), Figure 378 (SEQ ID NO:378), Figure 380 (SEQ ID NO:380), Figure 382 (SEQ ID NO:382), Figure 384 (SEQ ID NO:384), Figure 386 (SEQ ID NO:386), Figure 388 (SEQ ID NO:388), Figure 390 (SEQ ID NO:390), Figure 392 (SEQ ID NO:392), Figure 394 (SEQ ID NO:394), Figure 396 (SEQ ID NO:396), Figure 398 (SEQ ID NO:398), Figure 400 (SEQ ID NO:400), Figure 402 (SEQ ID NO:402), Figure 404 (SEQ ID NO:404), Figure 406 (SEQ ID NO:406), Figure 408 (SEQ ID NO:408), Figure 410 (SEQ ID NO:410), Figure 412 (SEQ ID NO:412), Figure 414 (SEQ ID NO:414), Figure 416 (SEQ ID NO:416), Figure 418 (SEQ ID NO:418), Figure 420 (SEQ ID NO:420), Figure 422 (SEQ ID NO:422), Figure 424 (SEQ ID NO:424), Figure 426 (SEQ ID NO:426), Figure 428 (SEQ ID NO:428), Figure 430 (SEQ ID NO:430), Figure 432 (SEQ ID NO:432), Figure 434 (SEQ ID NO:434), Figure 436 (SEQ ID NO:436), Figure 438 (SEQ ID NO:438), Figure 440 (SEQ ID NO:440), Figure 442 (SEQ ID NO:442), Figure 444 (SEQ ID NO:444), Figure 446 (SEQ ID NO:446), Figure 448 (SEQ ID NO:448), Figure 450 (SEQ ID NO:450), Figure 452 (SEQ ID NO:452), Figure 454 (SEQ ID NO:454), Figure 456 (SEQ ID NO:456), Figure 458 (SEQ ID NO:458), Figure 460 (SEQ ID NO:460), Figure 462 (SEQ ID NO:462), Figure 464 (SEQ ID NO:464), Figure 466 (SEQ ID NO:466), Figure 468 (SEQ ID NO:468), Figure 470 (SEQ ID NO:470), Figure 472 (SEQ ID NO:472), Figure 474 (SEQ ID NO:474), Figure 476 (SEQ ID NO:476), Figure 478 (SEQ ID NO:478), Figure 480 (SEQ ID NO:480), Figure 482 (SEQ ID NO:482), Figure 484 (SEQ ID NO:484), Figure 486 (SEQ ID NO:486), Figure 488 (SEQ ID NO:488), Figure 490 (SEQ ID NO:490), Figure 492 (SEQ ID NO:492), Figure 494 (SEQ ID NO:494), Figure 496 (SEQ ID NO:496), Figure 498 (SEQ ID NO:498), Figure 500 (SEQ ID NO:500), Figure 502 (SEQ ID NO:502), Figure 504 (SEQ ID NO:504), Figure 506 (SEQ ID NO:506), Figure 508 (SEQ ID NO:508), Figure 510 (SEQ ID NO:510), Figure 512 (SEQ ID NO:512), Figure 514 (SEQ ID NO:514), Figure 516 (SEQ ID NO:516), Figure 518 (SEQ ID NO:518), Figure 520 (SEQ ID NO:520), Figure 522 (SEQ ID NO:522), Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ ID NO:528), Figure 530 (SEQ ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534 (SEQ ID NO:534), Figure 536 (SEQ ID NO:536), Figure 538 (SEQ ID NO:538), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ ID NO:542), Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 548 (SEQ ID NO:548), Figure 550 (SEQ ID NO:550), Figure 552 (SEQ ID NO:552), Figure 554 (SEQ ID NO:554), Figure 556 (SEQ ID

NO:556), Figure 558 (SEQ ID NO:558), Figure 560 (SEQ ID NO:560), Figure 562 (SEQ ID NO:562), Figure 564 (SEQ ID NO:564), Figure 566 (SEQ ID NO:566), Figure 568 (SEQ ID NO:568), Figure 570 (SEQ ID NO:570), Figure 572 (SEQ ID NO:572), Figure 574 (SEQ ID NO:574), Figure 576 (SEQ ID NO:576), Figure 578 (SEQ ID NO:578), Figure 580 (SEQ ID NO:580), Figure 582 (SEQ ID NO:582), Figure 584 (SEQ ID NO:584), Figure 586 (SEQ ID NO:586), Figure 588 (SEQ ID NO:588), Figure 590 (SEQ ID NO:590), Figure 592 (SEQ ID NO:592), Figure 594 (SEQ ID NO:594), Figure 596 (SEQ ID NO:596), Figure 598 (SEQ ID NO:598), Figure 600 (SEQ ID NO:600), Figure 602 (SEQ ID NO:602), Figure 604 (SEQ ID NO:604), Figure 606 (SEQ ID NO:606), Figure 608 (SEQ ID NO:608), or Figure 610 (SEQ ID NO:610), lacking its associated signal peptide.

10 19. An isolated polypeptide having at least 80% amino acid sequence identity to:

(a) an amino acid sequence of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ
ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID
NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ
ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28
15 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure
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Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID
NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ
ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66
20 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure
74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80),
Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID
NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ
ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure
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118 (SEQ ID NO:118), Figure 120 (SEQ ID NO:120), Figure 122 (SEQ ID NO:122), Figure 124 (SEQ ID
NO:124), Figure 126 (SEQ ID NO:126), Figure 128 (SEQ ID NO:128), Figure 130 (SEQ ID NO:130), Figure
132 (SEQ ID NO:132), Figure 134 (SEQ ID NO:134), Figure 136 (SEQ ID NO:136), Figure 138 (SEQ ID
NO:138), Figure 140 (SEQ ID NO:140), Figure 142 (SEQ ID NO:142), Figure 144 (SEQ ID NO:144), Figure
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NO:152), Figure 154 (SEQ ID NO:154), Figure 156 (SEQ ID NO:156), Figure 158 (SEQ ID NO:158), Figure
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NO:166), Figure 168 (SEQ ID NO:168), Figure 170 (SEQ ID NO:170), Figure 172 (SEQ ID NO:172), Figure
35 174 (SEQ ID NO:174), Figure 176 (SEQ ID NO:176), Figure 178 (SEQ ID NO:178), Figure 180 (SEQ ID
NO:180), Figure 182 (SEQ ID NO:182), Figure 184 (SEQ ID NO:184), Figure 186 (SEQ ID NO:186), Figure
188 (SEQ ID NO:188), Figure 190 (SEQ ID NO:190), Figure 192 (SEQ ID NO:192), Figure 194 (SEQ ID

NO:194), Figure 196 (SEQ ID NO:196), Figure 198 (SEQ ID NO:198), Figure 200 (SEQ ID NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure 208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure 222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure 236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID NO:242), Figure 244 (SEQ ID NO:244), Figure 246 (SEQ ID NO:246), Figure 248 (SEQ ID NO:248), Figure 250 (SEQ ID NO:250), Figure 252 (SEQ ID NO:252), Figure 254 (SEQ ID NO:254), Figure 256 (SEQ ID NO:256), Figure 258 (SEQ ID NO:258), Figure 260 (SEQ ID NO:260), Figure 262 (SEQ ID NO:262), Figure 264 (SEQ ID NO:264), Figure 266 (SEQ ID NO:266), Figure 268 (SEQ ID NO:268), Figure 270 (SEQ ID NO:270), Figure 272 (SEQ ID NO:272), Figure 274 (SEQ ID NO:274), Figure 276 (SEQ ID NO:276), Figure 278 (SEQ ID NO:278), Figure 280 (SEQ ID NO:280), Figure 282 (SEQ ID NO:282), Figure 284 (SEQ ID NO:284), Figure 286 (SEQ ID NO:286), Figure 288 (SEQ ID NO:288), Figure 290 (SEQ ID NO:290), Figure 292 (SEQ ID NO:292), Figure 294 (SEQ ID NO:294), Figure 296 (SEQ ID NO:296), Figure 298 (SEQ ID NO:298), Figure 300 (SEQ ID NO:300), Figure 302 (SEQ ID NO:302), Figure 304 (SEQ ID NO:304), Figure 306 (SEQ ID NO:306), Figure 308 (SEQ ID NO:308), Figure 310 (SEQ ID NO:310), Figure 312 (SEQ ID NO:312), Figure 314 (SEQ ID NO:314), Figure 316 (SEQ ID NO:316), Figure 318 (SEQ ID NO:318), Figure 320 (SEQ ID NO:320), Figure 322 (SEQ ID NO:322), Figure 324 (SEQ ID NO:324), Figure 326 (SEQ ID NO:326), Figure 328 (SEQ ID NO:328), Figure 330 (SEQ ID NO:330), Figure 332 (SEQ ID NO:332), Figure 334 (SEQ ID NO:334), Figure 336 (SEQ ID NO:336), Figure 338 (SEQ ID NO:338), Figure 340 (SEQ ID NO:340), Figure 342 (SEQ ID NO:342), Figure 344 (SEQ ID NO:344), Figure 346 (SEQ ID NO:346), Figure 348 (SEQ ID NO:348), Figure 350 (SEQ ID NO:350), Figure 352 (SEQ ID NO:352), Figure 354 (SEQ ID NO:354), Figure 356 (SEQ ID NO:356), Figure 358 (SEQ ID NO:358), Figure 360 (SEQ ID NO:360), Figure 362 (SEQ ID NO:362), Figure 364 (SEQ ID NO:364), Figure 366 (SEQ ID NO:366), Figure 368 (SEQ ID NO:368), Figure 370 (SEQ ID NO:370), Figure 372 (SEQ ID NO:372), Figure 374 (SEQ ID NO:374), Figure 376 (SEQ ID NO:376), Figure 378 (SEQ ID NO:378), Figure 380 (SEQ ID NO:380), Figure 382 (SEQ ID NO:382), Figure 384 (SEQ ID NO:384), Figure 386 (SEQ ID NO:386), Figure 388 (SEQ ID NO:388), Figure 390 (SEQ ID NO:390), Figure 392 (SEQ ID NO:392), Figure 394 (SEQ ID NO:394), Figure 396 (SEQ ID NO:396), Figure 398 (SEQ ID NO:398), Figure 400 (SEQ ID NO:400), Figure 402 (SEQ ID NO:402), Figure 404 (SEQ ID NO:404), Figure 406 (SEQ ID NO:406), Figure 408 (SEQ ID NO:408), Figure 410 (SEQ ID NO:410), Figure 412 (SEQ ID NO:412), Figure 414 (SEQ ID NO:414), Figure 416 (SEQ ID NO:416), Figure 418 (SEQ ID NO:418), Figure 420 (SEQ ID NO:420), Figure 422 (SEQ ID NO:422), Figure 424 (SEQ ID NO:424), Figure 426 (SEQ ID NO:426), Figure 428 (SEQ ID NO:428), Figure 430 (SEQ ID NO:430), Figure 432 (SEQ ID NO:432), Figure 434 (SEQ ID NO:434), Figure 436 (SEQ ID NO:436), Figure 438 (SEQ ID NO:438), Figure 440 (SEQ ID NO:440), Figure 442 (SEQ ID NO:442), Figure 444 (SEQ ID NO:444), Figure 446 (SEQ ID NO:446), Figure 448 (SEQ ID NO:448), Figure 450 (SEQ ID NO:450), Figure 452 (SEQ ID NO:452), Figure 454 (SEQ ID NO:454), Figure 456 (SEQ ID NO:456), Figure 458 (SEQ ID NO:458), Figure 460 (SEQ ID

NO:460), Figure 462 (SEQ ID NO:462), Figure 464 (SEQ ID NO:464), Figure 466 (SEQ ID NO:466), Figure 468 (SEQ ID NO:468), Figure 470 (SEQ ID NO:470), Figure 472 (SEQ ID NO:472), Figure 474 (SEQ ID NO:474), Figure 476 (SEQ ID NO:476), Figure 478 (SEQ ID NO:478), Figure 480 (SEQ ID NO:480), Figure 482 (SEQ ID NO:482), Figure 484 (SEQ ID NO:484), Figure 486 (SEQ ID NO:486), Figure 488 (SEQ ID NO:488), Figure 490 (SEQ ID NO:490), Figure 492 (SEQ ID NO:492), Figure 494 (SEQ ID NO:494), Figure 496 (SEQ ID NO:496), Figure 498 (SEQ ID NO:498), Figure 500 (SEQ ID NO:500), Figure 502 (SEQ ID NO:502), Figure 504 (SEQ ID NO:504), Figure 506 (SEQ ID NO:506), Figure 508 (SEQ ID NO:508), Figure 510 (SEQ ID NO:510), Figure 512 (SEQ ID NO:512), Figure 514 (SEQ ID NO:514), Figure 516 (SEQ ID NO:516), Figure 518 (SEQ ID NO:518), Figure 520 (SEQ ID NO:520), Figure 522 (SEQ ID NO:522), Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ ID NO:528), Figure 530 (SEQ ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534 (SEQ ID NO:534), Figure 536 (SEQ ID NO:536), Figure 538 (SEQ ID NO:538), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ ID NO:542), Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 548 (SEQ ID NO:548), Figure 550 (SEQ ID NO:550), Figure 552 (SEQ ID NO:552), Figure 554 (SEQ ID NO:554), Figure 556 (SEQ ID NO:556), Figure 558 (SEQ ID NO:558), Figure 560 (SEQ ID NO:560), Figure 562 (SEQ ID NO:562), Figure 564 (SEQ ID NO:564), Figure 566 (SEQ ID NO:566), Figure 568 (SEQ ID NO:568), Figure 570 (SEQ ID NO:570), Figure 572 (SEQ ID NO:572), Figure 574 (SEQ ID NO:574), Figure 576 (SEQ ID NO:576), Figure 578 (SEQ ID NO:578), Figure 580 (SEQ ID NO:580), Figure 582 (SEQ ID NO:582), Figure 584 (SEQ ID NO:584), Figure 586 (SEQ ID NO:586), Figure 588 (SEQ ID NO:588), Figure 590 (SEQ ID NO:590), Figure 592 (SEQ ID NO:592), Figure 594 (SEQ ID NO:594), Figure 596 (SEQ ID NO:596), Figure 598 (SEQ ID NO:598), Figure 600 (SEQ ID NO:600), Figure 602 (SEQ ID NO:602), Figure 604 (SEQ ID NO:604), Figure 606 (SEQ ID NO:606), Figure 608 (SEQ ID NO:608), or Figure 610 (SEQ ID NO:610), lacking its associated signal peptide;

(b) an amino acid sequence of an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ

[illegible]

NO:382), Figure 384 (SEQ ID NO:384), Figure 386 (SEQ ID NO:386), Figure 388 (SEQ ID NO:388), Figure 390 (SEQ ID NO:390), Figure 392 (SEQ ID NO:392), Figure 394 (SEQ ID NO:394), Figure 396 (SEQ ID NO:396), Figure 398 (SEQ ID NO:398), Figure 400 (SEQ ID NO:400), Figure 402 (SEQ ID NO:402), Figure 404 (SEQ ID NO:404), Figure 406 (SEQ ID NO:406), Figure 408 (SEQ ID NO:408), Figure 410 (SEQ ID NO:410), Figure 412 (SEQ ID NO:412), Figure 414 (SEQ ID NO:414), Figure 416 (SEQ ID NO:416), Figure 418 (SEQ ID NO:418), Figure 420 (SEQ ID NO:420), Figure 422 (SEQ ID NO:422), Figure 424 (SEQ ID NO:424), Figure 426 (SEQ ID NO:426), Figure 428 (SEQ ID NO:428), Figure 430 (SEQ ID NO:430), Figure 432 (SEQ ID NO:432), Figure 434 (SEQ ID NO:434), Figure 436 (SEQ ID NO:436), Figure 438 (SEQ ID NO:438), Figure 440 (SEQ ID NO:440), Figure 442 (SEQ ID NO:442), Figure 444 (SEQ ID NO:444), Figure 446 (SEQ ID NO:446), Figure 448 (SEQ ID NO:448), Figure 450 (SEQ ID NO:450), Figure 452 (SEQ ID NO:452), Figure 454 (SEQ ID NO:454), Figure 456 (SEQ ID NO:456), Figure 458 (SEQ ID NO:458), Figure 460 (SEQ ID NO:460), Figure 462 (SEQ ID NO:462), Figure 464 (SEQ ID NO:464), Figure 466 (SEQ ID NO:466), Figure 468 (SEQ ID NO:468), Figure 470 (SEQ ID NO:470), Figure 472 (SEQ ID NO:472), Figure 474 (SEQ ID NO:474), Figure 476 (SEQ ID NO:476), Figure 478 (SEQ ID NO:478), Figure 480 (SEQ ID NO:480), Figure 482 (SEQ ID NO:482), Figure 484 (SEQ ID NO:484), Figure 486 (SEQ ID NO:486), Figure 488 (SEQ ID NO:488), Figure 490 (SEQ ID NO:490), Figure 492 (SEQ ID NO:492), Figure 494 (SEQ ID NO:494), Figure 496 (SEQ ID NO:496), Figure 498 (SEQ ID NO:498), Figure 500 (SEQ ID NO:500), Figure 502 (SEQ ID NO:502), Figure 504 (SEQ ID NO:504), Figure 506 (SEQ ID NO:506), Figure 508 (SEQ ID NO:508), Figure 510 (SEQ ID NO:510), Figure 512 (SEQ ID NO:512), Figure 514 (SEQ ID NO:514), Figure 516 (SEQ ID NO:516), Figure 518 (SEQ ID NO:518), Figure 520 (SEQ ID NO:520), Figure 522 (SEQ ID NO:522), Figure 524 (SEQ ID NO:524), Figure 526 (SEQ ID NO:526), Figure 528 (SEQ ID NO:528), Figure 530 (SEQ ID NO:530), Figure 532 (SEQ ID NO:532), Figure 534 (SEQ ID NO:534), Figure 536 (SEQ ID NO:536), Figure 538 (SEQ ID NO:538), Figure 540 (SEQ ID NO:540), Figure 542 (SEQ ID NO:542), Figure 544 (SEQ ID NO:544), Figure 546 (SEQ ID NO:546), Figure 548 (SEQ ID NO:548), Figure 550 (SEQ ID NO:550), Figure 552 (SEQ ID NO:552), Figure 554 (SEQ ID NO:554), Figure 556 (SEQ ID NO:556), Figure 558 (SEQ ID NO:558), Figure 560 (SEQ ID NO:560), Figure 562 (SEQ ID NO:562), Figure 564 (SEQ ID NO:564), Figure 566 (SEQ ID NO:566), Figure 568 (SEQ ID NO:568), Figure 570 (SEQ ID NO:570), Figure 572 (SEQ ID NO:572), Figure 574 (SEQ ID NO:574), Figure 576 (SEQ ID NO:576), Figure 578 (SEQ ID NO:578), Figure 580 (SEQ ID NO:580), Figure 582 (SEQ ID NO:582), Figure 584 (SEQ ID NO:584), Figure 586 (SEQ ID NO:586), Figure 588 (SEQ ID NO:588), Figure 590 (SEQ ID NO:590), Figure 592 (SEQ ID NO:592), Figure 594 (SEQ ID NO:594), Figure 596 (SEQ ID NO:596), Figure 598 (SEQ ID NO:598), Figure 600 (SEQ ID NO:600), Figure 602 (SEQ ID NO:602), Figure 604 (SEQ ID NO:604), Figure 606 (SEQ ID NO:606), Figure 608 (SEQ ID NO:608), or Figure 610 (SEQ ID NO:610), with its associated signal peptide; or

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure

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(SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108),
10 Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112), Figure 114 (SEQ ID NO:114), Figure 116 (SEQ
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NO:200), Figure 202 (SEQ ID NO:202), Figure 204 (SEQ ID NO:204), Figure 206 (SEQ ID NO:206), Figure
208 (SEQ ID NO:208), Figure 210 (SEQ ID NO:210), Figure 212 (SEQ ID NO:212), Figure 214 (SEQ ID
25 NO:214), Figure 216 (SEQ ID NO:216), Figure 218 (SEQ ID NO:218), Figure 220 (SEQ ID NO:220), Figure
222 (SEQ ID NO:222), Figure 224 (SEQ ID NO:224), Figure 226 (SEQ ID NO:226), Figure 228 (SEQ ID
NO:228), Figure 230 (SEQ ID NO:230), Figure 232 (SEQ ID NO:232), Figure 234 (SEQ ID NO:234), Figure
236 (SEQ ID NO:236), Figure 238 (SEQ ID NO:238), Figure 240 (SEQ ID NO:240), Figure 242 (SEQ ID
NO:242), Figure 244 (SEQ ID NO:244), Figure 246 (SEQ ID NO:246), Figure 248 (SEQ ID NO:248), Figure
30 250 (SEQ ID NO:250), Figure 252 (SEQ ID NO:252), Figure 254 (SEQ ID NO:254), Figure 256 (SEQ ID
NO:256), Figure 258 (SEQ ID NO:258), Figure 260 (SEQ ID NO:260), Figure 262 (SEQ ID NO:262), Figure
264 (SEQ ID NO:264), Figure 266 (SEQ ID NO:266), Figure 268 (SEQ ID NO:268), Figure 270 (SEQ ID
NO:270), Figure 272 (SEQ ID NO:272), Figure 274 (SEQ ID NO:274), Figure 276 (SEQ ID NO:276), Figure
278 (SEQ ID NO:278), Figure 280 (SEQ ID NO:280), Figure 282 (SEQ ID NO:282), Figure 284 (SEQ ID
35 NO:284), Figure 286 (SEQ ID NO:286), Figure 288 (SEQ ID NO:288), Figure 290 (SEQ ID NO:290), Figure
292 (SEQ ID NO:292), Figure 294 (SEQ ID NO:294), Figure 296 (SEQ ID NO:296), Figure 298 (SEQ ID
NO:298), Figure 300 (SEQ ID NO:300), Figure 302 (SEQ ID NO:302), Figure 304 (SEQ ID NO:304), Figure

[illegible]

572 (SEQ ID NO:572), Figure 574 (SEQ ID NO:574), Figure 576 (SEQ ID NO:576), Figure 578 (SEQ ID NO:578), Figure 580 (SEQ ID NO:580), Figure 582 (SEQ ID NO:582), Figure 584 (SEQ ID NO:584), Figure 586 (SEQ ID NO:586), Figure 588 (SEQ ID NO:588), Figure 590 (SEQ ID NO:590), Figure 592 (SEQ ID NO:592), Figure 594 (SEQ ID NO:594), Figure 596 (SEQ ID NO:596), Figure 598 (SEQ ID NO:598), Figure 600 (SEQ ID NO:600), Figure 602 (SEQ ID NO:602), Figure 604 (SEQ ID NO:604), Figure 606 (SEQ ID NO:606), Figure 608 (SEQ ID NO:608), or Figure 610 (SEQ ID NO:610), lacking its associated signal peptide.

20. A method for stimulating the release of TNF- α from human blood, said method comprising contacting said blood with a PRO1079, PRO827, PRO791, PRO1131, PRO1316, PRO1183, PRO1343, PRO1760, PRO1567 or PRO4333 polypeptide, wherein the release of TNF- α from said blood is stimulated.

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21. A method for stimulating the proliferation or differentiation of chondrocyte cells, said method comprising contacting said cells with a PRO6029 polypeptide, wherein the proliferation or differentiation of said cells is stimulated.

15

22. A method for detecting the presence of tumor in an mammal, said method comprising comparing the level of expression of any PRO polypeptide shown in Table 8 in (a) a test sample of cells taken from said mammal and (b) a control sample of normal cells of the same cell type, wherein a higher level of expression of said PRO polypeptide in the test sample as compared to the control sample is indicative of the presence of tumor in said mammal.

20

23. The method of Claim 22, wherein said tumor is adrenal tumor, lung tumor, colon tumor, breast tumor, prostate tumor, rectal tumor, cervical tumor or liver tumor.

24. An oligonucleotide probe derived from any of the nucleotide sequences shown in the accompanying figures.

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FIGURE 1

GAAGGCTGCCTCGCTGGTCCGAATTCGGTGGCGCCACGTCCGCCCGTCTCCGCCTTCTGCATCGCGGCTTCGGCG
GCTTCCACCTAGACACCTAACAGTCGCGGAGCCGGCCGCGTCGTGAGGGGGTCGGCACGGGGAGTCGGGCGGTCT
TGTGCATCTTGGCTACCTGTGGGTCTGAAGATGTCGGACATCGGAGACTGGTTCAGGAGCATCCCGGCGATCACGC
GCTATTGGTTCGCCGCCACCGTCGCCGTGCCCTTGGTCGGCAAACTCGGCCTCATCAGCCCGGCTACCTCTTCC
TCTGGCCCCGAAGCCTTCCCTTATCGCTTTCAGATTTGGAGGCCAATCACTGCCACCTTTATTTCCCTGTGGGTC
CAGGAACCTGGATTTCTTTATTTGGTCAATTTATATTTCTTATATCAGTATTCTACGCGACTTGAAACAGGAGCTT
TTGATGGGAGGCCAGCAGACTATTTATTCATGCTCCTCTTTAACTGGATTTGCATCGTGATTACTGGCTTAGCAA
TGGATATGCAGTTGCTGATGATTCCCTCTGATCATGTCAGTACTTTATGTCTGGGCCCAGCTGAACAGAGACATGA
TTGTATCATTTTGGTTTGGAAACACGATTTAAGGCTGCTATTTACCCTGGGTTATCCTTGGATTTCAACTATATCA
TCGGAGGCTCGGTAATCAATGAGCTTATTGGAAATCTGGTTGGACATCTTTATTTTTTCTAATGTTTCAGATACC
CAATGGACTTGGGAGGAAGAAATTTCTATCCACACCTCAGTTTTTGTACCGCTGGCTGCCAGTAGGAGAGGAG
GAGTATCAGGATTTGGTGTGCCCCCTGCTAGCATGAGGCGAGCTGCTGATCAGAATGGCGGAGGCGGGAGACACA
ACTGGGGCCAGGCTTTTCGACTTGGAGACCAGTGAAGGGGCGGCCCTCGGGCAGCCGCTCCTCTCAAGCCACATTT
CCTCCCAGTGTGGGTGCACTTAACAACCTGCGTTCTGGCTAACACTGTTGGACCTGACCCACACTGAATGTAGTC
TTTCAGTACGAGACAAAGTTTCTTAAATCCCGAAGAAAAATATAAGTGTTCACAAGTTTCACGATTCTCATTCA
AGTCCTTACTGCTGTGAAGAACAAATACCAACTGTGCAAAATGCAAACTGACTACATTTTTTGGTGTCTTCTCT
TCTCCCTTTCCGTCTGAATAATGGGTTTTAGCGGGTCCTAATCTGCTGGCATTGAGCTGGGGCTGGGTCACCAA
ACCCTTCCCAAAAGGACCTTATCTCTTTCTTGACACATGCCTCTCTCCCACTTTTCCCAACCCCCACATTTGCA
ACTAGAAAAAGTTGCCCATAAAATTGCTCTGCCCTTGACAGGTTCTGTTATTTATTGACTTTTGCCAAGGCTGGT
CACAACAATCATATTCACGTTATTTTCCCTTTTGGTGGCAGAACTGTTACCAATAGGGGGAGAAGACAGCCACG
GATGAAGCGTTTCTCAGCTTTTGAATTGCTTCGACTGACATCCGTTGTTAACCCTTTGCCACTCTTCAGATATT
TTTTATAAAAAAGTACCACTGAGTTCATGAGGGCCACAGATTGGTTATTAATGAGATACGAGGGTTGGTGTCTGG
GTGTTTGTTCCTGAGCTAAGTGATCAAGACTGTAGTGGAGTTGCAGCTAACATGGGTTAGGTTTAAACCATGGG
GGATGCACCCCTTTCGCTTTCATATGTAGCCCTACTGGCTTGTGTAGCTGGAGTAGTTGGGTGCTTGTGTGTTA
GGAGGATCCAGATCATGTTGGCTACAGGGAGATGCTCTCTTTGAGAGGTCCTGGGCATTGATTCCCATTTCATC
TCATTCTGGATATGTGTTTCATTGAGTAAAGGAGGAGAGACCCTCATACGCTATTTAAATGTCACTTTTTGCCTA
TCCCCCGTTTTTGGTTCATGTTTCAATTAATTGTGAGGAAGGCGCAGCTCCTCTCTGCACGTAGATCATTTTTTA
AAGCTAATGTAAGCACATCTAAGGGAATAACATGATTTAAGGTTGAAATGGCTTTAGAATCATTTGGGTTTGAGG
GTGTGTTATTTGAGTCATGAATGTACAAGCTCTGTGAATCAGACCAGCTTAAATACCCACACCTTTTTTTCGTA
GGTGGGCTTTTCTATCAGAGCTTGGCTCATAACCAATAAAGTTTTTTGAAGGCCATGGCTTTTACACAGTTA
TTTTATTTTATGACGTTATCTGAAAGCAGACTGTTAGGAGCAGTATTGAGTGGCTGTCACACTTTGAGGCAACTA
AAAAGGCTTCAAACGTTTTGATCAGTTTCTTTTCAGGAAACATTGTGCTCTAACAGTATGACTATTTCTTTCCCC
ACTCTTAAACAGTGTGATGTGTGTTATCCTAGGAAATGAGAGTTGGCAAACAACCTTCTCATTTTGAATAGAGTTT
GTGTGTACTTCTCCATATTTAATTTATATGATAAAATAGGTGGGGAGAGTCTGAACCTTAACTGTCATGTTTTGT
TGTTTCATCTGTGGCCACAATAAAGTTTACTTGTAAAATTTTAGAGGCCATTACTCCAATTATGTTGCACGTACAC
TCATTGTACAGGCGTGGAGACTCATTGTATGTATAAGAATATTTCTGACAGTGAGTGACCCGGAGTCTCTGGTGT
ACCCTCTTACCAGTCAGCTGCCTGCGAGCAGTCATTTTTTCTTAAAGGTTTACAAGTATTTAGAAGTTTTTCAGTT
CAGGGCAAAATGTTTCATGAAGTTATTCTCTTAAACATGGTTAGGAAGCTGATGACGTTATTGATTTTGTCTGGA
TTATGTTTCTGGAATAATTTTACCAAACAAGCTATTTGAGTTTTTGAAGTTGACAAGGCAAAACATGACAGTGGAT
TCTCTTTACAAATGGAAAAAAAATCCTTATTTGTATAAAGGACTTCCCTTTTTTGTAACTAATCCTTTTTTAT
TGGTAAAAATGTAAATTAATGTGCAACTTG

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FIGURE 2

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLGKISPAYLFLWPEAFLYRFQIWRPITATFYFPVGP GTGFLYLVN
LYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIPLIMSVLYVWAQLNRDMIVSFWFGTRF
KACYLPWVILGFNYIIGGSVINELIGNLVGHLYFFLMFRYPMDLGGRNFLSTPQFLYRWLPSSRRGGVSGFGVPPA
SMRRAADQNGGGGRHNWGGQGFRLGDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

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FIGURE 3

GAGCGAGGCCGGGGACTGAAGGTGTGGGTGTGAGCCCTCTGGCAGAGGGTTAACCTGGGTCAAATGCACGGATT
CTCACCTCGTACAGTTACGCTCTCCCGCGGCACGTCCGCGAGGACTTGAAGTCCTGAGCGCTCAAGTTTGTCCGT
AGGTCGAGAGAAGGCCATGGAGGTGCCGCCACCGGCACCGCGAGCTTTCTCTGTAGAGCATTGTGCCTATTTCC
CCGAGTCTTTGCTGCCGAAGCTGTGACTGCCGATTCCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGT
CCCAGAGCCCTATTACCCGGAATCTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAAT
TTCAAAGGACCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTTGGCTGGGTGTATGGGGGAATACC
AGCTTTTATTTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATCATAACCGGTTTGATGCTGT
GCAATCTGCACATCGTGCTGCCACACGAGGCTTCATTTCGTTATGGCTGGCGCTGGGGTTGGAGAACTGCAGTGTT
TGTGACTATATTCAACACAGTGAACACTAGTCTGAATGTATACCGAAATAAAGATGCCTTAAGCCATTTTGTAAAT
TGCAGGAGCTGTCACGGGAAGTCTTTTAGGATAAACGTAGGCCTGCGTGGCCTGGTGGCTGGTGGCATAATTGG
AGCCTTGCTGGGCACTCCTGTAGGAGGCCTGCTGATGGCATTTCAGAAGTACGCTGGTGAGACTGTTTCAGGAAAG
AAAACAGAAGGATCGAAAGGCACTCCATGAGCTAAACTGGAAGAGTGGAAAGGCAGACTACAAGTTACTGAGCA
CCTCCCTGAGAAAATTGAAAGTAGTTTACGGGAAGATGAACCTGAGAATGATGCTAAGAAAATTGAAGCACTGCT
AAACCTTCCTAGAAACCCTTCAGTAATAGATAAACAAGACAAGGACTTGAAAGTCTCTGAACCTGAAACTCACTG
GAGAGCTGAAGGGAGCTGCCATGTCCGATGAATGCCAACAGACAGGCCACTCTTTGGTCAGCCTGCTGACAAATT
TAAGTGCTGGTACCTGTGGTGGCAGTGGCTTGCTCTTGTCTTTTTCTTTCTTTTAACTAAGAATGGGGCTGTT
GTACTCTCACTTTACTTATCCTTAAATTTAAATACATACTTATGTTTGTATTAATCTATCAATATATGCATACAT
GGATATATCCACCCACCTAGATTTTAAGCAGTAAATAAACATTTTCGCAAAAGATTAAAGTTGAATTTTACAGTTT

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FIGURE 4

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23318
><subunit 1 of 1, 285 aa, 1 stop
><MW: 32190, pI: 9.03, NX(S/T): 2
MEVPPPPAPRSFLCRALCLFPRVFAAEAVTADSEVLEERQKRLPYVPEPYYPESGWDRLRELFQKDEQQRISKDLA
NICKTAATAGIIGWVYGGIPAFIHAKQQYIEQSQAETIYHNRFDAVQSAHRAATRGFIYGRWGWRTAVFVTIFN
TVNTSLNVYRNKDALSHEFVIAGAVTGSLFRINVGLRGLVAGGIIGALLGTPVGGLLMAFQKYAGETVQERKQKDR
KALHELKLEEWKGRLQVTEHLPEKIESSLREDEPENDAKKIEALLNLPRNPSVIDKQDKD
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Important Features:**Signal Peptide:**

amino acids 1-24

Transmembrane domains:

amino acids 76-96 and 171-195

N-glycosylation site:

amino acids 153-156

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FIGURE 5

CGGACGCGTGGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTTCCTGCGCGCGCGCCTGAAGTCGGC
GTGGGCGTTTTGAGGAAGCTGGGATACAGCATTTAATGAAAAATTTATGCTTAAGAAGTAAAAATGGCAGGCTTCC
TAGATAATTTTCGTTGGCCAGAATGTGAATGTATTGACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTCTG
CAGGTATATTGTTTTTACAGGCTGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAAGCCAGAACAGTTGA
ACCATGCCTTTCACACATGTGGTGTATTTCCACATTGGCTTTCTTCATGATAAATGCTGTATCCAATGCTCAGG
TGAGAGGTGATAGCTATGAAAGCGGCTGTTTAGGAAGAACAGGTGCTCGAGTTTGGCTTTTCATTGGTTTCATGT
TGATGTTTGGGTCACTTATTGCTTCCATGTGGATTCTTTTTGGTGCATATGTTACCCAAAATACTGATGTTTATC
CGGGACTAGCTGTGTTTTTCAAATGCACTTATATTTTTTAGCACTCTGATCTACAAATTTGGAAGAACCGAAG
AGCTATGGACCTGAGATCACTTCTTAAGTCACATTTTCCTTTTGTATATTCTGTTTGTAGATAGGTTTTTTATC
TCTCAGTACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTTTGTTTCTTTACATTTTTATGTTCTGAGTT
TTGAAATAGTTTTATGAAATTTCTTTATTTTTCATTGCATAGACTGTTAATATGTATATAATACAAGACTATATG
AATTGGATAATGAGTATCAGTTTTTTATTCCTGAGATTTAGAACTTGATCTACTCCCTGAGCCAGGGTTACATCA
TCTTGTCATTTTAGAAAGTAACCACTCTTGTCTCTCTGGCTGGGCACGGTGGCTCATGCCTGTAATCCCAGCACTT
TGGGAGGCCGAGGCCGGCCGATTGCTTGAGGTCAAGTGTGAGACCAGCCTGGCCAACATGGCGAAACCCCATC
TACTAAAAATACAAAAATTAGCCAGGCATGGTGGTGGGTGCCTGTAATCCCAGCTACCTGGGAGGCTGAGGCAGG
AGAATCGCTTGAACCCGGGGGGCAGAGGTTGCAGTGAGCTGAGTTTGCGCCACTGCACTCTAGCCTGGGGGAGAA
AGTGAAACTCCCTCTCAAAAAAAGACCACTCTCAGTATCTCTGATTTCTGAAGATGTACAAAAAATATAGCTT
CATATATCTGGAATGAGCACTGAGCCATAAAAGGTTTTAGCAAGTTGTAACCTATTTTGGCCTAAAAATGAGGT
TTTTTTGGTAAAGAAAAAATATTTGTTCTTATGTATTGAAGAAGTGACTTTTATATAATGATTTTTTAAATGCC
CAAAGGACTAGTTTGAAAGCTTCTTTTAAAAAGAATTCCTCTAATATGACTTTATGTGAGAA

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FIGURE 6

MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWWMIDAADVYPKPEQLNHAFHTCGVFSTLAFMINAV
SNAQVRGDSYESGCLGRTGARVWLFIFGMLMFGSLIASMWILFGAYVTQNTDVYPGLAVFFQNALIFFSTLIYKF
GRTEELWT

Important features:

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 23-42 (type II), 60-80, 97-117, 128-148

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FIGURE 7

CGGTGGTTTTTGTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTGTAGCTTCTCCAGG
TATGGACCCATAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAGGATGTGCGTCTCTC
CACTAGAAGCTCTTCTGAGGGAGGTAATTAACAGTGGAAATGGAAAAACAGTGCTGTAGTCATCCTGTAATA
TGCTCCTTGTCAACAATGTATACATTCTGCTAGGTGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTA
GTGAAGTATTCTGCAATGAAGAAAACAAGTATGATTATCTTCCAACACTGTGAATGTGTGCTCAGAACTGGTG
AAGCTAGTTTTCTGTGTGCTTGTGTCAATCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATATGCT
TCCTGGAAGGAATCTCTGATTTTCATGAAGTGGTCCATTCTCGCCTTTCTTTATTTCTGGATAACTTGATTGTC
TTCTATGTCCTGTCCTATCTTCAACCAGCCATGGCTGTTATCTTCTCAAATTTTAGCATTATAACAACAGCTCTT
CTATTCAAGATAGTGCTGAAGAGGCGTCTAACTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATT
GTGGCCTTGACTGCCGGGACTAAAACCTTTACAGCACAACTTGGCAGGACGTGGATTTTCATCACGATGCCCTTTTC
AGCCCTTCCAATTCCTGCCTTCTTTTCAGAAGTGAGTGTCCAGAAAAGACAATTGTACAGCAAAGGAATGGACT
TTTCTGAAGCTAAATGGAACACCACAGCCAGAGTTTTTCAGTCACATCCGTCTTGGCATGGGCCATGTTCTTATT
ATAGTCCAGTGTTTTATTTCTTCAATGGCTAATATCTATAATGAAAAGATACTGAAGGAGGGGAACAGCTCACT
GAAAGCATCTTCATACAGAACAGCAAACTCTATTTCTTTGGCATTCTGTTTAATGGGCTGACTCTGGGCCTTCAG
AGGAGTAACCGTGATCAGATTAAAGAACTGTGGATTTTTTATGGCCACAGTGCATTTTCAGTAGCCCTATTTTTT
GTAAGTGCATTCAGGGCCTTTTCAGTGGCTTTTCATTCTGAAGTTCCTGGATAACATGTTCCATGTCTTGATGGCC
CAGGTTACCACTGTCTATTATCACAACTGTCTGTCTGGTCTTTGACTTCAGGCCCTCCCTGGAATTTTCTTTG
GAAGCCCCATCAGTCCCTTCTCTATATTTATTTATAATGCCAGCAAGCCTCAAGTTCGGGAATACGCACCTAGG
CAAGAAAGGATCCGAGATCTAAGTGGCAATCTTTGGGAGCGTTCAGTGGGGATGGAGAAGAACTAGAAAAGACTT
ACCAAACCAAGAGTGATGAGTCAGATGAAGATACTTTCTAACTGGTACCCACATAGTTTGCAGCTCTCTTGAAC
CTTATTTTTCATTTTTCAGTGTGTAATATTTATCTTTTCACTTTGATAAACCAGAAATGTTTCTAAATCCTAA
TATTCTTTGCATATATCTAGCTACTCCCTAAATGGTTCATCCAGGCTTAGAGTACCAAAGGCTAAGAAATTC
TAAAGAACTGATACAGGAGTAACAATATGAAGAATTCATTAATATCTCAGTACTTGATAAATCAGAAAGTTATAT
GTGCAGATTATTTTCTTGGCCTTCAAGCTTCCAAAAAACTTGTAAATAATCATGTTAGCTATAGCTTGTATATAC
ACATAGAGATCAATTTGCCAAATATTCACAATCATGTAGTTCTAGTTTACATGCCAAAGTCTTCCCTTTTAAACA
TTATAAAAGCTAGGTTGTCTCTTGAATTTTGGGCCCCAGAGATAGTCATTTTGAAGTAAAGAGCAACGGGACC
CTTTCTAAAAACGTTGGTTGAAGGACCTAAATACCTGGCCATACCATAGATTTGGGATGATGTAGTCTGTGCTAA
ATATTTTGTCTGAAGAAGCAGTTTCTCAGACACAACATCTCAGAATTTTAATTTTGAAGATTCATGGGAAATTTGG
ATTTTTGTAATAATCTTTTGATGTTTTAAACATTGGTTCCCTAGTCACCATAGTTACCACTTGATTTTTAAGTCA
TTTAAACAAGCCACGGTGGGGCTTTTTCTCCTCAGTTTGAGGAGAAAAATCTTGATGTCTTACTCCTGAATTA
TTACATTTTGGAGAATAAGAGGGCATTTTATTTTATTAGTTACTAATTCAGCTGTGACTATTGTATATCTTTCC
AAGAGTTGAAATGCTGGCTTCAGAATCATACCAGATTGTGAGTGAAGCTGATGCCTAGGAACCTTTTAAAGGGATC
CTTTCAAAGGATCACTTAGCAAACACATGTTGACTTTTAACTGATGTATGAATATTAATACTCTAAAAATAGAA
AGACCAGTAATATATAAGTCACTTTACAGTGCTACTTCACACTTAAAAGTGCATGGTATTTTTCATGGTATTTTG
CATGCAGCCAGTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATATTAAAAATTAGCAAACAAAAGTGAC
TTGCTCAGGGTCATGCAGCTGGGTGATGATAGAAGAGTGGGCTTTAACTGGCAGGCCTGTATGTTTACAGACTAC
CATACTGTAATATAGGCTTTATGGTGTCTATTCTCAGAACTTATACATTTCTGCTCTCCTTTCTCCTAAGTTTC
ATGCAGATGAATATAAGGTAATATACTATTATATAATTCATTTGTGATATCCACAATAATATGACTGGCAAGAAT
TGGTGGAAATTTGTAATTAATAATTTATTAACCT

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FIGURE 8

MEKQCCSHPVICSLSTMYTFLLGAIFIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVKLVFCVLVSFCVIK
KDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLQPAMAVIFS NFSIITALLFRIVLKRRRLNWIQ
WASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDAFFSPSNSCLLFRSECPRKDNCTAKEWTFPEAKWNNTARVFS
HIRLGMGHVLIIVQCFISSMANIYNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFY
GHSAFSVALIFVTAFQGLSVAFILKFLDNMFHVLMAQVTTVIIITTVSVLVFDFRPSLEFFLEAPSVLLSIFIYNA
SKPQVPEYAPRQERIRDL SGNLWERS SSGDGEELERLTKPKSDESDETF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293, 298-318,
328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

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FIGURE 9

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGTATGAGCAGGTCTG
AAGACTAACATTTTGTGAAGTTGTAAAACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTTC
CTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCTTCATATTTTCATACATTACTGCAGTAACACTCCACCAT
ATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTA
AATATTGCGGCAGTTTATGCATTGCTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAAGAG
AACGTTATCATCAAATTAACAAGGCTGGCCTTGTAAGTGGAGCTGTGCTTACCTTTGGTATGGGCTCATTATAT
AACTTCCAGAAAACAACCCTTTTGTCTGCACATGTAAGTGGAGCTGTGCTTACCTTTGGTATGGGCTCATTATAT
ATGTTTGTTCAGACCATCCTTTCTACCAAATGCAGCCCAAATCCATGGCAAACAAGTCTTCTGGATCAGACTG
TTGTTGGTTATCTGGTGTGGAGTAAGTGCACCTTAGCATGCTGACTTGCTCATCAGTTTGCACAGTGGCAATTT
GGGACTGATTTAGAACAGAACTCCATTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACTACTGCA
GCAGAATGGTCTATGTCATTTTCCTTCTTTGGTTTTTTCCTGACTTACATTCGTGATTTTCAGAAAAATTTCTTTA
CGGGTGGAAGCCAATTTACATGGATTAACCCTCTATGACACTGCACCTTGCCCTATTAACAATGAACGAACACGG
CTACTTTCCAGAGATATTTGATGAAAGGATAAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGG
TTCACAGAAGTTGCTTATTTCTTCTCTGAAATTTTCAACCACTTAATCAAGGCTGACAGTAACACTGATGAATGCT
GATAATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCATCAAGAAGACTATTA AAAACA
CCTATGCCTATACTTTTTTATCTCAGAAAATAAAGTCAAAAGACTATG

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FIGURE 10

MWWFQQGLSFLPSALVIWTSAAFI FSYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNIAAVLCIATIIYVRY
KQVHALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVSGAVLTFGMGSLYMFVQTILSYQMOPKI
HGKQVFWIRLLLVIWCGVSALSMLTCSSVLHSGNFGTDLEQKLHWNPEDKGYVLHMITTAAEWSMSFSFFGFFLT
YIRDFQKISLRVEANLHGLTLYDTAPCPINNERTRLLSRDI

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FIGURE 11

CCCACGCGTCCGCCCCCGCTGCGTCCCGGAGTGCAAGTGAGCTTCTCGGCTGCCCCGCGGGCCGGGGTGCGGAG
CCGACATGCGCCCCGCTTCTCGGCCTCCTTCTGGTCTTCGCCGGGTGCACCTTCGCCTTGACTTGCTGTCGACGC
GACTGCCCCGCGGGCGGAGACTGGGCTCCACCGAGGAGGCTGGAGGCAGGTGCTGTGGTCCCCCTCCGACCTGG
CAGAGCTGCGGGAGCTCTCTGAGGTCCTTCGAGAGTACCGGAAGGAGCACCAGGCCTACGTGTTCTGCTCTTCT
GCGGCGCCTACCTCTACAAACAGGGCTTTGCCATCCCCGGCTCCAGCTTCCTGAATGTTTTAGCTGGTGCCTTGT
TTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGTGACCTCGGTGGGTGCCACATGCTGCTACCTGCTCTCCA
GTATTTTTGGCAAACAGTTGGTGGTGTCTACTTTCTTGATAAAGTGGCCCTGCTGCAGAGAAAGGTGGAGGAGA
ACAGAAACAGCTTGTTTTTTTTCTTATTGTTTTTGAGACTTTTCCCCATGACACCAAACCTGGTTCTTGAACCTCT
CGGCCCCAATTCTGAACATTCCCATCGTGCAAGTTCTTCTCTCAGTTCTTATCGGTTTGATCCCATATAATTTCA
TCTGTGTGCAGACAGGGTCCATCCTGTCAACCCTAACCTCTCTGGATGCTCTTTCTCCTGGGACACTGTCTTTA
AGCTGTTGGCCATTGCCATGGTGGCATTAAATCCTGGAACCCTCATTAAAAAATTTAGTCAGAAACATCTGCAAT
TGAATGAAACAAGTACTGCTAATCATATACACAGTAGAAAAGACACATGAATCTGGATTTTCTGTTTGCCACATCC
CTGGACTCAGTTGCTTATTTGTGTAATGGATGTGGTCTCTAAAGCCCCTCATTGTTTTTGATTGCCTTCTATAG
GTGATGTGGACACTGTGCATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGTATTACATC
AGGTTTTCAAACCAGCCCTGGTGTAGCAGACACTGCAACAGATGCCTCCTAGAAAATGCTGTTTGTGGCCGGGCG
CGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCCGGTGATTCAACAAGGTCAGGAGTTCAAGACC
AGCCTGGCCAAGATGGTGAAATCCTGTCTCTAATAAAAAATACAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGT
AATCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATTGCTTGAACCAAGGTGGCAGAGGTTGCAGTAAGCCAAGAT
CACACCACTGCACTCCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

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FIGURE 12

MRPLLGLLLVFAGCTFALYLLSTRLPGRRLGSTEEAGGRSLWFPSDLAELRELSEVLREYRKEHQAYVFLFCG
AYLYKQGFAIPGSSFLNVLGALFGPWLGLLLCCVLTSVGATCCYLLSSIFGKQLVVSYPDKVALLQRKVEENR
NSLFFFLLFLRLFPMTPNWFLNLSAPILNIPVQFFSVLIGLIPYNFICVQTGSILSTLTSLDALFSWDTVEKL
LAIAMVALIPGTLIKKEFSQKHLQLNETSTANHIHSRKDT

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31

Sugar transport proteins.

amino acids 162-172

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FIGURE 13

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGAGTCCCGGCTGCAGCACCTGGGAGAAGGCAGACCGTGTGAG
GGGGCCTGTGGCCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAGGCAGGAGCCTTCCTTACACTTCGCCA
TGAGTTTTCTCATCGACTCCAGCATCATGATTACCTCCCAGATACTATTTTTTGGATTTGGGTGGCTTTTCTTCA
TGCGCCAATTGTTTAAAGACTATGAGATACGTGAGTATGTTGTACAGGTGATCTTCTCCGTGACGTTTGCATTTT
CTTGCACCATGTTTGAGCTCATCATCTTTGAAATCTTAGGAGTATTGAATAGCAGCTCCCGTTATTTTCACTGGA
AAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTTTTCATGGTGCCTTTTACATTGGCTATTTTATTGTGAGCA
ATATCCGACTACTGCATAAAACAAGACTGCTTTTTTCTGTCTCTTATGGCTGACCTTTATGTATTTCTTCTGGA
AACTAGGAGATCCCTTTCCCATCTCAGCCCAAAACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTTG
GTGTGATTGGAGTGACTCTCATGGCTCTCTTTCTGGATTTGGTGCTGTCAACTGCCCATACACTTACATGTCTT
ACTTCCTCAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATATGATCA
TAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAAGTGCATAACAAACCATCAG
GTTTCTGGGGAATGATAAAAAGTGTTACCACTTCAGCATCAGGAAGTGAATACTTACTCTTATTCAACAGGAAG
TGGATGCTTTGGAAGAATTAAGCAGGCAGCTTTTTCTGGAAACAGCTGATCTATATGCTACCAAGGAGAGAATAG
AATACTCCAAAACCTTCAAGGGGAAATATTTAATTTTCTTGGTTACTTTTTCTCTATTTACTGTGTTTGGAAAA
TTTTTCATGGCTACCATCAATATTGTTTTGATCGAGTTGGGAAAACGGATCCTGTCAAGAGGCATTGAGATCA
CTGTGAATTATCTGGGAATCCAATTTGATGTGAAGTTTTGGTCCCAACACATTTCTTCTATTCTTGTGGAATAA
TCATCGTCACATCCATCAGAGGATTGCTGATCACTCTTACCAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCCT
CCAATGTCATTGTCTGCTATTAGCACAGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGA
GTATGCCTTTAGAATACCGCACCATTAATCACTGAAGTCCTTGGAGAACTGCAGTTCAACTTCTATCACCGTTGGT
TTGATGTGATCTTCTGGTCAGCGCTCTCTCTAGCATACTCTTCTCTATTTGGCTCACAAACAGGCACCAGAGA
AGCAAATGGCACCT**TGA**ACTTAAGCCTACTACAGACTGTTAGAGGCCAGTGGTTTCAAATTTAGATATAAGAGG
GGGGAAAAATGGAACCAGGGCCTGACATTTTATAAACAAACAAAATGCTATGGTAGCATTTTTCACCTTCATAGC
ATACTCCTTCCCCGTGAGGTGATACTATGACCATGAGTAGCATCAGCCAGAACATGAGAGGGAGAACTAACTCAA
GACAATACTCAGCAGAGAGCATCCCGTGTGGATATGAGGCTGGTGTAGAGGCGGAGAGGAGCCAAGAACTAAAG
GTGAAAAATACACTGGAACCTCTGGGGCAAGACATGTCTATGGTAGCTGAGCCAAACACGTAGGATTTCCGTTTTA
AGGTTACATGGAAGGTTATAGCTTTGCCTTGAGATTGACTCATTAATCAGAGACTGTAACAAAAA
AAAAAAGGGCGCGGCGACTCTAGAGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCACTTGTTTATTG
CAGCTTATAATG

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FIGURE 14

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEILGVLNSSSRYPFH
KMNL CVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTFMYFFWKLGDFFPILSPKHGILSIEQLISRV
GVIGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDILALERRLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPS
GFWGMIKSVTTSASGSENLTLIQQEVDLEELSRQLFLETADLYATKERIEYSKTFKGKYNFLGYFFSIYCVWK
IFMATINIVFDRVGKTDVPTRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKFFYAISSSKS
SNVIVLLLAQIMGMYFVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSALSSILFLYLAHKQAPE
KQMAP

Important features:**Signal peptide:**

amino acids 1-23

Potential transmembrane domains:

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398, 425-444

N-glycosylation sites.

amino acids 67-70, 180-183 and 243-246

Eukaryotic cobalamin-binding proteins

amino acids 151-160

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FIGURE 15

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCGGGACATGCGGCCC
CAGGAGCTCCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGTTGCTGCTGCTGCCGCCGCCGCGTGCCTGCC
CACAGCGCCACGCGCTTCGACCCACCTGGGAGTCCCTGGACGCCGCCAGCTGCCGCGTGGTTTGACCAAGGCC
AAGTTCGGCATCTTCATCCACTGGGGAGTGTTTTCCGTGCCAGCTTCGGTAGCGAGTGGTTCTGGTGGTATTGG
CAAAAGGAAAAGATACCGAAGTATGTGGAATTTATGAAAGATAATTACCCTCCTAGTTTCAAATATGAAGATTTT
GGACCACTATTTACAGCAAAATTTTTTAATGCCAACCAGTGGGCAGATATTTTTTCAGGCCTCTGGTGCCAAATAC
ATTGTCTTAACTTCCAAACATCATGAAGGCTTTACCTTGTGGGGTCAAGATATTCGTGGAACTGGAATGCCATA
GATGAGGGGGCCCAAGAGGGACATTGTCAAGGAACCTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTTTGGA
CTGTACTATTCCTTTTTGAATGGTTTCATCCGCTCTTCTTGAGGATGAATCCAGTTCATTCCATAAGCGGCAA
TTTCCAGTTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACATATCAGCCTGAGGTTCTGTGGTCCGAT
GGTGACGGAGGAGCACCGGATCAATACTGGAACAGCACAGGCTTCTTGGCCTGGTTATATAATGAAAGCCAGTT
CGGGGCACAGTAGTCACCAATGATCGTTGGGGAGCTGGTAGCATCTGTAAGCATGGTGGCTTCTATACCTGCAGT
GATCGTTATAACCCAGGACATCTTTGCCACATAAATGGGAAAACCTGCATGACAATAGACAAACTGTCTGGGGC
TATAGGAGGGAAGCTGGAATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTGTAGAGACAGTTTCA
TGTGGAGGAAATCTTTGATGAATATTGGGCCCACACTAGATGGCACCATTCTGTAGTTTTTGAGGAGCGACTG
AGGCAAGTGGGGTCTGGCTAAAAGTCAATGGAGAAGCTATTTATGAAACCTATACCTGGCGATCCCAGAATGAC
ACTGTCACCCCAGATGTGTGGTACACATCCAAGCCTAAAGAAAAATTAGTCTATGCCATTTTTCTTAAATGGCCC
ACATCAGGACAGCTGTTCTTGGCCATCCCAAAGCTATTCTGGGGGCAACAGAGGTGAACTACTGGGCCATGGA
CAGCCACTTAACTGGATTTCTTGGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTCATCAGATG
CCGTGTAAATGGGGCTGGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTGATGCTGCAAGTT
ATGTCTAAGGCTAGGAACATATCAGGTGTCTATAATTGTAGCACATGGAGAAAGCAATGTAACTGGATAAGAAAA
TTATTTGGCAGTTCAGCCCTTTCCCTTTTTCCCACTAAATTTTTCTTAAATTACCCATGTAAACCATTTTAACTCT
CCAGTGCACCTTTGCCATTAAAGTCTCTTCACATTGATTTGTTTCCATGTGTGACTCAGAGGTGAGAATTTTTTCA
CATTATAGTAGCAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTTTATGTTGAAGCCATATCCCCATGAT
TATATAGTTATGCATCACTTAATATGGGGATATTTTCTGGGAAATGCATTGCTAGTCAATTTTTTTTTGTGCCAA
CATCATAGAGTGTATTTACAAAATCCTAGATGGCATAGCCTACTACACACCTAATGTGTATGGTATAGACTGTTG
CTCCTAGGCTACAGACATATACAGCATGTTACTGAATACTGTAGGCAATAGTAACAGTGGTATTTGTATATCGAA
ACATATGGAACATAGAGAAGGTACAGTAAAAATACTGTAAATAAATGGTGACCTGTATAGGGCACTTACCAC
GAATGGAGCTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTATTGAA
CACTGCCAGACGTTATAAAATACTGTATGCTTAGGCTACACTACATTTATAAAAAAAGTTTTTCTTCTTCAATT
ATAAATTAACATAAGTGTACTGTAACCTTTACAAACGTTTTAATTTTTTAAACCTTTTTGGCTCTTTGTAATAAC
ACTTAGCTTAAACATAAACTCATTGTGCAATGTAA

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FIGURE 16

MRPQELPRLAFPLLLLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHGVSFVPSFGSEWFW
WYWQKEKIPKYVEFMKDNYPSPFKYEDFGPLFTAKFFNANQWADIFQASGAKYIVLTSKHHEGFTLWGSEYSWNW
NAIDEGPKRDIVKELEVAIRNRTDLRFGLYYSLFEWFHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVL
WSDGDGGAPDQYWNSTGFLAWLYNESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKL
SWGyrREAGISDYLTIIEELVKQLVETVSCGNNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYTWRS
QNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWISLEQNGIMVELPQITI
HQMPCCKWGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319, 375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 17

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCCCTCTAAAGCAGATTTAGAGTGGTAAAAAAGCAAAACACA
 CCAAACGCTCGCAGCCACAAAGGGATGAAATTTCTTCTGGACATCCTCCTGCTTCTCCCGTTACTGATCGTCTG
 CTCCCTAGAGTCCTTCGTGAAGCTTTTTATTCTTAAGAGGAGAAAATCAGTCACCGCGCAAATCGTGTCTGATTAC
 AGGAGCTGGGCATGGAATTTGGGAGACTGACTGCCTATGAATTTGCTAAACTTTAAAGCAAGCTGGTTCTCTGGGA
 TATAAATAAGCATGGACTGGAGGAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTTCATACCTTTGTGGT
 AGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAGAGGTTGAAGCGAGAATTTGGAGATGTTAGTATTTTT
 AGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTGTCTACACAAGATCCTCAGATTTGAAAGACTTTTGA
 AGTTAATGTACTTGCACATTTCTGGACTACAAAGGCATTTCTTCTGCAATGACGAAGAATAACCATGGCCATAT
 TGTCACTGTGGCTTCGGCAGCTGGACATGTCTCGGTCCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGCTGC
 TGTGGATTTTCATAAACTTTGACAGATGAACCTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATGTCTGTG
 TCCTAATTTTCTGAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTTGGGACCCACTCTGGAACCTGAGGAAGT
 GGTAACAGGCTGATGCATGGGATTTCTGACTGAGCAGAGATGATTTTATTCATCTTCTATAGCTTTTATTAAC
 AACATTGGAAGGATCCTTCCTGAGCGTTTCCTGGCAGTTTTTAAACGAGAAAATCAGTGTTAAGTTTGATGCAGT
 TATTGGATATAAAATGAAAGCGCAATTAAGCACCCTAGTTTTCTGAAAACCTGATTTACCAGGTTTAGGTTGATGTCA
 TCTAATAGTGCCAGAAATTTAATGTTTGAACCTCTGTTTTTCTAATTATCCCCATTTCTTCAATATCATTTTTG
 AGGCTTTGGCAGTCTTCATTTACTACCACCTTGTCTTTAGCCAAAAGCTGATTACATATGATATAAACAGAGAAA
 TACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAGAACCAAAATGACTTTATTAATAAATATTTTCCAAGATTA
 TTTGTGGCTCACCTGAAGGCTTTGCAAAATTTGTACCTTAACGGTTTATTAAACATATATTTTATTTTGTATTG
 CACTTAAATTTTGTATAATTTGTGTTTCTTTTTCTGTTCTACATAAAATCAGAACTTCAAGCTCTTAAATAAA
 ATGAAGGACTATATCTAGTGGTATTTTACAATGAATATCATGAACCTCTCAATGGGTAGGTTTCATCCTACCCATT
 GCCACTCTGTTTCTGAGAGATACCTTCACATTTCCAATGCCAACATTTCTGCACAGGGAAGCTAGAGGTGGATAC
 ACGTGTGTCAGTATAAAAGCATCACTGGGATTTAAGGAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAA
 TAAATGGATCACACTTAAAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAA
 AAAAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAAAGCAAA

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FIGURE 18

MKFLLDILLLLPLLVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSKL
VLWDINKHGLEETAACKCKGLGAKVHTFVVDSCNREDIYSSAKKVKAIEIGDVSILVNNAGVVYT
SDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYCSSK
FAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRMLMHGILT
EQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

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FIGURE 19

CCCACGCGTCCGCTCCGCGCCCTCCCCCGCCTCCCGTGCGGTCCGTCGGTGGCCTAGAGAT
GCTGCTGCCGCGGTTGCAGTTGTCGCGCACGCCTCTGCCCGCCAGCCCGCTCCACCGCCGTAG
CGCCCGAGTGTCGGGGGGCGCACCCGAGTCGGGGCC**ATG**AGGCCGGGAACCGCGCTACAGGCCG
TGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCCGCGACGGGTGCGCTGCTGAGTGCCTCGG
ATTTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGGAGGGACACAGAGGCCTTGTATATAAG
TCATTTACTTCCATGATACTTCTCGAAGACTGAACTTTGAGGAAGCCAAAAGAAGCCTGCAGGA
GGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAAAAGTTCA
TTGAAAACCTCTTGCCATCTGATGGTGACTTCTGGATTGGGCTCAGGAGGCGTGAGGAGAAAC
AAAGCAATAGCACAGCCTGCCAGGACCTTTATGCTTGGACTGATGGCAGCATATCACAATTTA
GGAAGTGGTATGTGGATGAGCCGTCCTGCGGCAGCGAGGTCTGCGTGGTCATGTACCATCAGC
CATCGGCACCCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAATGATGACCGGTGCAACA
TGAAGAACAATTTTCAATTTGCAAATATTCTGATGAGAAACCAGCAGTTTCTTCTAGAGAAGCTG
AAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAGGAAGAAGATGCCA
AAAAAACATTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCTACATCCTAATCCCAGCA
TTCCCTTCTCCTCCTCCTTGTGGTCACCACAGTTGTATGTTGGGTTTGGATCTGTAGAAAAA
GAAAACGGGAGCAGCCAGACCTAGCACAAAGAAGCAACACACCATCTGGCCCTCTCCTCACC
AGGGAAACAGCCCGGACCTAGAGGTCTACAATGTCATAAGAAAACAAAGCGAAGCTGACTTAG
CTGAGACCCGGCCAGACCTGAAGAATATTTCAATCCGAGTGTGTTCTGGGAGAAGCCACTCCCG
ATGACATGTCTTGTGACTATGACAACATGGCTGTGAACCCATCAGAAAGTGGGTTTGTGACTC
TGGTGAGCGTGGAGAGTGGATTTGTGACCAATGACATTTATGAGTTCTCCCCAGACCAAATGG
GGAGGAGTAAGGAGTCTGGATGGGTGGAAAATGAAATATATGGTTAT**TAG**GACATATAAAAAA
CTGAAACTGACAACAATGGAAAAGAAATGATAAGCAAAATCCTCTTATTTTCTATAAGGAAAA
TACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCCTGTGGATGAGCATGTGGTCCCCACGA
CCTCCTGTTGGACCCCCACGTTTTTGGCTGTATCCTTTATCCCAGCCAGTCATCCAGCTCGACC
TTATGAGAAGGTACCTTGCCAGGTCTGGCACATAGTAGAGTCTCAATAAATGTCACTTGGTT
GGTTGTATCTAACTTTTAAGGGACAGAGCTTTACCTGGCAGTGATAAAGATGGGCTGTGGAGC
TTGGAAAACACCTCTGTTTTTCTTGCTCTATACAGCAGCACATATTATCATACAGACAGAAA
ATCCAGAATCTTTTCAAAGCCCACATATGGTAGCACAGGTTGGCCTGTGCATCGGCAATTCTC
ATATCTGTTTTTTTCAAAGAATAAAATCAAATAAAGAGCAGGAAAAAAAAA

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FIGURE 20

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLDLRGGQPVCRRGGTQRPCYKVIYFHDTSRRLN
FEEAKEACRRDGGQLVSI ESEDEQK LIEKF IENLLPSDGD F WIGLRRREEKQSNSTACQDLYA
WTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKYSDE
KPAVPSREAEGEETELTPVLPEETQEEDAKKTFKESREAA NLAYILIPSIPLLLLLLVVTTV
VCWWICRKRKREQPD PSTKKQHTIWPSPHQGN SPDLEVYNVIRKQSEADLAETRPDLKNISF
RVCSGEATPDDMSCDYDNMAVNPSESGFVTLVSVESGFVTNDIYEFSPDQMGRSKESGWVENE
IYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327**N-myristoylation site.**

amino acids 18-24, 37-43, 76-82, 146-152

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FIGURE 21

AGGCTCCCGCGCGCGGCTGAGTGCGGACTGGAGTGGGAACCCGGGTCCCGCGCTTAGAGAACACGCG**ATG**ACCA
CGTGGAGCCTCCGGCGGAGGCCGGCCGCGCAGCTGGGACTCCTGCTGCTGGTTCGTCTTGGGCTTCCTGGTGCTCC
GCAGGCTGGACTGGAGCACCTTGGTCCCTCTGCGGCTCCGCCATCGACAGCTGGGGCTGCAGGCCAAGGGCTGGA
ACTTCATGCTGGAGGATTCCACCTTCTGGATCTTCGGGGCTCCATCCACTATTTCCGTGTGCCAGGGAGTACT
GGAGGGACCGCCTGCTGAAGATGAAGGCCTGTGGCTTGAACCCCTCACCACCTATGTTCCGTGGAACTGCATG
AGCCAGAAAGAGGCAAATTTGACTTCTCTGGGAACCTGGACCTGGAGGCCTTCGTCTGATGGCCGCAGAGATCG
GGCTGTGGGTGATTCTGCGTCCAGGCCCTACATCTGCAGTGAGATGGACCTCGGGGGCTTGCCAGCTGGCTAC
TCCAAGACCCTGGCATGAGGCTGAGGACAACCTTACAAGGGCTTCACCGAAGCAGTGGACCTTTATTTTGACCACC
TGATGTCCAGGGTGGTGCCACTCCAGTACAAGCGTGGGGGACCTATCATTGCCGTGCAGGTGGAGAATGAATATG
GTTCTATAATAAAGACCCCGCATACATGCCCTACGTCAAGAAGGCACTGGAGGACCGTGGCATTGTGGAACCTGC
TCCTGACTTCAGACAACAAGGATGGGCTGAGCAAGGGGATTGTCCAGGGAGTCTTGCCACCATCAACTTGCAGT
CAACACACGAGCTGCAGTACTGACCACCTTTCTCTTCAACGTCCAGGGGACTCAGCCCAAGATGGTGATGGAGT
ACTGGACGGGGTGGTTTGAAGTCTGAGGAGGCGCTCACAATATCTTGGATTCTTCTGAGGTTTTGAAAACCGTGT
CTGCCATTGTGGACGCGGGCTCCTCCATCAACCTCTACATGTTCCACGAGGCACCAACTTTGGCTTCATGAATG
GAGCCATGCACTTCCATGACTACAAGTCAGATGTCAACAGCTATGACTATGATGCTGTGCTGACAGAAGCCGGCG
ATTACACGGCCAAGTACATGAAGCTTCGAGACTTCTTCGGCTCCATCTCAGGCATCCCTCTCCCTCCCCACCTG
ACCTTCTTCCCAAGATGCCGTATGAGCCCTTAACGCCAGTCTTGACCTGTCTCTGTGGGACGCCCTCAAGTACC
TGGGGGAGCCAATCAAGTCTGAAAAGCCCATCAACATGGAGAACCTGCCAGTCAATGGGGGAAATGGACAGTCCCT
TCGGGTACATTCTCTATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGCATGATCGGGGGCAGG
TGTTTGTGAACACAGTATCCATAGGATTCTTGGACTACAAGACAACGAAGATTGCTGTCCCCCTGATCCAGGGTT
ACACCGTGCTGAGGATCTTGGTGGAGAATCGTGGGCGAGTCAACTATGGGGAGAATATTGATGACCAGCGCAAAG
GCTTAATTGGAAATCTCTATCTGAATGATTACCCCTGAAAACCTTCAGAATCTATAGCCTGGATATGAAGAAGA
GCTTCTTTCAGAGGTTCCGCCTGGACAAATGGNGTTCCCTCCAGAAACACCCACATTACCTGCTTTCTTCTTGG
TAGCTTGTCCATCAGCTCCACGCCCTTGTGACACCTTTCTGAAGCTGGAGGGCTGGGAGAAGGGGGTTGTATTCA
TCAATGGCCAGAACCTTGGACGTTACTGGAACATTGGACCCAGAACGCTTTACCTCCAGGTCCCTGGTTGA
GCAGCGGAATCAACCAGGTCACTGTTTTTGGAGGACGATGGCGGGCCCTGCATTACAGTTCACGGAAACCCCC
ACCTGGGCAGGAACCACTACATTAAG**TGAG**CGGTGGCACCCCTCCTGCTGGTGCCAGTGGGAGACTGCCGCCCTC
CTCTTGACCTGAAGCCTGGTGGCTGCTGCCCCACCCCTCACTGCAAAAGCATCTCCTTAAGTAGCAACCTCAGGG
ACTGGGGGCTACAGTCTGCCCCGTCTCAGCTCAAAACCCTAAGCCTGCAGGGAAAGGTGGGATGGCTCTGGGCC
TGGCTTTGTGATGATGGCTTTCTTACAGCCCTGCTCTTGTGCCGAGGCTGTGCGGCTGTCTTAGGGTGGGAGC
AGCTAATCAGATCGCCCAGCCTTTGGCCCTCAGAAAAAGTGCTGAAACGTGCCCTTGACCCGGACGTACAGCCC
TGCGAGCATCTGCTGGACTCAGGCGTGCTCTTTGCTGGTTCCTGGGAGGCTTGCCACATCCCTCATGGCCCCAT
TTTATCCCCGAAATCCTGGGTGTGTCAACAGTGTAGAGGGTGGGGAAGGGGTGTCTCACCTGAGCTGACTTTGTT
CTTCCTTCAACCTTCTGAGCCTTCTTTGGGATTCTGGAAGGAACTCGGCGTGAGAAACATGTGACTTCCCTT
TCCCTTCCCACTCGCTGCTTCCACAGGGTGACAGGCTGGGCTGGAGAAACAGAAATCTCACCTGCGTCTTCC
CAAGTTAGCAGGTGTCTCTGGTGTTCAGTGAGGAGGACATGTGAGTCCTGGCAGAAGCCATGGCCCATGTCTGCA
CATCCAGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCCTGGCAGAAGCCATGGCCCATGTCTGCACATCC
AGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCCTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGA
GGAGGACAGAAGGCCAGCTCACATGTGAGTCCTGGCAGAAGCCATGGCCCATGTCTGCACATCCAGGGAGGAGG
ACAGAAGGCCAGCTCAGTGGCCCCGCTCCCCACCCCCACGCCGAACAGCAGGGGCAGAGCAGCCCTCCTTC
GAAGTGTGTCCAAGTCCGCATTTGAGCCTTGTTCTGGGGCCAGCCCAACACCTGGCTTGGGCTCACTGTCTGA
GTTGCAGTAAAGCTATAACCTTGAATCACA

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FIGURE 22

MTTWSLRRRPPARTLGLLLLVLGFLVLRRLDWSTLVPLRLRHRQLGLQAKGWNFMLEDSTFWI
FGGSIHYFRVPREYWRDRLKMKACGLNTLTITYVPWNLHEPERGKFDGSGNLDLEAFVLMMAE
IGLWVILRPGPYICSEMDLGGLP SWLLQDPGMRLRTTYKGFTEAVDLYFDHLSRVVPLQYKR
GGPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLTSDNKGDL SKGIVQGVLATINLQ
STHELQLLTFFLFNVQGTQPKMVMEYWTGWFD SWGGPHNILD SSEVLKTVSAIVDAGSSINLY
MFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDY TAKYMKLRDFFGSI SGIPLP PPPD
LLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNGQSFGYILYETSITSSG
ILSGHVHDRGQVFVNTV SIGFLDYKTTKIAVPLIQGYTVLRILVENRGRVNYGENIDDQRKGL
IGNLYLNDSP LKNFRIYS LDMKKSFFQRFGLDKWXS L PETPTLP AFFLGSL SISSTPCDTFLK
LEGWEKGVVFINGQNLGRYWNIGPQKTLYLP GPWLSSGINQVIVFEETMAGPALQFTETPHLG
RNQYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

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FIGURE 24

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPENF
TELSYNYGSGSVKNCCPLNWEYFQSSCYFFSTDTISWALSLKNCSAMGAHLVVINSQEEQEF
LSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPPNIATLEDCAIMRDSSNPR
QNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

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FIGURE 25

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACCC
TGGTGAGGGTTCTCTACTTGGCCTTCGGTGGGGGTCAAGACGCAGGCACCTACGCCAAAGGGG
AGCAAAGCCGGGCTCGGCCCCGAGGCCCCAGGACCTCCATCTCCCAATGTTGGAGGAATCCGA
CACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCCAAGA
AGCTGTCTGCCTTCGTTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCCAGGCAG
ACACTCGGTCTGTTCTAGTGGATAGGGGTTCATGACCGGTTTCTCCTAGACGGGGCCCCGTTCC
GCTATGTGTCTGGCAGCCTGCACTACTTTCGGGTACCGCGGGTGCTTTGGGCCGACCGGCTTT
TGAAGATGCGATGGAGCGGCCTCAACGCCATACAGTTTTATGTGCCCTGGAACCTACCACGAGC
CACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGGACCTCATTGCCTTTCTGAATGAGGCAG
CTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTTACATCTGTGCAGAGTGGGAGATGG
GGGGTCTCCCATCCTGGTTGCTTCGAAAACCTGAAATTCATCTAAGAACCTCAGATCCAGACT
TCCTTGCCGCACTGGACTCCTGGTTCAAGGTCTTGCTGCCCAAGATATATCCATGGCTTTATC
ACAATGGGGGCAACATCATTAGCATTGAGGTGGAGAATGAATATGGTAGCTACAGAGCCTGTG
ACTTCAGCTACATGAGGCACTTGGCTGGGCTCTTCCGTGCACTGCTAGGAGAAAAGATCTTGC
TCTTCACCACAGATGGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGGGACTCTATACCACTG
TAGATTTTGGCCCAGCTGACAACATGACCAAATCTTTACCCTGCTTCGGAAGTATGAACCCC
ATGGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTACTGGGGCCAGAATCACT
CCACACGGTCTGTGTCAGCTGTAACCAAAGGACTAGAGAACATGCTCAAGTTGGGAGCCAGTG
TGAACATGTACATGTTCCATGGAGGTACCAACTTTGGATATTGGAATGGTGGCGATAAGAAGG
GACGCTTCCTTCCGATTACTACCAGCTATGACTATGATGCACCTATATCTGAAGCAGGGGACC
CCACACCTAAGCTTTTGTCTCTTCGAGATGTCATCAGCAAGTTCCAGGAAGTTCTTTGGGAC
CTTTACCTCCCCCGAGCCCCAAGATGATGCTTGGACCTGTGACTCTGCACCTGGTTGGGCATT
TACTGGCTTTCTAGACTTGCTTTGCCCCCGTGGGCCCATTCATTCAATCTTGCCAATGACCT
TTGAGGCTGTCAAGCAGGACCATGGCTTCATGTTGTACCGAACCTATATGACCCATACCATTT
TTGAGCCAACACCATTCTGGGTGCCAAATAATGGAGTCCATGACCGTGCCTATGTGATGGTGG
ATGGGGTGTTCAGGGTGTGTTGGGAGCGAAATATGAGAGACAACTATTTTGGACGGGGAAAC
TGGGGTCCAACTGGATATCTTGGTGGAGAACATGGGGAGGCTCAGCTTTGGGTCTAACAGCA
GTGACTTCAAGGGCCTGTTGAAGCCACCAATTCTGGGGCAAACAATCCTTACCCAGTGGATGA
TGTTCCCTCTGAAAATTGATAACCTTGTGAAGTGGTGGTTTCCCCTCCAGTTGCCAAAATGGC
CATATCCTCAAGCTCCTTCTGGCCCCACATTCTACTCCAAAACATTTCCAATTTTAGGCTCAG
TTGGGGACACATTTCTATATCTACCTGGATGGACCAAGGGCCAAGTCTGGATCAATGGGTTTA
ACTTGGGCCGGTACTGGACAAAGCAGGGGCCACAACAGACCCTCTACGTGCCAAGATTCCTGC
TGTTTCCTAGGGGAGCCCTCAACAAAATTACATTGCTGGAAGTAGAAGATGTACCTCTCCAGC
CCCAAGTCCAATTTTGGATAAGCCTATCCTCAATAGCACTAGTACTTTGCACAGGACACATA
TCAATTCCCTTTTCACTGATACACTGAGTGCCTCTGAACCAATGGAGTTAAGTGGGCACTGAA
AGGTAGGCCGGGCATGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCTGAGACGGGTG
GATTACCTGAGGTCAGGACTTCAAGACCAGCCTGGCCAACATGGTGAAACCCCGTCTCCACTA
AAAATACAAAATTAGCCGGGCGTGATGGTGGGCACCTCTAATCCCAGCTACTTGGGAGGCTG
AGGGCAGGAGAATTGCTTGAATCCAGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCACTG
CACTCCAGCCTGGCTGACAGTGAGACACTCCATCTCAAAAAAAAAAAAA

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FIGURE 26

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDRGHDREFLLDGAPFRYVSGSLHYFRVPRVLW
ADRLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYICA
EWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENEYGS
YRACDFS YMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDGFPADNMTKI FTLLR
KYEPHGPLVNSEYYTGWLDYWGQNHSTRSVSAVTKGLENMLKLGASVNM YMFHGGTNFGYWNG
ADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLPPPSPKMMLGPVTLH
LVGHLLAFLDLLCPRGP IHSILPMTFEAVKQDHGFMLYRTYMTHTI FEPTPFWVPNNGVHDRA
YVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRLSFGSNSSDFKGLLKPPILGQ TIL
TQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGD TFLYLPGWTKGQVW
INGFNLGRYWTQGPQOTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLDKPILNSTSTL
HRTHINSLSADTL SASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648**Tyrosine kinase phosphorylation site.**

amino acids 191-198

N-myristoylation site.amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

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FIGURE 27

GGACAGCTCGCGGCCCCCGAGAGCTCTAGCCGTCGAGGAGCTGCCTGGGGACGTTTGCCCTGG
GGCCCCAGCCTGGCCCGGGTCACCCTGGCATGAGGAG**AT**GGGCCTGTTGCTCCTGGTCCCATT
GCTCCTGCTGCCCCGGCTCCTACGGACTGCCCTTCTACAACGGCTTCTACTACTCCAACAGCGC
CAACGACCAGAACCTAGGCAACGGTCATGGCAAAGACCTCCTTAATGGAGTGAAGCTGGTGGT
GGAGACACCCGAGGAGACCCTGTTACCTACCAAGGGGGCCAGTGTGATCCTGCCCTGCCGCTA
CCGCTACGAGCCGGCCCTGGTCTCCCCGCGGCGTGTGCGTGTCAAATGGTGGAAAGCTGTCGGA
GAACGGGGCCCCAGAGAAGGACGTGCTGGTGGCCATCGGGCTGAGGCACCGCTCCTTTGGGGA
CTACCAAGGCCGCGTGCACCTGCGGCAGGACAAAGAGCATGACGTCTCGCTGGAGATCCAGGA
TCTGCGGCTGGAGGACTATGGGCGTTACCGCTGTGAGGTCATTGACGGGCTGGAGGATGAAAG
CGGTCTGGTGGAGCTGGAGCTGCGGGGTGTGGTCTTTCCTTACCAGTCCCCCAACGGGCGCTA
CCAGTTCAACTTCCACGAGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCGGTGGTGGCCTCCTT
TGAGCAGCTCTTCCGGGCTGGGAGGAGGGCCTGGACTGGTGCACGCGGGCTGGCTGCAGGA
TGCTACGGTGCAGTACCCCATCATGTTGCCCGGCGAGCCCTGCGGTGGCCAGGCCTGGCACC
TGGCGTGCAGAGCTACGGCCCCCGCCACCGCCGCTGCACCGCTATGATGTATTCTGCTTCGC
TACTGCCCTCAAGGGGCGGGTGTACTACCTGGAGCACCCCTGAGAAGCTGACGCTGACAGAGGC
AAGGGAGGCCTGCCAGGAAGATGATGCCACGATCGCCAAGGTGGACAGCTCTTTGCCGCTG
GAAGTTCCATGGCCTGGACCGCTGCGACGCTGGCTGGCTGGCAGATGGCAGCGTCCGCTACCC
TGTGGTTACCCGCGATCCTAACTGTGGGCCCCAGAGCCTGGGGTCCGAAGCTTTGGCTTCCC
CGACCCGCGAGCCGCTTGTACGGTGTCTTACTGCTACCGCCAGCAC**TAG**GACCTGGGGCCCTC
CCCTGCCGCATTCCCTCACTGGCTGTGTATTTATTGAGTGGTTCGTTTTCCCTTGTGGGTTGG
AGCCATTTTAACTGTTTTTTATACTTCTCAATTTAAATTTCTTTAAACATTTTTTTACTATTT
TTTGTAAGCAAACAGAACCCAATGCCTCCCTTTGCTCCTGGATGCCCCACTCCAGGAATCAT
GCTTGCTCCCCTGGGCCATTTGCGGTTTTGTGGGCTTCTGGAGGGTTCCCCGCCATCCAGGCT
GGTCTCCCTCCCTTAAGGAGGTGGTGCCAGAGTGGGCGGTGGCCTGTCTAGAATGCCGCCG
GGAGTCCGGGCATGGTGGGCACAGTTCTCCCTGCCCTCAGCCTGGGGGAAGAAGAGGGCCTC
GGGGGCTCCGGAGCTGGGCTTTGGGCCTCTCCTGCCACCTCTACTTCTCTGTGAAGCCGCT
GACCCAGTCTGCCCACTGAGGGGCTAGGGCTGGAAGCCAGTTCTAGGCTTCCAGGCGAAATC
TGAGGGAAGGAAGAACTCCCTCCCGTTCCCTTCCCTCTCGGTTCCAAAGAATCTGTTT
TGTTGTCATTTGTTTCTCCTGTTTCCCTGTGTGGGGAGGGGCCCTCAGGTGTGTGTACTTTGG
ACAATAAATGGTGCTATGACTGCCTTCGCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA
AAA

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FIGURE 28

MGLLLLVPLLLLPGSYGLPFYNGFYYSNSANDQNLGNGHGKDLLNGVKLVVETPEETLFTYQG
ASVILPCRYRYEPALVSPRRVRVKWWKLENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQDKE
HDVSLEIQDLRLLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQVCA
EQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPRHRL
HRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDRCDAGW
LADGSVRYPPVHHPNCGPPEPGVRSFGFPDQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.amino acids 36-42, 184-190, 208-214, 237-243, 297-303,
307-313

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FIGURE 29

GCAAGCGGCGAAATGGCGCCCTCCGGGAGTCTTGCAAGTTCCCCTGGCAGTCCTGGTGCTGTTG
CTTTGGGGTGCTCCCTGGACGCACGGGCGGCGGAGCAACGTTTCGCGTCATCACGGACGAGAAC
TGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTTATGCCCCGTGGTGCCCTGCTTGT
CAAAATCTTCAACCGGAATGGGAAAGTTTTGCTGAATGGGGAGAAGATCTTGAGGTTAATATT
GCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTTATCATAACTGCTCTTCCT
ACTATTTATCATTGTAAAGATGGTGAATTTAGGCGCTATCAGGGTCCAAGGACTAAGAAGGAC
TTCATAAACTTTATAAGTGATAAAGAGTGGAAGAGTATTGAGCCCGTTTCATCATGGTTTGGT
CCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTTCAGCTATCTATGTGGATCAGGACG
TGCCATAACTACTTTATTGAAGACCTTGGATTGCCAGTGTGGGGATCATATACTGTTTTTGCT
TTAGCAACTCTGTTTTCCGGACTGTTATTAGGACTCTGTATGATATTTGTGGCAGATTGCCTT
TGTCTTCAAAAAGGCGCAGACCACAGCCATACCCATACCCTTCAAAAAAATTATTATCAGAA
TCTGCACAACCTTTGAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAAGATGTTTCAGAA
GAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTTCCACAGAATGCCATAAGACAACGC
TCTCTGGGTCCATCATTGGCCACAGATAAATCCTAGTTAAATTTTATAGTTATCTTAATATTA
TGATTTTGATAAAACAGAAGATTGATCATTTTGTGGTTTGAAGTGAAGTGTGACTTTTTT
GAATATTGCAGGGTTCAGTCTAGATTGTCAATTAATTGAAGAGTCTACATTCAGAACATAAAA
GCACTAGGTATACAAGTTTGAAATATGATTTAAGCACAGTATGATGGTTTAAATAGTTCTCTA
ATTTTTGAAAAATCGTGCCAAGCAATAAGATTTATGTATATTTGTTTAAATAAACCTATTTT
AAGTCTGAGTTTTGAAAATTTACATTTCCCAAGTATTGCATTATTGAGGTATTTAAGAAGATT
ATTTTAGAGAAAAATATTTCTCATTTGATATAATTTTTCTCTGTTTCACTGTGTGAAAAAAG
AAGATATTTCCCATAAATGGGAAGTTTGCCATTGTCTCAAGAAATGTGTATTTCACTGACAA
TTTCGTGGTCTTTTTAGAGGTATATTCCAAAATTTCCCTTGATTTTTTAGGTTATGCAACTAAT
AAAACTACCTTACATTAATTAATTACAGTTTTCTACACATGGTAATACAGGATATGCTACTG
ATTTAGGAAGTTTTTAAGTTCATGGTATTCTCTTGATTCCAACAAAGTTTGATTTTCTCTTGT
ATTTTTCTTACTTACTATGGGTACATTTTTTATTTTTCAAATTGGATGATAATTTCTTGGAA
ACATTTTTTATGTTTTAGTAAACAGTATTTTTTTTGTGTTTCAAACGAAGTTTACTGAGAGA
TCCATCAAATTGAACAATCTGTTGTAATTTAAATTTTGGCCACTTTTTTCAGATTTTACATC
ATTCCTTGCTGAACCTCAACTGAAATTGTTTTTTTTTCTTTTTGGATGTGAAGGTGAACATT
CCTGATTTTTGTCTGATGTGAAAAAGCCTTGGTATTTTACATTTTGAAAAATTCAAAGAAGCTT
AATATAAAAGTTTGCATTCTACTCAGGAAAAGCATCTTCTGTATATGTCTTAAATGTATTT
TTGTCTCATATACAGAAAGTTCTTAATTGATTTTACAGTCTGTAATGCTTGATGTTTTAAAA
TAATAACATTTTTATATTTTTTAAAGACAACTTCATATTATCCTGTGTCTTTCTGACTG
GTAATATTGTGTGGGATTTTACAGGTAAAAGTCAGTAGGATGGAACATTTTAGTGTATTTTA
CTCCTTAAAGAGCTAGAATACATAGTTTTTACCTTAAAGAAGGGGGAAAAATCATAAATACAA
TGAATCAACTGACCATACGTAGTAGACAATTTCTGTAATGTCCCCTTCTTCTAGGCTCTGT
TGCTGTGTGAATCCATTAGATTTACAGTATCGTAATATAACAAGTTTTCTTAAAGCCCTCTCC
TTTAGAATTTAAATATTGTACCATTAAAGAGTTTGGATGTGTAAGTTGTGATGCCTTAGAAA
AATATCCTAAGCACAAAATAAACCTTTCTAACCACCTTCATTAAAGCTGAAAAA

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FIGURE 30

MAPSGSLAVPLAVLVLLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNLO
PEWESFAEWGEDLEVNIKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFINF
ISDKEWKSIEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFALATL
FSGLLLGLCMIFVADCLCPSKRRRPQYPYPYPSKKLLSESAQPLKKVEEEQEADVEDVSEEEAE
SKEGTNKDFPQNAIQRSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

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FIGURE 31

AG**ATG**GCGGTCTTGGCACCTCTAATTGCTCTCGTGATTTCGGTGCCGCGACTTTCACGATGGC
TCGCCCCAACCTTACTACCTTCTGTGCGGCCCTGCTCTCTGCTGCCTTCCTACTCGTGAGGAAAC
TGCCGCGCTCTGCCACGGTCTGCCACCCAACGCGAAGACGGTAACCCGTGTGACTTTGACT
GGAGAGAAGTGGAGATCCTGATGTTTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGATCCA
TCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTAGTAAAGTGGCCAACACAATTCTTT
TCTTCCGCTTGGATATTGCGATGGGCCTACTTTACATCACACTCTGCATAGTGTTCTTGATGA
CGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAAACCATTG
ATGAGGAACTAGAACGGGACAAGAGGGTCACCTGGATTGTGGAGTTCTTTGCCAATTGGTCTA
ATGACTGCCAATCATTTGCCCCATCTATGCTGACCTCTCCCTTAAATACAACGTACAGGGC
TAAATTTTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTACAAAGTGAGCA
CATCACCCCTCACCAAGCAACTCCCTACCCTGATCCTGTTCCAAGGTGGCAAGGAGGCAATGC
GGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTTCTCTGAGGAGAATGTGA
TCCGAGAATTTAACTTAAATGAGCTATACCAGCGGGCCAAGAACTATCAAAGGCTGGAGACA
ATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCCACCACAGTGTGAGATGGGGAAAACAAGA
AGGATAAA**TAA**GATCCTCACTTTGGCAGTGCTTCCTCTCCTGTCAATTCCAGGCTCTTTCCAT
AACCACAAGCCTGAGGCTGCAGCCTTTNATTNATGTTTTCCCTTTGGCTGNGACTGGNTGGGG
CAGCATGCAGCTTCTGATTTTAAAGAGGCATCTAGGGAATTGTCAGGCACCCTACAGGAAGGC
CTGCCATGCTGTGGCCAACTGTTTCACTGGAGCAAGAAAGAGATCTCATAGGACGGAGGGGGA
AATGGTTTCCCTCCAAGCTTGGGTCACTGTGTTAACTGCTTATCAGCTATTCAGACATCTCCA
TGGTTTCTCCATGAACTCTGTGGTTTCATCATTCCCTCTTAGTTGACCTGCACAGCTTGGTT
AGACCTAGATTTAACCCTAAGGTAAGATGCTGGGGTATAGAACGCTAAGAATTTTCCCCAAG
GACTCTTGCTTCCTTAAGCCCTTCTGGCTTCGTTTATGGTCTTCATTAAAAGTATAAGCCTAA
CTTTGTGCTAGTCCTAAGGAGAAACCTTTAACCACAAAGTTTTATCATTGAAGACAATATT
GAACAACCCCTATTTTGTGGGGATTGAGAAGGGGTGAATAGAGGCTTGAGACTTTCCTTTGT
GTGGTAGGACTTGGAGGAGAAATCCCCTGGACTTTCACCTAACCCCTCTGACATACTCCCCACAC
CCAGTTGATGGCTTTCGGTAATAAAAAGATTGGGATTCCTTTTG

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FIGURE 32

MAVLAPLIALVYSVPRLSRWLAQPYYLLSALLSAAFLLVRLPPLCHGLPTQREDGNPCDFDW
REVEILMFLSAIVMMKNRRSITVEQHIGHNIFMFSKVANTILFFRLDIRMGLLYITLCIVFLMT
CKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYNCTGL
NFGKVDVGRYTDVSTRYKVSTSP LTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSEENVI
REFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

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FIGURE 33

CGGACGCGTGGGGTGCCCGAC**ATG**GCGAGTGTAGTGCTGCCGAGCGGATCCCAGTGTGCGGCG
GCAGCGGCGGCGGCGGCGCCTCCCGGGCTCCGGCTTCTGCTGTTGCTCTTCTCCGCCGCGGCA
CTGATCCCCACAGGTGATGGGCAGAATCTGTTTACGAAAGACGTGACAGTGATCGAGGGAGAG
GTTGCGACCATCAGTTGCCAAGTCAATAAGAGTGACGACTCTGTGATTGAGCTACTGAATCCC
AACAGGCAGACCATTATTTTCAGGGACTTCAGGCCTTTGAAGGACAGCAGGTTTCAGTTGCTG
AATTTTTCTAGCAGTGAACCTCAAAGTATCATTGACAAACGTCTCAATTTCTGATGAAGGAAGA
TACTTTTGCCAGCTCTATAACCGATCCCCACAGGAAAGTTACACCACCATCACAGTCCTGGTC
CCACCACGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGGAGATTGAA
GTCAACTGCACTGCTATGGCCAGCAAGCCAGCCACGACTATCAGGTGGTTCAAAGGGAACACA
GAGCTAAAAGGCAAATCGGAGGTGGAAGAGTGGTCAGACATGTACACTGTGACCAGTCAGCTG
ATGCTGAAGGTGCACAAGGAGGACGATGGGGTCCCAGTGATCTGCCAGGTGGAGCACCCCTGCG
GTCAGTGGAAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCTCAAGTGCACATT
CAGATGACTTATCCTCTACAAGGCTTAACCCGGGAAGGGGACGCGCTTGAGTTAACATGTGAA
GCCATCGGGAAGCCCCAGCCTGTGATGGTAACCTTGGGTGAGAGTCGATGATGAAATGCCTCAA
CACGCCGTACTGTCTGGGCCCAACCTGTTTCATCAATAACCTAAACAAAACAGATAATGGTACA
TACCGCTGTGAAGCTTCAAACATAGTGGGGAAAGCTCACTCGGATTATATGCTGTATGTATAC
GATCCCCCACAACCTATCCCTCCTCCCACAACAACCACCACCACCACCACCACCACCACCACC
ACCATCCTTACCATCATCACAGATTCCTCGAGCAGGTGAAGAAGGCTCGATCAGGGCAGTGGAT
CATGCCGTGATCGGTGGCGTCGTGGCGGTGGTGGTGTTCGCCATGCTGTGCTTGCTCATCATT
CTGGGGCGCTATTTTGCCAGACATAAAGGTACATACTTCACTCATGAAGCCAAAGGAGCCGAT
GACGCAGCAGACGCAGACACAGCTATAATCAATGCAGAAGGAGGACAGAACAACCTCCGAAGAA
AAGAAAGAGTACTTCATCT**AGAT**CAGCCTTTTTGTTTCAATGAGGTGTCCAACCTGGCCCTATT
TAGATGATAAAGAGACAGTGATATTGG

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FIGURE 34

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39518
<subunit 1 of 1, 440 aa, 1 stop
<MW: 48240, pI: 4.93, NX(S/T): 7
MASVVLPSGSQCAAAAAAAPPGLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQ
VNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYT
DPPQESYTTITVLVPPRNLMDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSE
VEEWSDMYTVTSQMLMKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQ
GLTREGDALELTCEAIGKPQPMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASN
IVGKAHSDYMLYVYDPPTTIPPTTTTTTTTTTTTTTTTILTIITDSRAGEEGSIRAVDHAIVIGGV
VAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADATAINAEGGQNNSEEKKEYFI
```

Signal sequence.

amino acids 1-36

Transmembrane domain.

amino acids 372-393

N-glycosylation sites.amino acids 65-69, 99-103, 111-115, 163-167, 302-306, 306-310,
430-434**Tyrosine kinase phosphorylation sites.**

amino acids 233-240, 319-328

N-myristoylation sites.amino acids 9-15, 227-233, 307-313, 365-371, 376-382, 402-408,
411-417, 427-433, 428-432

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FIGURE 35

GGTTGCCACAGCTGGTTTAGGGCCCCGACCACTGGGGCCCCCTTGTCTAGGAGGAGACAGCCTCCCGGCCCGGGGAG
GACAAGTCGCTGCCACCTTTGGCTGCCGACGTGATCCCTGGGACGGTCCGTTTCTGCCGTGAGCTGCCGGCCG
AGTTGGGTCTCCGTGTTTCAGGCCGGCTCCCCCTTCTGGTCTCCCTTCTCCCGCTGGGCCGGTTTATCGGGAGG
AGATTGTCTTCCAGGGCTAGCAATTGGACTTTTGATGATGTTTGACCCAGCGGCAGGAATAGCAGGCAACGTGAT
TTCAAAGCTGGGCTCAGCCTCTGTTTCTTCTCTCGTGTAATCGCAAAACCCATTTTGAGCAGGAATTCCAATCA
TGTCTGTGATGGTGGTGAGAAAGAAGGTGACACGGAAATGGGAGAACTCCAGGCAGGAACACCTTTTGCTGTG
ATGGCCGCGTCATGATGGCCCGCAAAAGGGCATTCTTCTACCTGACCCTTTTCTCATCCTGGGGACATGTACAC
TCTTCTTCGCCCTTTGAGTGCCGCTACCTGGCTGTTTCAGCTGTCTCCTGCCATCCCTGTATTTGTGCCATGCTCT
TCCTTTTCTCCATGGCTACACTGTTGAGGACCAGCTTCAGTGACCCTGGAGTGATTCTCGGGCGCTACCAGATG
AAGCAGCTTTCATAGAAATGGAGATAGAAGCTACCAATGGTGCGGTGCCCCAGGGCCAGCGACCACCGCTCGTA
TCAAGAATTTCCAGATAAAACAACCAGATTGTGAACTGAAATACTGTTACACATGCAAGATCTTCGGCCTCCCC
GGGCTCCCATTGCAGCATCTGTGACAACTGTGTGGAGCGCTTCGACCATCACTGCCCCCTGGGTGGGGAATTGTG
TTGGAAAGAGGAACTACCGCTACTTCTACCTCTTCATCCTTTCTCTCTCCCTCCTCACAATCTATGTCTTCGCCT
TCAACATCGTCTATGTGGCCCTCAAATCTTTGAAAATTGGCTTCTTGAGACATTGAAAGAACTCCTGGAACTG
TTCTAGAAGTCCTCATTTGCTTCTTTACACTCTGGTCCGTCGTGGGACTGACTGGATTTCTACTTTCTCGTGG
CTCTCAACCAGACAACCAATGAAGACATCAAAGGATCATGGACAGGGAAGAATCGCGTCCAGAATCCCTACAGCC
ATGGCAATATTGTGAAGAACTGCTGTGAAGTGCTGTGTGGCCCCCTTGCCCCCAGTGTGCTGGATCGAAGGGGTA
TTTTGCCACTGGAGGAAAGTGGAGTGCACCTCCAGTACTCAAGAGACCAGTAGCAGCCTCTTGCCACAGAGCC
CAGCCCCACAGAACACCTGAACTCAAATGAGATGCCGGAGGACAGCAGCACTCCCGAAGAGATGCCACCTCCAG
AGCCCCCAGAGCCACCACAGGAGGCAGCTGAAGCTGAGAAG**TAG**CCTATCTATGGAAGAGACTTTTGTGTGTG
TAATTAGGGCTATGAGAGATTTAGGTGAGAAGTTAAACCTGAGACAGAGAGCAAGTAAGCTGTCCCTTTTAACT
GTTTTTCTTTGGTCTTTAGTCAACAGTTGCACACTGGCATTCTTCTGCTGCAAGCTTTTTTAAATTTCTGAACT
CAAGGCAGTGGCAGAAGATGTCAGTCACCTCTGATAACTGGAAAAATGGGTCTCTTGGGCCCTGGCACTGGTTCT
CCATGGCCTCAGCCACAGGGTCCCTTGGACCCCCCTCTCTCCCTCCAGATCCAGCCCTCCTGCTTGGGGTCAC
TGGTCTCATTCTGGGGCTAAAAGTTTTTGGAGCTGGCTCAAATCCTCCCAAGCTGCTGCACGTGCTGAGTCCAGA
GGCAGTCACAGAGACCTCTGGCCAGGGGATCCTAACTGGGTCTTGGGGTCTTCAGGACTGAAGAGGAGGGAGAG
TGGGGTCAGAAGATTCTCCTGGCCACCAAGTGCCAGCATTGCCACAAATCCTTTTAGGAATGGGACAGGTACCT
TCCACTTGTTGTANNNNNNNNNNNNNNNNNNNNNNNNNNNNTGTTTTCTTTTGACTCCTGCTCCCATAGGAG
CAGGAATGGCAGTAATAAAAGTCTGCACTTTGGTCATTTCTTTTCTCAGAGGAAGCCCCAGTGCTCACTTAAAC
ACTATCCCCCTCAGACTCCCTGTGTGAGGCCTGCAGAGGCCCTGAATGCACAAATGGGAAACCAAGGCACAGAGAG
GCTCTCCTCTCCTCTCCTCTCCCCGATGTACCCTCAAAAAAAAAAAAAATGCTAACCAGTCTTCCATTAAAGCCT
CGGCTGAGTGAGGGAAAGCCCAGCACTGCTGCCCTCTCGGGTAACTCACCTAAGGCCTCGGCCACCTCTGGCT
ATGGTAACCACACTGGGGCTTCTCCAAGCCCCGCTCTTCAGCACTTCCACCGGCAGAGTCCAGAGCCACTT
CACCTGGGGGTGGGCTGTGGCCCCCAGTCAGCTCTGCTCAGGACCTGCTCTATTTAGGGAAGAAGATTTATGT
ATTATATGTGGCTATATTTCTAGAGCACCTGTGTTTTCTCTTTCTAAGCCAGGGTCTGTCTGGATGACTTAT
GCGGTGGGGGAGTGTAACCGGAACTTTTCTATCTATTTGAAGGCGATTAACTGTGTCTAATGCA

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FIGURE 36

MSVMVVRKKVTRKWEKLPGRNTFCCDGRVMMARQKGIFYLTFLILGTCTLFFAFECRYLAVQ
LSPAIPVFAAMLFLFSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPPRI
KNFQINNQIVKLKYCYTCKIFRPPRASHCSICDNCVERFDHHC PWVGNCVGKRNRYFYLFIL
SLSLLTIYVFAFNIVYVALKSLKIGFLETLPKTPGTVLEVLI CFFTLWSVGLTGFHTFLVAL
NQT TNEDIKGSWTGKNRVQNPYSHGNIVKNCCEVLCGPLPPSVLDRRGILPLEESGSRPPSTQ
ETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPEPPEPPEPPQEAAEAEK

Putative transmembrane domains:

amino acids 36-55 (type II TM), 65-84, 188-208, 229-245

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FIGURE 37

GGCGGAGCAGCCCTAGCCGCCACCGTCGCTCTCGCAGCTCTCGTCCGCACTGCCACCGCCGCCGCCGTCCTACTGCG
TCCTGGCTCCGGCTCCCGCGCCCTCCCGGCCGGCCATGCGAGCCCCGCCGCGCCAGGCGCCCGGTGCGCAGCTGC
TGCCCCGCGCTGGCCCTGCTGCTGCTGCTGCTCGGAGCGGGGCCCGAGGCAGCTCCCTGGCCAAACCGGTGCCCG
CCGCGCCCTTGTCTGCGCCCGGCCGTGCGCCGCGCAGCCCTGCCGGAATGGGGGTGTGTGCACCTCGCGCCCTG
AGCCGGACCCGAGCACCCGGCCCCCGCCGGCGAGCCTGGCTACAGCTGCACCTGCCCCGCCGGGATCTCCGGCG
CCAACTGCCAGCTTGTGAGATCCTTGTGCCAGCAACCTTGTCAACATGGCAACTGCAGCAGCAGCAGCAGCA
GCAGCAGCGATGGCTACCTCTGCATTTGCAATGAAGGCTATGAAGGTCCCAACTGTGAACAGGCACCTTCCAGTC
TCCCAGCCACTGGCTGGACCGAATCCATGGCACCCCGACAGCTTACGCTGTTCTGCTACTCAGGAGCCTGACA
AAATCCTGCCTCGCTCTCAGGCAACGGTGACACTGCCTACCTGGCAGCCGAAAACAGGGCAGAAAGTTGTAGAAA
TGAAATGGGATCAAGTGGAGGTGATCCCAGATATTGCCTGTGGGAATGCCAGTTCTAACAGCTCTGCCGGTGGCC
GCCTGGTATCCTTTGAAGTGCCACAGAACACCTCAGTCAAGATTGCGCAAGATGCCACTGCCTCACTGATTTTGC
TCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAGTGTGACCCCTTCAAGCTT
CAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAATAATCACTTTATTGGTTTTGTGAATGATTCTG
TGACTAAGTCTATTGTGGCTTTGCGCTTAACCTCTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACG
CAAATGACTTGGAGTGTTCAGGAAAAGGAAAATGCACCACGAAGCCGTCAGAGGCAACTTTTTCTGTACCTGTG
AGGAGCAGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAACGCGAGCT
GTATTGATGCAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCCTTCTGGTTATACTGGAGAGCTTT
GCCAGTCCAAGATTGATTACTGCATCCTAGACCCATGCAGAAATGGAGCAACATGCATTTCCAGTCTCAGTGGAT
TCACCTGCCAGTGTCCAGAAGGATACTTCGGATCTGCTTGTGAAGAAAAGGTGGACCCCTGCGCCTCGTCTCCGT
GCCAGAACAACGGCACCTGCTATGTGGACGGGGTACACTTTACCTGCAACTGCAGCCCGGGCTTCACAGGGCCGA
CCTGTGCCAGCTTATTGACTTCTGTGCCCTCAGCCCTGTGCTCATGGCACGTGCCGACGCTGGGCACCAGCT
ACAAATGCCTCTGTGATCCAGGTTACCATGGCCTCTACTGTGAGGAGGAATATAATGAGTGCCTCTCCGCTCCAT
GCCTGAATGCAGCCACCTGCAGGGACCTCGTTAATGGCTATGAGTGTGTGTGCCTGGCAGAATACAAAGGAACAC
ACTGTGAATTGTACAAGGATCCCTGCGCTAACGTCACTGTCTGAACGGAGCCACCTGTGACAGCGACGGCCTGA
ATGGCACGTGCATCTGTGCACCCGGGTTTACAGGTGAAGAGTGCGACATTGACATAAATGAATGTGACAGTAACC
CCTGCCACCATGGTGGGAGCTGCCTGGACCAGCCCAATGGTTATAACTGCCACTGCCCGCATGGTTGGGTGGGAG
CAAATGTGAGATCCACCTCCAATGGAAGTCCGGGCACATGGCGGAGAGCCTCACCAACATGCCACGGCACTCCC
TCTACATCATCATTGGAGCCCTCTGCGTGGCCTTCATCCTTATGCTGATCATCCTGATCGTGGGGATTTGCCGCA
TCAGCCGCATTGAATACCAGGGTTCTTCCAGGCCAGCCTATGAGGAGTTCTACAACCTGCCGACGATCGACAGCG
AGTTTCAGCAATGCCATTGCATCCATCCGGCATGCCAGGTTTGGAAAGAAATCCCGGCCGCAATGTATGATGTA
GCCCCATCGCCTATGAAGATTACAGTCTGATGACAAACCCTTGGTCACACTGATTAAGAACTAAAGATTTGTAAAT
CTTTTTTTGGATTATTTTTCAAAAAGATGAGATACTACACTCATTTAAATATTTTTAAGAAAATAAAAAGCTTAA
GAAATTTAAATGCTAGCTGCTCAAGAGTTTTTCAGTAGAATATTTAAGAACTAATTTTCTGCAGCTTTTAGTTTG
GAAAAAATATTTTTAAAAACAAATTTGTGAAACCTATAGACGATGTTTTAATGTACCTTCAGCTCTCTAAACTGT
GTGCTTCTACTAGTGTGTGCTCTTTTCACTGTAGACACTATCACGAGACCCAGATTAATTTCTGTGGTGTGTACA
GAATAAGTCTAATCAAGGAGAAGTTTCTGTTTGACGTTTGAGTGCCGGCTTCTGAGTAGAGTTAGGAAAACCAC
GTAACTAGCATATGATGTATAATAGAGTATACCCGTTACTTTAAAAAGAAAGTCTGAAATGTTTCGTTTTGTGGAAA
AGAACTAGTTAAATTTACTATTCTTAACCCGAATGAAATTAGCCTTTGCCTTATTCTGTGCATGGGTAAGTAAC
TTATTTCTGCAGTGTGTTGTGAACTTTGTGGAACATTTCTTCGAGTTTGTGTTTGTGCTATTTCGTAACAGTCG
TCGAACTAGGCCTCAAAAACATACGTAACGAAAAGGCCCTAGCGAGGCAAAATCTGATTGATTTGAATCTATATTT
TTCTTTAAAAAGTCAAGGGTTCTATATTGTGAGTAAATTAATTTACATTTGAGTTGTTTGTGCTAAGAGGTAG
TAAATGTAAGAGAGTACTGGTTCCTTCAGTAGTGAGTATTTCTCATAGTGCAGCTTTATTTATCTCCAGGATGTT
TTTGTGGCTGTATTGATTGATATGTGCTTCTTCTGATTCTTGCTAATTTCCAACCATATTGAATAAATGTGATC
AAGTCA

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FIGURE 38

><subunit 1 of 1, 737 aa, 1 stop
><MW: 78475, pI: 5.09, NX(S/T): 11
MQPRRAQAPGAQLLPALALLLLLLGAGPRGSSLANPVPAAPLSAPGPCAAQPCRNGGVCTSRP
EPDPQHPAPAGEPGYSCTCPAGISGANCQLVADPCASNPCHHGNCSSSSSSSSSDGYLCICNEG
YEGPNCEQALPSLPATGWTESMAPRQLQVPATQEPDKILPRSQATVTLPTWQPKTGQKVVEM
KWDQVEVIPDIACGNASSNSSAGGRLVSFEVPQNTSVKIRQDATASLILLWKVTATGFQQCSL
IDGRSVTPLQASGGLVLLLEMLALGNNHFIGFVNDVSVTKSIVALRLTLVVKVSTCVPGESHAN
DLECSGKGKCTTKPSEATFSCTCEEQYVGTFCEEYDACQRKPCQNNASCIDANEKQDGSNFTC
VCLPGYTGELCQSKIDYCIDLPCRNGATCISSLSGFTCQCPEGYFGSACEEKVDPCASSPCQN
NGTCYVDGVHFTCNCSPGFTGPTCAQLIDFCALSPCAHGTCRSVGTSYKCLCDPGYHGLYCEE
EYNECLSAPCLNAATCRDLVNGYECVCLA EYKGTHCELYKDPCANVSCLNGATCDS DGLNGTC
ICAPGFTGEECDIDINECDSNPCHHGGSCLDQPNGYNCHCPHG WVGANCEIHLQWKS GHMAES
LTNMPRHS LYIIIGALCVAFILMLIILIVGICRISRIEYQGSSRPAYEEFYNCRSIDSEFSNA
IASIRHARFGKKS RPAMYDVSP IAYEDYS PDDKPLVTLIKTKDL

Signal sequence.

amino acids 1-28

Transmembrane domain.

amino acids 641-660

N-glycosylation sites.amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,
375-379, 442-446, 549-553, 564-568**Glycosaminoglycan attachment site.**

amino acids 320-324

Tyrosine kinase phosphorylation sites.

amino acids 490-498, 674-682

N-myristoylation sites.amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,
373-379, 449-455, 480-486, 562-568, 565-571**Amidation site.**

amino acids 702-706

Aspartic acid and asparagine hydroxylation site.

amino acids 520-532, 596-608

EGF-like domain cysteine pattern signatures.amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,
491-503, 529-541, 567-579, 605-617

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FIGURE 39

GAGCGCCGCCGCCGCCGCCGCCGCCGCCGCGCACTGCAGCCCCAGGCCCCCGGCCCCCCACCCACGTCGTG
CGTTGCTGCCCGCCTGGGCCAGGCCCAAAGGCAAGGACAAAGCAGCTGTCAGGGAACCTCC
GCCGGAGTCGAATTTACGTGCAGCTGCCGGCAACCACAGGTTCCAAGATGGTTTGCGGGGGGCT
TCGCGTGTTCCAAGAACTGCCTGTGCGCCCTCAACCTGCTTTACACCTTGGTTAGTCTGCTGC
TAATTGGAATTGCTGCGTGGGGCATTGGCTTCGGGGCTGATTTCCAGTCTCCGAGTGGTCGGCG
TGGTCATTGCAGTGGGCATCTTCTTGTTCCTGATTGCTTTAGTGGGTCTGATTGGAGCTGTAA
AACATCATCAGGTGTTGCTATTTTTTTTATATGATTATTCTGTTACTTGTATTTATTGTTCAGT
TTTCTGTATCTTGCGCTTGTTTAGCCCTGAACCAGGAGCAACAGGGTCAGCTTCTGGAGGTTG
GTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAATCTAAACTGCTGTGGGTTC
GAAGTGTTAACCCAAATGACACCTGTCTGGCTAGCTGTGTTAAAGTGACCACTCGTGCTCGC
CATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTTGAGATTTGTTGGTGGCATTGGCC
TGTTCTTCAGTTTTACAGAGATCCTGGGTGTTTTGGCTGACCTACAGATACAGGAACCAGAAAG
ACCCCCGCGCGAATCCTAGTGCATTCTTTTGAATGAGAAAAACAAGGAAGATTTCTTTTCGTATT
ATGATCTTGTTACATTTCTGTAATTTTCTGTTAAGCTCCATTTGCCAGTTTAAGGAAGGAAAC
ACTATCTGGAAAAGTACCTTATTGATAGTGGAATTATATATTTTTTACTCTATGTTTCTCTACA
TGTTTTTTTTCTTTCCGTTGCTGAAAAATATTTGAAACTTGTGGTCTCTGAAGCTCGGTGGCAG
CTGGAATTTACTGTATTCATTGTGCGGCACTGTCCACTGTGGCCTTTCTTAGCATTTTTTACCT
GCAGAAAAACTTTGTATGGTACCCTGTGTTGGTTATATGGTGAATCTGAACGTACATCTCAC
TGGTATAATTATATGTAGCACTGTGCTGTGTAGATAGTTCCACTGGA AAAAGAGTGGA AATT
TATTA AAATCAGAAAGTATGAGATCCTGTTATGTTAAGGGAAATCCAAATTCCCAATTTTTTTT
TGGTCTTTTTTAGGAAAGATTGTTGTGGTAAAAAGTGTTAGTATAAAAAATGATAATTTACTTGT
AGTCTTTTATGATTACACCAATGTATTCTAGAAATAGTTATGTCTTAGGAAATTGTGGTTTTAA
TTTTTGACTTTTACAGGTAAAGTGCAAAGGAGAAAGTGGTTTTCATGAAATGTTCTAATGTATAAT
AACATTTACCTTCAGCCTCCATCAGAATGGAACGAGTTTTGAGTAATCAGGAAGTATATCTAT
ATGATCTTGATATTGTTTTTATAATAAATTTGAAGTCTAAAAGACTGCATTTTTTAAACAAGTTAG
TATTAATGCGTTGGCCACCGTAGCAAAAAGATATTTGATTATCTTAAAAATTGTAAATACCG
TTTTTCATGAAATTTCTCAGTATTGTAACAGCAACTTGTCAAACCTAAGCATATTTGAATATGA
TCTCCCATAAATTTGAAATTGAAATCGTATTGTGTGGCTCTGTATATTCTGTTAAAAAATTAA
GGACAGAAACCTTTCTTTGTGTATGCATGTTTGAATTAAAAAGAAAGTAATGGAAG

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FIGURE 40

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39979

><subunit 1 of 1, 204 aa, 1 stop

><MW: 22147, pI: 8.37, NX(S/T): 3

MVCGGFACSKNCLCALNLLYTLVSLLLIGIAAWGIGFGLISSLRVVGVIAGVIFLFLIALVG
LIGAVKHHQVLLFFYMIILLVFIIVQFSVSCACLALNQEQQGQLLEVGNNTASARNDIQRN
NCCGFRSVNPNDTCLASCVKSDHSCSPCAPIIGEYAGEVLRVGGIGLFFSFTEILGVWLT
YRNQKDPRANPSAFL

Signal Peptide:

amino acids 1-34

Transmembrane domains:

amino acids 47-63, 72-95 and 162-182

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FIGURE 41

CAGTCACCA**ATGA**AGCTGGGCTGTGTCCTCATGGCCTGGGCCCTCTACCTTTCCCTTGGTGTGC
TCTGGGTGGCCAGATGCTACTGGCTGCCAGTTTTGAGACGCTGCAGTGTGAGGGACCTGTCT
GCACTGAGGAGAGCAGCTGCCACACGGAGGATGACTTGACTGATGCAAGGGAAGCTGGCTTCC
AGGTCAAGGCCTACACTTTTCAGTGAACCCCTCCACCTGATTGTGTCCTATGACTGGCTGATCC
TCCAAGGTCCAGCCAAGCCAGTTTTTTGAAGGGGACCTGCTGGTTCTGCGTGCCAGGCCTGGC
AAGACTGGCCACTGACTCAGGTGACCTTCTACCGAGATGGCTCAGCTCTGGGTCCCCCGGGC
CTAACAGGGGAATTCTCCATCACCGTGGTACAAAAGGCAGACAGCGGGCACTACCACTGCAGTG
GCATCTTCCAGAGCCCTGGTCTGGGATCCCAGAAACAGCATCTGTTGTGGCTATCACAGTCC
AAGAAGTGTTCAGCGCCAATTCTCAGAGCTGTACCCTCAGCTGAACCCCAAGCAGGAAGCC
CCATGACCCTGAGTTGTCAGACAAAGTTGCCCTGCAGAGGTGAGCTGCCCGCCTCCTCTTCT
CCTTCTACAAGGATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAATTCCAGATCCCCA
CAGCTTCAGAAGATCACTCCGGGTCATACTGGTGTGAGGCAGCCACTGAGGACAACCAAGTTT
GGAAACAGAGCCCCCAGCTAGAGATCAGAGTGCAGGGTGCTTCCAGCTCTGCTGCACCTCCCA
CATTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGAAGTCTCCTGAGGAGGCCCTGGGC
CTCTGCCTCCGCCGCCAACCCCATCTTCTGAGGATCCAGGCTTTTCTTCTCCTCTGGGGATGC
CAGATCCTCATCTGTATCACAGATGGGCCTTCTTCTCAAACACATGCAGGATGTGAGAGTCC
TCCTCGGTACCTGCTCATGGAGTTGAGGGAATTATCTGGCCACCAGAAGCCTGGGACCACAA
AGGCTACTGCTGAAT**AGA**AGTAAACAGTTCATCCATGATCTCACTTAACCACCCCAATAAATC
TGATTCTTTATTTTCTCTTCTGTCCTGCACATATGCATAAGTACTTTTACAAGTTGTCCAG
TGTTTTGTAGATAATGTAGTTAGGTGAGTGTAAATAAATTTATATAAAGTGAGAATTAGAG
TTTAGCTATAATTGTGTATTCTCTCTTAACACAACAGAATTCTGCTGTCTAGATCAGGAATTT
CTATCTGTTATATCGACCAGAATGTTGTGATTTAAAGAGAACTAATGGAAGTGGATTGAATAC
AGCAGTCTCAACTGGGGGCAATTTTGGCCCCCAGAGGACATTGGGCAATGTTTGGAGACATTT
TGGTCATTATACTTGGGGGGTTGGGGGATGGTGGGATGTGTGTCTACTGGCATCCAGTAAATA
GAAGCCAGGGGTGCCGCTAAACATCCTATAATGCACAGGGCAGTACCCACAACGAAAAATAA
TCTGGCCCCAAAATGTCAGTTGTACTGAGTTTGAGAAACCCAGCCTAATGAAACCCTAGGTGT
TGGGCTCTGGAATGGGACTTTGTCCCTTCTAATTATTATCTCTTTCCAGCCTCATTAGCTAT
TCTTACTGACATAACAGTCTTTAGCTGGTGCTATGGTCTGTTCTTTAGTTCTAGTTTGTATCC
CCTCAAAAGCCATTATGTTGAAATCCTAATCCCCAAGGTGATGGCATTAGAAGTGGGCCTTT
GGGAAGTGATTAGATCAGGAGTGCAGAGCCCTCATGATTAGGATTAGTGCCCTTATTTAAAAA
GGCCCCAGAGAGCTAACTCACCCCTCCACCATATGAGGACGTGGCAAGAAGATGACATGTATG
AGAACCAAAAAACAGCTGTCGCCAAACACCGACTCTGTCGTTGCCTTGATCTTGAAGTTCCAG
CCTCCAGAACTATGAGAAATAAAATCTGGTTGTTTGTAGCCTAA

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FIGURE 42

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40594
><subunit 1 of 1, 359.aa, 1 stop
><MW: 38899, pI: 5.21, NX(S/T): 0
MKLGCVLMAWALYLSLGVLWVAQMLLAASFETLQCEGPVCTEESCHTEDDLTDAREAGFQVK
AYTFSEPFHLIVSYDWLILQGPAKPVFEGDLLVLRQAWQDWPLTQVTFYRDGSALGPPGPNR
EFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGSPMT
LSCQTKLPLQRSAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQVWKQ
SPQLEIRVQGASSAAPTTLNPAPQKSAAPGTAPEEAPGPLPPPPTPSSDPGFSSPLGMPDP
HLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE
```

Signal sequence:

amino acids 1-17

Leucine zipper pattern sequence:

amino acids 12-33

Protein kinase C phosphorylation site:

amino acids 353-355

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FIGURE 43

GCGAGTGTCCAGCTGCGGAGACCCGTGATAATTCGTTAACTAATTCAACAAACGGGACCCTTC
TGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGGACAGGCGGATTGGAAGAGCGGGAA
GGTCCTGGCCCAGAGCAGTGTGACACTTCCCTCTGTGACCATGAACTCTGGGTGTCTGCATT
GCTGATGGCCTGGTTTGGTGTCTGAGCTGTGTGCAGGCCGAATTCTTCACCTCTATTGGGCA
CATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATCCTTGT
GGAGGAAGCCAAGCTTTCCAAGATTAAGAGCTGGGCCAACAAAATGGAAGCCTTGACTAGCAA
GTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAACTGGTGAAGCG
GCTAAACACAGACTGGCCTGCGCTGGAGGACCTTGTCTGCAGGACTCAGCTGCAGGTTTTAT
CGCCAACTCTCTGTGCAGCGGCAGTTCTTCCCCACTGATGAGGACGAGATAGGAGCTGCCAA
AGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTTCCAGAGGGGAACT
TCCAGGAACCAAGTACCAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATGGGCCGCTCGGC
CTACAATGAAGGGGACTATTATCATACGGTGTGGTGGATGGAGCAGGTGCTAAAGCAGCTTGA
TGCCGGGGAGGAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCAGCTATGCTGTCTT
CCAGTTGGGTGATCTGCACCGTGCCCTGGAGCTCACCCGCCGCTGCTCTCCCTTGACCCAAG
CCACGAACGAGCTGGAGGGAATCTGCGGTACTTTGAGCAGTTATTGGAGGAAGAGAGAGAAAA
AACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAAAGGCATCTATGAGAGGCCTGT
GGACTACCTGCCTGAGAGGGATGTTTACGAGAGCCTCTGTCTGGGGAGGGTGTCAAACCTGAC
ACCCCGTAGACAGAAGAGGCTTTTCTGTAGGTACCAACATGGCAACAGGGCCCCACAGCTGCT
CATTGCCCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCGCACATCGTCAGGTACTACGATGT
CATGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAACCTAAACTTGCACGAGCCAC
CGTTCGTGATCCCAAGACAGGAGTCTCACTGTGCCAGCTACCGGGTTTCCAAAAGCTCCTG
GCTAGAGGAAGATGATGACCCTGTTGTGGCCCGAGTAAATCGTCGGATGCAGCATATCACAGG
GTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAATTATGGAGTGGGAGGACAGTATGA
ACCGCACTTCGACTTCTCTAGGCGACCTTTTGACAGCGGCCTCAAACAGAGGGGAATAGGTT
AGCGACGTTTCTTAACCTACATGAGTGATGTAGAAGCTGGTGGTGCCACCGTCTTCCCTGATCT
GGGGGCTGCAATTTGGCCTAAGAAGGGTACAGCTGTGTTCTGGTACAACCTCTTGCGGAGCGG
GGAAGGTGACTACCGAACAAGACATGCTGCCTGCCCTGTGCTTGTGGGCTGCAAGTGGGTCTC
CAATAAGTGGTTCCATGAACGAGGACAGGAGTTCTTGAGACCTTGTGGATCAACAGAAGTTGA
CTGACATCCTTTTCTGTCTTCCCCTTCCCTGGTCCCTCAGCCCATGTCAACGTGACAGACACC
TTTGTATGTTCTTTGTATGTTCTTATCAGGCTGATTTTTGGAGAAATGAATGTTTGTCTGGA
GCAGAGGGAGACCATACTAGGGCGACTCCTGTGTGACTGAAGTCCAGCCCTTCCATTAGCC
TGTGCCATCCCTGGCCCCAAGGCTAGGATCAAAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGC
CTAGCAAGGTGCCTTTGTACCTCAGGTGTTTTAGGTGTGAGATGTTTCAGTGAACCAAAGTTC
TGATACCTTGTTTACATGTTTGTATTTTATGGCATTCTATCTATTGTGGCTTTACCAAAAAAT
AAAATGTCCCTACCAGAAAAA

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FIGURE 44

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEEKELVQSLKEYILVEEAKLSKIKSWAN
KMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALDVLQDSAAGFIANLSVQRQFFPTD
EDEIGAALKMRLQDITYRLDPGTISRGEIPGTYQAMLSVDDCFGMGRSAYNEGDIYHTVLWM
EQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLRYFEQ
LLEEEREKTLTNQTEAELATPEGIYERPDYLPDVEYSLCRGEGVKLTTPRRQKRLFCRYHH
GNRAPQLLIAPFKEEWDSPHIVRYDVMSDEEIERIKEIAKPKLARATVRDPKTGVLTVAS
YRVSKSSWLEEDDDPVVARVNRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFSRRPFDSG
LKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGECDYRTRHAACP
LVGCKWVSNKWFHERGQEFRLPCGSTVD

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534**Tyrosine kinase phosphorylation site.**

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

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FIGURE 45

GGGGCCTTGCCTTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGGG
CGGCGGGCGCGGGTGCAGGGATCCCTGACGCCTCTGTCCCTGTTTCTTTGTGCTCCAGCC
TGTCTGTCGTGTTTTGGCGCCCCCGCCTCCCCGCGGTGCGGGGTTGCACACCGATCCTGGGC
TTCGCTCGATTTGCCGCCGAGGCGCCTCCCAGACCTAGAGGGGCGCTGGCCTGGAGCAGCGGG
TCGTCTGTGTCTCTCTCCTCTGCGCCGCGCCGGGGATCCGAAGGGTGCGGGGCTCTGAGGA
GGTGACGCGCGGGGCTCCCGCACCCCTGGCCTTGCCCGCATCTCCCTCTCTCCAGGTGTGA
GCAGCCTATCAGTCACC**ATG**TCCGCAGCCTGGATCCCGGCTCTCGGCCTCGGTGTGTGTCTGC
TGCTGCTGCCGGGGCCCCGCGGGCAGCGAGGGAGCCGCTCCCATTGCTATCACATGTTTTACCA
GAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCCTCTGCCAGGGGGCTGCCCTCTTGAGG
AATTCTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGGGCTGCTGTCC
ACAGGGGAGTAATCAGCAACTCAGGGGGACCTGTACGAGTCTATAGCCTACCTGGTCGAGAAA
ACTATTCCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTTCTAGATGGTCTGCTTCTT
TCACAGTAACTAAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCAGTGTCCACAGCAC
ATCCACCAACAGGTAAACGACTAAAGAAAACACCCGAGAAGAAAACCTGGCAATAAAGATTGTA
AAGCAGACATTGCATTTCTGATTGATGGAAGCTTTAATATTGGGCAGCGCCGATTTAATTTAC
AGAAGAATTTTGTGGAAAAGTGGCTCTAATGTTGGGAATTGGAACAGAAGGACCACATGTGG
GCCTTGTTCAAGCCAGTGAACATCCCAAAATAGAATTTTACTTGAAAACTTTACATCAGCCA
AAGATGTTTTGTTGGCATAAAGGAAGTAGGTTTCAGAGGGGGTAATTCCAATACAGGAAAAG
CCTTGAAGCATACTGCTCAGAAATTCTTCACGGTAGATGCTGGAGTAAGAAAAGGGATCCCCA
AAGTGGTGGTGGTATTTATTGATGGTTGGCCTTCTGATGACATCGAGGAAGCAGGCATTGTGG
CCAGAGAGTTTGGTGTCAATGTATTTATAGTTTCTGTGGCCAAGCCTATCCCTGAAGAACTGG
GGATGGTTCAGGATGTCACATTTGTTGACAAGGCTGTCTGTGCGGAATAATGGCTTCTTCTCTT
ACCACATGCCCAACTGGTTTGGCACCAAAAATACGTAAAGCCTCTGGTACAGAAGCTGTGCA
CTCATGAACAAATGATGTGCAGCAAGACCTGTTATAACTCAGTGAACATTGCCTTTCTAATTG
ATGGCTCCAGCAGTGTTGGAGATAGCAATTTCCGCCTCATGCTTGAATTTGTTTCCAACATAG
CCAAGACTTTTGAATCTCGGACATTGGTGCCAAGATAGCTGCTGTACAGTTTACTTATGATC
AGCGCACGGAGTTCAGTTTCACTGACTATAGCACCAAGAGAATGTCCTAGCTGTCATCAGAA
ACATCCGCTATATGAGTGGTGGAACAGCTACTGGTGATGCCATTTCTTCACTGTTAGAAATG
TGTTTGGCCCTATAAGGGAGAGCCCCAACAAGAACTTCCTAGTAATTGTCACAGATGGGCAGT
CCTATGATGATGTCCAAGGCCCTGCAGCTGCTGCACATGATGCAGGAATCACTATCTTCTCTG
TTGGTGTGGCTTGGGCACCTCTGGATGACCTGAAAGATATGGCTTCTAAACCGAAGGAGTCTC
ACGCTTTCTTCAAGAGAGTTCACAGGATTAGAACCAATTGTTTCTGATGTCATCAGAGGCA
TTTGTAGAGATTTCTTAGAATCCAGCAA**TAA**TGGTAACATTTTGACAACCTGAAAGAAAAAGT
ACAAGGGGATCCAGTGTGTAATTTGTATTCTCATAATACTGAAATGCTTTAGCATACTAGAAT
CAGATACAAAACCTATTAAGTATGTCAACAGCCATTTAGGCAAATAAGCACTCCTTTAAAGCCG
CTGCCTTCTGGTTACAATTTACAGTGTACTTTGTTAAAACACTGCTGAGGCTTCATAATCAT
GGCTCTTAGAAACTCAGGAAAGAGGAGATAATGTGGATTAAACCTTAAGAGTTCTAACCATG
CCTACTAAATGTACAGATATGCAAATTCATAGCTCAATAAAGAATCTGATACTTAGACCAA
AAAAAAA

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FIGURE 46

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPPGGCPLEEF SVYG
NIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVTKG
KSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRRFNLQKNFVG
KVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAlKEVGFRGGNSNTGKALKHTA
QKFFTVDAGVRKGIPKVVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELGMVQDV
TFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLIDGSSSV
GDSNFRMLLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTFSFTDYSTKENVLAVIRNIRYMS
GGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAAHDAGITIFSVGVAVA
PLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532**N-myristoylation site.**amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449**Amidation site.**

amino acids 145-149

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FIGURE 47

GCCCCGCGCCCGGCGCCGGGCGCCCCGAAGCCGGGAGCCACCGCC**ATG**GGGGCCTGCCTGGGAG
CCTGCTCCCTGCTCAGCTGCGCGTCCTGCCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAGCT
GCTGCCCCGCCAGCCGCAACTCCACCGTGAGCCGCCTCATCTTCACGTTCTTCCTCTTCCTGG
GGGTGCTGGTGTCCATCATTTATGCTGAGCCCGGGCGTGGAGAGTCAGCTCTACAAGCTGCCCT
GGGTGTGTGAGGAGGGGGCCGGGATCCCCACCGTCCTGCAGGGCCACATCGACTGTGGCTCCC
TGCTTGGCTACCGCGCTGTCTACCGCATGTGCTTCGCCACGGCGGCCTTCTTCTTCTTCTTTT
TCACCTTGCTCATGCTCTGCGTGAGCAGCAGCCGGGACCCCCGGGCTGCCATCCAGAATGGGT
TTTGGTTCTTTAAGTTCCTGATCCTGGTGGGCCTCACCGTGGGTGCCTTCTACATCCCTGACG
GCTCCTTCACCAACATCTGGTTCTACTTCGGCGTCGTGGGCTCCTTCTTCTTCATCCTCATCC
AGCTGGTGCTGCTCATCGACTTTGCGCACTCCTGGAACCAGCGGTGGCTGGGCAAGGCCGAGG
AGTGCGATTCCCGTGCTGGTACGCAGGCCTCTTCTTCTTCACTCTCCTCTTCTACTTGCTGT
CGATCGCGGCCGTGGCGCTGATGTTTATGTACTACACTGAGCCCAGCGGCTGCCACGAGGGCA
AGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCTGCTGTCTGCCCCA
AGGTCCAGGACGCCCAGCCCAACTCGGGTCTGCTGCAGGCCTCGGTCATCACCTCTACACCA
TGTTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCAACCCCCATTGCCAA
CCCAGCTGGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAGACCCAGTGGTGGGATG
CCCCGAGCATTGTGGGCCTCATCATCTTCTCCTGTGCACCCTCTTCATCAGTCTGCGCTCCT
CAGACCACCGGCAGGTGAACAGCCTGATGCAGACCGAGGAGTGCCACCTATGCTAGACGCCA
CACAGCAGCAGCAGCAGCAGGTGGCAGCCTGTGAGGGCCGGGCCTTTGACAACGAGCAGGACG
GCGTCACCTACAGCTACTCCTTCTTCCACTTCTGCCTGGTGCTGGCCTCACTGCACGTCATGA
TGACGCTCACCAACTGGTACAAGCCCGGTGAGACCCGGAAGATGATCAGCACGTGGACCGCCG
TGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCTCCTCTACCTGTGGACCCTGGTAGCCC
CACTCCTCCTGCGCAACCGCGACTTCAGCT**TGAG**GGCAGCCTCACAGCCTGCCATCTGGTGCCTC
CTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACCTGCCCCCTCCCCACACCAATCAGCC
AGGCTGAGCCCCCACCCTGCCCCAGCTCCAGGACCTGCCCCCTGAGCCGGGCCTTCTAGTCGT
AGTGCCCTCAGGGTCCGAGGAGCATCAGGCTCCTGCAGAGCCCCATCCCCCGCCACACCCAC
ACGGTGGAGCTGCCTCTTCTTCCCCTCCTCCCTGTTGCCATACTCAGCATCTCGGATGAAA
GGGCTCCCTTGTCTCAGGCTCCACGGGAGCGGGGCTGCTGGAGAGAGCGGGGAACTCCCACC
ACAGTGGGGCATCCGGCACTGAAGCCCTGGTGTTCCTGGTCACGTCCCCCAGGGGACCCTGCC
CCCTTCTGGACTTCGTGCCTTACTGAGTCTCTAAGACTTTTCTAATAAACAAGCCAGTGCG
TGTAACAAAAA

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FIGURE 48

MGACLGACSLLSASCCLCGSAPCILCSCCPASRNSTVSRIFTFFLFLGVLVSIIMLSPGVES
QLYKLPWVCEEGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFFTLLMLCVSSSRDPR
AAIQNGEWF^WFKFLILVGLTVGAFYIPDGSTNIWFYFGVVGSFLFILIQLVLLIDFAHSWNQR
WLGKAEECDSRAWYAGL^WFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTFVCVVS
IAAVLPKVQDAQPN^WSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVAGPEGY
ETQWWDAPSIVGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQQVAACEGRA
FDNEQDGV^WTYSYSFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVWVKICASWAGLLLY
LWTLVAPLLLNRDFS

Signal sequence:
amino acids 1-20

Transmembrane domains:
amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,
272-283, 324-340, 391-406, 428-444

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FIGURE 49

[illegible]

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FIGURE 50

MAGIPGLLFLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVSS
SCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIIYLSSSGDGAQHRDSGSSGKSRR
KRQIYGYSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKGTQK
LRVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPGWIKGNANDIGMDYDYALLEL
KKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCDAQPGA
SGSGVYVRMWKRQQQKWERKIIGIFSGHQWDMNGSPQDFNVAVRITPLKYAQICYWIKGNYL
DCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

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FIGURE 51

GGGAGGGGGCTCCGGGCGCGCGCAGCAGACCTGCTCCGGCCGCGCGCCTCGCCGCTGTCTCCGGGAGCGGCAG
CAGTAGCCCCGGGCGGCGAGGGCTGGGGGTTCTCGAGACTCTCAGAGGGGCGCCTCCCATCGGCGCCCCACCACCC
CAACCTGTTCTCGCGCGCCACTGCGCTGCGCCCCAGGACCCGCTGCCAACATGGATTTTCTCTGGCGCTGGT
GCTGGTATCCTCGCTCTACCTGCAGGCGGCGCGCGAGTTCGACGGGAGGTGGCCAGGCAATAGTGTCTATCGAT
TGGCCTATGTGTTATGGTGGGAGGATTGACTGCTGCTGGGGCTGGGCTCGCCAGTCTTGGGGACAGTGTGAGCC
TGTGTGCCAACCACGATGCAAACATGGTGAATGTATCGGGCCAAACAAGTGCAAGTGTCTCTGGTTATGCTGG
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCCTGAAGCCCCGGCCCTGTAAGCACAGGTGCATGAACACTTA
CGGCAGCTACAAGTGCTACTGTCTCAACGGATATATGCTCATGCCGGATGGTTCTGCTCAAGTGCCCTGACCTG
CTCCATGGCAAACCTGTCAGTATGGCTGTGATGTTGTTAAAGGACAAATACGGTGCCAGTGCCCATCCCCTGGCCT
GCACCTGGCTCCTGATGGGAGGACCTGTGTAGATGTTGATGAATGTGCTACAGGAAGAGCCTCCTGCCCTAGATT
TAGGCAATGTGTCAACACTTTTGGGAGCTACATCTGCAAGTGTCTATAAAGGCTTCGATCTCATGTATATTGGAGG
CAAATATCAATGTCATGACATAGACGAATGCTCACTTGGTCAGTATCAGTGCAGCAGCTTTGCTCGATGTTATAA
CGTACGTGGGTCCCTACAAGTGCAAATGTAAAGAAGGATACCAGGGTGATGGACTGACTTGTGTGTATATCCCAAA
AGTTATGATTGAACCTTCAGGTCCAATTCATGTACCAAAGGGAATGGTACCATTTTAAAGGGTGACACAGGAAA
TAATAATTGGATTCTGTATGTTGGAAGTACTTGGTGGCCTCCGAAGACACCATATATCTCTCTATCATTACCAA
CAGGCCTACTTCTAAGCCAACAACAAGACCTACACCAAGCCAACACCAATTCCTACTCCACCACCACCACCACC
CCTGCCAACAGAGCTCAGAACACCTCTACCACCTACAACCCAGAAAGGCCAACACCACCGGACTGACAACCTATAGC
ACCAGCTGCCAGTACACCTCCAGGAGGGATTACAGTTGACAACAGGGTACAGACAGACCCTCAGAAACCCAGAGG
AGATGTGTTTCAAGTGTCTGGTACACAGTTGTAATTTTGACCATGGACTTTGTGGATGGATCAGGGAGAAAGACAA
TGACTTGCACTGGGAACCAATCAGGGACCCAGCAGGTGGACAATATCTGACAGTGTGGCAGCCAAAGCCCCAGG
GGGAAAAGCTGCACGCTTGGTGCTACCTCTCGGCCGCTCATGCATTGAGGGGACCTGTGCTGTCTATTGAGGCA
CAAGGTGACGGGGCTGCACTCTGGCACACTCCAGGTGTTTGTGAGAAAACACGGTGCCACGGAGCAGCCCTGTG
GGGAAGAAATGGTGGCCATGGCTGGAGGCAAACACAGATCACCTTGCGAGGGGCTGACATCAAGAGCGAATCACA
AAGATGATTAAAGGGTTGGAAAAAAGATCTATGATGGAAAATTAAGGAACTGGGATTATTGAGCCTGGAGAAG
AGAAGACTGAGGGGCAAACCATTTGATGGTTTTCAAGTATATGAAGGGTTGGCACAGAGAGGGTGGCGACCAGCTG
TTCTCCATATGCACTAAGAATAGAACAAGAGGAACTGGCTTAGACTAGAGTATAAGGGAGCATTCTTGGCAGG
GGCCATTGTTAGAACTTCTATAAAAAAAGAGTGTGAAAATCTCAGTATCTCTCTCTCTTTCTAAAAAATTAGA
TAAAAATTTGTCTATTTAAGATGGTTAAAGATGTTCTTACCCAAGGAAAAGTAACAAATTATAGAATTTCCCAAA
AGATGTTTTGATCCTACTAGTAGTATGCAGTGAAAATCTTTAGAACTAAATAATTTGGACAAGGCTTAATTTAGG
CATTTCCCTCTTGACCTCCTAATGGAGAGGGATTGAAAGGGGAAGAGCCACCAATGCTGAGCTCACTGAAATA
TCTCTCCCTTATGGCAATCCTAGCAGTATTAAAGAAAAAGGAACTATTTATTCCAAATGAGAGTATGATGGAC
AGATATTTTAGTATCTCAGTAATGTCCTAGTGTGGCGGTGGTTTTCAATGTTTCTTCATGGTAAAGGTATAAGCC
TTTCATTTGTTCAATGGATGATGTTTCAGATTTTTTTTTTTTTTAAGAGATCCTTCAAGGAACACAGTTCAGAGAG
ATTTTCATCGGGTGCATTCTCTCTGCTTCGTGTGTGACAAGTTATCTTGGCTGCTGAGAAAGAGTGCCCTGCCCC
ACACCGGCAGACCTTTCTCTCACCTCATCAGTATGATTCACTTTCTCTTATCAATTGGACTCTCCAGGTTCCAC
AGAACAGTAATATTTTTTGAACAATAGGTACAATAGAAGGTCTTCTGTCAATTAACCTGGTAAAGGCAGGGCTGG
AGGGGGAAAATAAATCATTAAGCCTTTGAGTAACGGCAGAAATATATGGCTGTAGATCCATTTTAAATGGTTCATT
TCCTTTATGGTCATATAACTGCACAGCTGAAGATGAAAGGGGAAAATAAATGAAAATTTTACTTTTCGATGCCAA
TGATACATTGCACTAAACTGATGGAAGAAGTTATCCAAGTACTGTATAACATCTTGTGTTATTTAATGTTTT
CTAAAATAAAAAATGTTAGTGGTTTTCCAAATGGCCTAATAAAAAACAATTATTTGTAAATAAAAAACTGTTAGTAAT

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FIGURE 52

MDFLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQPR
CKHGEICIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPDGS
CSSALTCSMANCQYGCDVVKGQIRCQCPSPGLHLAPDGRTCVDVDECATGRASCPFRQCVNT
FGSYICKCHKGFDLMYIGGKYQCHDIDEC SLGQYQCSSFARCYNVRGSYKCKKEGYQGDGLT
CVYIPKVMIEPSGPIHVPKNGTILKGD TGNNNWIPDVGSTWWPPKTPYIIPPIITNRPTSKPT
TRPTPKPTPIPTPPPPPLPTLRTPLPPTTPERPTTGLTTIAPAASTPPGGITVDNRVQTD
QKPRGDFVSVLVHSCNFDHGLCGWIREKDNDLHWEPIRDPAGGQYLTVSAAKAPGGKAARLVL
PLGRLMHSGDLCLSFHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQITLRGADIK
SESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482**Aspartic acid and asparagine hydroxylation site.**

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

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FIGURE 53

CGGGCCGCCCCGGCCCCCATTCGGGCGGGCCTCGCTGCGGCGGGCGACTGAGCCAGGCTGGG
CCGCGTCCCTGAGTCCCAGAGTCGGCGCGGCGCGGCAGGGGCAGCCTTCCACCACGGGGAGCC
CAGCTGTCAGCCGCTCACAGGAAGATGCTGCGTGGCGGGGCAGCCCTGGCATGGGTGTGCA
TGTGGGTGCAGCCCTGGGAGCACTGTGGTTCTGCCTCACAGGAGCCCTGGAGGTCCAGGTCCC
TGAAGACCCAGTGGTGGCACTGGTGGGCACCGATGCCACCCTGTGCTGCTCCTTCTCCCTGA
GCCTGGCTTCAGCCTGGCACAGCTCAACCTCATCTGGCAGCTGACAGATACCAAACAGCTGGT
GCACAGCTTTGCTGAGGGCCAGGACCAGGGCAGCGCCTATGCCAACCGCACGGCCCTCTTCCC
GGACCTGCTGGCACAGGGCAACGCATCCCTGAGGCTGCAGCGCGTGCCTGTGGCGGACGAGGG
CAGCTTCACCTGCTTCGTGAGCATCCGGGATTTTCGGCAGCGCTGCCGTGACCTGCAGGTGGC
CGCTCCCTACTCGAAGCCAGCATGACCCTGGAGCCCAACAAGACCTGCGGCCAGGGGACAC
GGTGACCATCACGTGCTCCAGCTACCAGGGCTACCCTGAGGCTGAGGTGTTCTGGCAGGATGG
GCAGGGTGTGCCCCCTGACTGGCAACGTGACCACGTGCGAGATGGCCAACGAGCAGGGCTTGTT
TGATGTGCACAGCGTCCTGCGGGTGGTGTGGGTGCGAATGGCACCTACAGCTGCCTGGTGCG
CAACCCCGTGCTGCAGCAGGATGCGCACRGCTCTGTCAACATCACAGGGCAGCCTATGACATT
CCCCCAGAGGCCCTGTGGGTGACCGTGGGGCTGTCTGTCTGTCTCATTGCACTGCTGGTGGC
CCTGGCTTTCGTGTGCTGGAGAAAGATCAAACAGAGCTGTGAGGAGGAGAATGCAGGAGCTGA
GGACCAGGATGGGGAGGGAGAAGGCTCCAAGACAGCCCTGCAGCCTCTGAAACACTCTGACAG
CAAAGAAGATGATGGACAAGAAATAGCC**TGAC**CCATGAGGACCAGGGAGCTGCTACCCCTCCCT
ACAGCTCCTACCCTCTGGCTGCAATGGGGCTGCACTGTGAGCCCTGCCCCAACAGATGCATC
CTGCTCTGACAGGTGGGCTCCTTCTCAAAGGATGCGATACACAGACCACTGTGCAGCCTTAT
TTCTCCAATGGACATGATTCCCAAGTCATCCTGCTGCCTTTTTTCTTATAGACACAATGAACA
GACCACCCACAACCTTAGTTCTCTAAGTCATCCTGCCTGCTGCCTTATTTACAGTACATACA
TTTCTTAGGGACACAGTACACTGACCACATCACCACCCTCTTCTTCCAGTGCTGCGTGGACCA
TCTGGCTGCCTTTTTTCTCCAAAAGATGCAATATTCAGACTGACTGACCCCTGCCTTATTTT
ACCAAAGACACGATGCATAGTCACCCCGGCCCTTGTTTCTCCAATGGCCGTGATACACTAGTGA
TCATGTTTCAGCCCTGCTTCCACCTGCATAGAATCTTTTCTTCTCAGACAGGGACAGTGCGGCC
TCAACATCTCCTGGAGTCTAGAAGCTGTTTCCCTTTCCCTCCTTCCCTGCCCAAGTGAA
GACAGGGCAGGGCCAGGAATGCTTTGGGGACACCGAGGGGACTGCCCCCACCACCATGG
TGCTATTCTGGGGCTGGGGCAGTCTTTTCTGGCTTGCCCTCTGGCCAGCTCCTGGCCTCTGGT
AGAGTGAGACTTCAGACGTTCTGATGCCTTCGGATGTCATCTCTCCCTGCCCCAGGAATGGA
AGATGTGAGGACTTCTAATTTAAATGTGGGACTCGGAGGGATTTTGTAACCTGGGGGTATATT
TTGGGGAAAATAAATGTCTTTGTAAAAAAAAAAAAAAAAAAAAA

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FIGURE 54

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41386
><subunit 1 of 1, 316 aa, 1 stop, 1 unknown
><MW: -1, pI: 4.62, NX(S/T): 4
MLRRRGSPGMGVHVGAAALGALWFCLTGALEVQVPEDPVVALVGTDATLCCSFSPPEPGFSLAQL
NLIWQLTDTKQLVHSFAEGDQGSAYANRTALFPDLLAQGNASLRLQVRVADGSGFTCFVSI
RDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDVTITCSSYQGYPEAEVFWQDGQGVPLTGN
VTTSQMANEQGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDAHXSVTITGQPMTFPPEALWVT
VGLSVCLIALLLVALAFVCWRKIKQSCEEENAGAEDQDGEGEKSKTALQPLKHSDSKEDDGQEIA
```

Important features:**Signal peptide:**

amino acids 1-28

Transmembrane domain:

amino acids 251-270

N-glycosylation site.

amino acids 91-94, 104-107, 189-192 and 215-218

Homologous region to Immunoglobulins and MHC

amino acids 217-234

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FIGURE 55

GAGTCTTGACCGCCGCGGGCTCTTGGTACCTCAGCGCGAGCGCCAGGCGTCCGGCCGCGCGTG
GCT**ATG**TTTCGTGTCCGATTTCCGCAAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTT
CTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCCAG
TGTGACCACGTGCAATATACGCTGGTTCCAGTTTCTGGGTGGCAAGAAGCTTGAACTGCATTT
CTTGAGCATAAAGAACAGTTTCATTATTTTATTCTCATAAACTGTGGAGCTAATGTAGACCTA
TTGGATATTCTTCAACCTGATGAAGACACTATATTCTTTGTGTGTGACTCCCATAGGCCAGTC
AATGTCGTCAATGTATACAACGATACCCAGATCAAATTACTCATTAACAAGATGATGACCTT
GAAGTTCCCGCCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATTTCAGGAAAT
GACAGTGATGGGTCAGAGCCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATAGTGGAGCAA
ACCATGCGGAGGAGGCAGCGGCGAGAGTGGGAGGCCCGGAGAAGAGACATCCTCTTTGACTAC
GAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGGCTTGGATGCTG
TCCAAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGACCAGTGGGTGCAA
GACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTGTCAGCGCCACGTTTCCCGC
CACAACCACCGGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCACACGGATCTCCTTT
GAGTATGACCTCCGCCTGGTGCTCTACCAGCACTGGTCCCTCCATGACAGCCTGTGCAACACC
AGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAAGCGGCTCCAGGAGTTC
CTTGACAGACATGGGTCTTCCCCTGAAGCAGGTGAAGCAGAAGTTCCAGGCCATGGACATCTCC
TTGAAGGAGAATTTGCGGGAAATGATTGAAGAGTCTGCAAATAAATTTGGGATGAAGGACATG
CGCGTGACAGACTTTCAGCATTTCATTTTGGGTTCAAGCACAAAGTTTCTGGCCAGCGACGTGGTC
TTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCTCAGGGACAGATCACTTCATC
CAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTGTACCATGGCCTGGAACCTCGCC
AAGAAGCAGCTGCGAGCCACCCAGCAGACCATTGCCAGCTGCCTTTGCACCAACCTCGTCATC
TCCCAGGGGCCTTTTCTGTACTGCTCTCTCATGGAGGGCACTCCAGATGTCATGCTGTTCTCT
AGGCCGGCATCCCTAAGCCTGCTCAGCAAACACCTGCTCAAGTCCTTTGTGTGTTTCGACAAAG
AACCGGCGCTGCAAACCTGCTGCCCCCTGGTGATGGCTGCCCCCCTGAGCATGGAGCATGGCACA
GTGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTCGGACAGGAAGAAGCTTTTTTGGGAGG
GCGTTTGAGAAGGCAGCGGAAAGCACCAGCTCCCGGATGCTGCACAACCATTTTGACCTCTCA
GTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTTCTGGACGCACTTATTTCCCTCCTGTCC
TAGGAAATTTGATTCTTCCAGAATGACCTTCTTATTTATGTAAGTGGCTTTTCAATTTAGATTGTA
AGTTATGGACATGATTTGAGATGTAGAAGCCATTTTTTTATTAAATAAAATGCTTATTTTAGGAAA

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FIGURE 56

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELET AFL
EHKEQFHYFILINCGANVDLLDILQPD EDTIFFVCDSHRPVNVVNVYNDTQIKLLIKQDD DLE
VPAYEDI FRDEEEDEEHSGNDS DGSEPSEK RTRLEEEIVEQTMRRRQRREWEARRRDILFDYE
QY EYHGTSSAMVMFELAWMLSKDLNDMLWWAIVGLTDQWVQDKITQMKYVTDVGV LQRHVSRH
NHRNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSL CNTSYTAARFKLWSVHGQKRLQEFL
ADMGLPLKQVKQKFQAMDISLKENLREMIEESANKFGMKDMRVQTF SIHFGFKHKFLASDVVF
ATMSLMESPEKDGSGTDHFIQALDSLRSNLDKLYHGLELAKKQLRATQQT IASCLCTNLVIS
QGPFLYCSLMEGTPDVMLFSRPASLSLLSKHLLKS FVCSTKNRRCKLLPLVMAAPLSMEHGT V
TVVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLHNHFDLSVIELKAEDRSKFLDALISLLS

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FIGURE 57

CGCCGCCGTTGGGGCTGGAAGTTCCCGCCAGGTCCGTGCCGGGCGAGAGAGATGCTGCCCGGC
CCGCCTCGGCTTTGAGGCGAGAGAAGTGTCCAGACCCATTTGCGCTTGCTGACGGCGTTCGAG
CCCTGGCCAGAC**ATGT**CCACAGGGTTCTCCTTCGGGTCCGGGACTCTGGGCTCCACCACCGTG
GCCGCCGGCGGGACCAGCACAGGCGGCGTTTTCTCCTTCGGAACGGGAACGTCTAGCAACCCT
TCTGTGGGGCTCAATTTTGGAAATCTTGGAAAGTACTTCAACTCCAGCAACTACATCTGCTCCT
TCAAGTGGTTTTTGGAAACGGGCTCTTTGGATCTAAACCTGCCACTGGGTTCACTCTAGGAGGA
ACAAATACAGGTGCCTTGACACCAAGAGGCCTCAAGTGGTCACCAAATATGGAACCCCTGCAA
GGAAACAGATGCATGTGGGGAAGACACCCATCCAAGTCTTTTTAGGAGTCCCCTTCTCCAGA
CCTCCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCGGAGCCCTGGAAAGGAATCAGA
GATGCTACCACCTACCCGCTGGATGGAGTCTCGCTCTGTGCCAGGCTGGAGTGCAGTGGCA
CGATCTCGGCTCACTGCAACCTCCGCTCCCGGGTTCAAGCGAGTCTCCTGCCTCAGCCTCTG
AGTGTCTGGGGCTACAGGTGCCTGCAGGAGTCTGGGGCCAGCTGGCCTCGATGTACGTACGC
ACGCGGGAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTCTGTACCTGAACGTGTACGCG
CCGGCGCGCGCGCCCGGGGATCCCCAGCTGCCAGTGGTCTGGTTCCCGGGAGGCGCCTTC
ATCGTGGGCGCTGCTTCTTCGTACGAGGGCTCTGACTTGGCCGCGCCGAGAAAGTGGTGCTG
GTGTTTTCTGCAGCACAGGCTCGGCATCTTCGGCTTCCTGAGCACGGACGACGCCACGCGCGC
GGAACTGGGGGCTGCTGGACCAGATGGCGGCTCTGCGCTGGGTGCAGGAGAACATCGCAGCC
TTCGGGGGAGACCCAGGAAATGTGACCCCTGTTTCGGCCAGTCCGCGGGGGCCATGAGCATCTCA
GGACTGATGATGTACCCCTAGCCTCGGGTCTCTTCCATCGGGCCATTTCCAGAGTGGCACC
GCGTTATTCAAGCTTTTCATCACTAGTAACCCACTGAAAGTGGCCAAGAAGGTTGCCACCTG
GCTGGATGCAACCACAACAGCACACAGATCCTGGTAAACTGCCTGAGGGCACTATCAGGGACC
AAGGTGATGCGTGTGTCCAACAAGATGAGATTCTCCAAGTGAACCTCCAGAGAGACCCGGAA
GAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGGTGTATCCAGATGACCCCTTGGTG
CTCCTGACCCAGGGGAAGGTTTTATCTGTGCCCTACCTTCTAGGTGTCAACAACCTGGAATTC
AATTGGCTCTTGCCCTTATAATATACCAAGGAGCAGGTACCACTTGTGGTGGAGGAGTACCTG
GACAATGTCAATGAGCATGACTGGAAGATGCTACGAAACCGTATGATGGACATAGTTCAAGAT
GCCACTTTCGTGTATGCCACACTGCAGACTGCTCACTACCACCGAGAAACCCCAATGATGGGA
ATCTGCCCTGCTGGCCACGCTACAACAAGGATGAAAAGTACCTGCAGCTGGATTTTACCACAA
GAGTGGGCAT**TGA**AGCTCAAGGAGAAGAAGATGGCTTTTTGGATGAGTCTGTACCAGTCTCAA
GACCTGAGAAGCAGAGGCAATTCTAAGGGTGGCTATGCAGGAAGGAGCCAAAGAGGGGTTTGC
CCCCACCATCCAGGCCCTGGGGAGACTAGCCATGGACATACCTGGGGACAAGAGTTCTACCCA
CCCCAGTTTAGAACTGCAGGAGCTCCCTGCTGCCTCCAGGCCAAAGCTAGAGCTTTTGCCTGT
TGTGTGGGACCTGCACTGCCCTTCCAGCCTGACATCCATGATGCCCTCTACTTCACTGTT
GACATCCAGTTAGGCCAGGCCCTGTCAACACCACACTGTGCTCAGCTCTCCAGCCTCAGGACA
ACCTCTTTTTTTCCCTTCTTCAAATCCTCCCACCCTCAATGTCTCCTTGTGACTCCTTCTTA
TGGGAGGTCGACCCAGACTGCCACTGCCCCGTGCTACTGCACCCAGCTTGGCATTTACCATCCA
TCCTGCTCAACCTTGTTCCTGTCTGTTACATTGGCCTGGAGGCCTAGGGCAGGTTGTGACAT
GGAGCAAACCTTTTGGTAGTTTGGGATCTTCTCTCCCACCCACACTTATCTCCCCCAGGGCCAC
TCCAAAGTCTATACACAGGGGTGGTCTCTTCAATAAAGAAGTGTGATTAGAAAAAAAAAAAA

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FIGURE 58

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44179
<subunit 1 of 1, 545 aa, 1 stop
<MW: 58934, pI: 9.45, NX(S/T): 4
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GTGLFSGSKPATGFTLGSTNTGALHTKRPQVVTKYGT LQGKQMHVGKTPIQVFLGVPF SRPPLG
ILRFAPPEPPEPWKGIRDATTYPGWSLALSPGWSA VARSRLTATSASRVQASLLPQPLSVWG
YRCLQESWGQLASMYVSTRERYKWLRFSEDCLYLNVYAPARAPGDPQLPVMVWFPGGAFIVGA
ASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLLDQMAALRWVQENIAAFGGD
PGNVTLFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVAHLAGCN
HNSTQILVNCLRALSGTKVMRVS NKMRFQLNFQRPDEEIIWSMSPVVDGVVIPDDPLVLLTQ
GKVSSVPYLLGVNNLEFNWLLPYNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMDIVQDATFV
YATLQTAHYHRETPMMGICPAGHATTRMKSTCSWILPQEWA
```

Important features:**Signal peptide:**

amino acids 1-29

Carboxylesterases type-B serine active site.

amino acids 312-327

Carboxylesterases type-B signature 2.

amino acids 218-228

N-glycosylation sites.

amino acids 318-321, 380-383 and 465-468

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FIGURE 60

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44192

<subunit 1 of 1, 694 aa, 1 stop

<MW: 77400, pI: 9.54, NX(S/T): 6

MLLLGLCLGLSLCVGSQEEAQSWGHSSEQDGLRVPRQVRLQLRLKTKPLMTEFSVKSTIISR
YAFTTVSCRMLNRRASEDQDIEFQMQUIPAAAFITNFTMLIGDKVYQGEITEREKKSGDRVKEKR
NKTTEENGEKGTETFRASAVIPSKDKAAFFLSYEELLQRRLGKYEHSISVRPQQLSGRLSVDV
NILESAGIASLEVLPLHNSRQRGSGRGEDDSGPPPSTVINQNETFANIIFKPTVVQQARIAQN
GILGDFIIRYDVNREQSIGDIQVLNGYFVHYFAPKDLPLPKNVVFLDSSASMVGTKLRQTK
DALFTILHDLRPQDRFSIIGFSNRIKVKDHLISVTPDSIRDGKVYIHHMSPTGGTDINGALQ
RAIRLLNKYVAHSGIGDRSVSLIVFLTDGKPTVGETHTLKLNNNTREAARGQVCIFTIGIGND
VDFRLLLEKLSLENCGLTRRVHEEEDAGSQLIGFYDEIRTPLLSDIRIDYPPSSVVQATKTLFP
NYFNGSEIIIIAGKLVDRKLDHLHVEVTASNSKKFIILKTDVPVRPQKAGKDVGTGSPRGGDGE
GDTNHIERLWSYLTTKELLSSWLQSDDEPEKERLRQRAQALAVSYRFLTPFTSMKLRGPVPRM
DGLEEAHGMSAAMGPEPVVQSVRGAGTQPGPLLKKPNSVKKKQNKTKKRHRDGVFPLHHLGIR

Signal sequence.

amino acids 1-14

N-glycosylation sites.

amino acids 97-101, 127-131, 231-235, 421-425, 508-512, 674-678

Glycosaminoglycan attachment sites.

amino acids 213-217, 391-395

N-myristoylation sites.

amino acids 6-12, 10-16, 212-218, 370-376, 632-638, 638-644

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FIGURE 61

CAGGAACCCCTCTCTTTGGGTCTGGATTGGGACCCCTTTCCAGTACCATTTTTTCTAGTGAACC
ACGAAGGGACGATACCAGAAAAACACCCTCAACCCAAAGGAAATAGACTACAGCCCCAATTGGC
TGACTTTGGCTATAGAAAAAAGAAAGGAACGAAAAGAGACAGTTTTTTTTTGGAAAGCTAAGTC
TTCCCTTTATCGAGTCAAGAAACCCCCCTTCTTGAGCTATTTACAGCTTTTAACAATTGAGT
AAAGTACGCTCCGGTCAACC**ATGGT**GACAGCCGCCCTGGGTCCCGTCTGGGCAGCGCTCCTGCT
CTTTCTCCTGATGTGTGAGATCCGTATGGTGGAGCTCACCTTTGACAGAGCTGTGGCCAGCGG
CTGCCAACGGTGTGTGACTCTGAGGACCCCTGGATCCTGCCCATGTATCCTCAGCCTCTTC
CTCCGGCCGCCCCACGCCCTGCCTGAGATCAGACCCTACATTAATATCACCATCCTGAAGGG
TGACAAAGGGGACCCAGGCCCAATGGGCCTGCCAGGGTACATGGGCAGGGAGGGTCCCCAAGG
GGAGCCTGGCCCTCAGGGCAGCAAGGGTGACAAGGGGGAGATGGGCAGCCCCGGCGCCCCGTG
CCAGAAGCGCTTCTTCGCCTTCTCAGTGGGCCGCAAGACGGCCCTGCACAGCGCGAGGACTT
CCAGACGCTGCTCTTCGAAAGGGTCTTTGTGAACCTTGATGGGTGCTTTGACATGGCGACCGG
CCAGTTTGCTGCTCCCCCTGCGTGGCATCTACTTCTTCAGCCTCAATGTGCACAGCTGGAATTA
CAAGGAGACGTACGTGCACATTATGCATAACCAGAAAGAGGCTGTATCCTGTACGCGCAGCC
CAGCGAGCGCAGCATCATGCAGAGCCAGAGTGTGATGCTGGACCTGGCCTACGGGGACCGCGT
CTGGGTGCGGCTCTTCAAGCGCCAGCGCGAGAAGCCCATCTACAGCAACGACTTCGACACCTA
CATCACCTTCAGCGGCCACCTCATCAAGGCCGAGGACGACT**GA**AGGGCCTCTGGGCCACCCTCC
CGGCTGGAGAGCTCAGGTGCTGGTCCCGTCCCTGCAGGGCTCAGTTTGCAGTGTGTGAAGC
AGGAAGGCCAGGGAGGTCCCCGGGGACCTGGCATTTCTGGGGAGACCCTGCTTCTATCTTGGCT
GCCATCATCCCTCCCAGCCTATTTCTGCTCCTCTCTTCTCTCTTGGACCTATTTTAAGAAGCT
TGCTAACCTAAATATTCTAGAACTTTCCAGCCTCGTAGCCCAGCACTTCTCAAACCTGGAAA
TGATGGGAATCACC CGGGGTTTCGTGTTAAATGCAGATTCTGACTCAGCAGGTCTGAGTGGGT
CCAGGATTCTGTGTTTCTCATATGTTCTGGGTGATGCTGATGGGGTCAGTCTATGAACCACA
CTGGAGCAACCAGGTTCTAGGACTTTCTCAATATTCTAGTACTTTCTGAACATTCTGGAATCC
TCCCCACATTCTAGAATTCTCCCAACATTTTTTTTTTCTTGAGACAGAGTCTTGCTCTGTTGCC
CAGGCTAGAGTGCAGTGGTGCAATCTCAGTTCAGTGCACCTCTGCCTCCCGGGTTCAAGCGA
TTCTTCTGCCCTCAGCCTCCCTAGTGGCTGGGATTACAGGCGCCTGCTACCATGCCTGGCTAAT
TTTTGTATTTTTAGTAGAGATGGGGTTTACCATATTGGCCAGGCTGGTCTTGAACCTCCTGAC
TTCAGGTGACCCACCCGCTCGGCCTCTCAAAATGCTGGGATTACAGGTGTGAGCCACCGTGC
CTGGCCAATTCCAACATTCTTAAATCTCTCATCCCTCCAGGGCTCCCCGTGCTATGTTCTCT
TTACCCCTTCCCCCTCTTCTCTTGCTCAGGCCTGCACCACTGCAGCCACCGTTCAATTTATTCA
TTCATTAAACACTGAGCACTCACTCTGTGCTGGGTCCCGGGAAGGGTGAGGGGGTCAGACACA
GGCCCTGCCCCTGCCCTCAGTGAAGTGGCCAGTCCAGCCAGGCGGGGAGAGATGTGTACATAG
GTTTTAAAGCAGACCCAGAGCTCATGGGGGCTGTGTTCTGGGTGTTCAAGGTGCTGCTGGTCC
TCCATTACCCACTGCTCCCCAAGGCTGGTGGGACGGGGTCCCGGTGGCAGGGGAGGTATCTC
CTTCCCGTTCCCTCATCCACCTGCCAGTGCTCATCGTTACAGCAAACCCAGGGGGCTTGGC
CAGGTCAAGGGTTCTGTGAGGAGAGGACCCAGGAGTGTGGGGGCATTTGGGGGGTGAAGTGGC
CCCCGAAGAATGGAACCCACACCCATAGCTCTCCCCACAGCTGATACGGCATCCTGCGAGAAG
ACCTGCCCTCCTCACTGGGATCCCCCTTCCCTGCCTCCTCCCAGGGCTCTGCCAGGGCCTTGCTC
AGTCCCTTCCACCAAAGTCATCTGAACCTCCGTTTCCCCAGGGCCTCCAGCTGCCCTCAGACA
CTGATGTCTGTCCCCAGGTGCTCTCTGCCCTCATGCCCCCTCTCACCGGCCAGTGCCCCGAC
TCTCCAGGCTTTATCAAGGTGCTAAGGCCCGGGTGGGCAGCTCCTCGTCTCAGAGCCCTCCTC
CGGCCTGGTGCTGCCTTTACAAACACCTGCAGGAGAAGGGCCACGGAAGCCCCAGGCTTTAGA
GCCCTCAGCAGGTCTGGGGAGCTAGAGCAAAGGAGGGACCTCAGGCCTTCCGTTTCTTCTTCC
AGGGTGGGGTGGCCTGGTGTTCCTTAGCCTTCCAAACCCAGGTGGCCTGCCCTTCTCCCCAG
AGGGAGGCGGCCTCCGCCATTGGTGCTCATGCAGACTCTGGGGCTGAGGTGCCCGGGGGGT
GATCTCTGGTGCTCACAGCCGAGGGAGCCGTGGCTCCATGGCCAGATGACGGAACAGGGTCT
GACCAAGTGCCAGGAAGACCTGTGCTATAAACCACCCTGCCTGATCCTGCCCTGCCTGACCC
CGCCACGCCCTGCCGTCCAGCATGATTAAAGAATGCTGTCTCCTCTTGAAAAA

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FIGURE 62

MVTAALGPVWAALLLFLLMCEIRMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSSGRPHA
LPEIRPYINITILKGDKGDPGPMGLPGYMGREGPQGEPPGQSGDKGEMGSPGAPCQKRFFA
FSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKETVH
IMHNQKEAVILYAQPSESRIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITFSGH
LIKAEDD

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 72-75

Clq domain proteins.

amino acids 144-178, 78-111 and 84-117

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FIGURE 63

ATGGAAGCCAGTAACACTGTGGCCTACTATCTCTTCCGTGGTGCCATCTACATTTTTTGGGAC
TCGGGAATTATGAGGTAGAGGTGGAGGCGGAGCCGGATGTCAGAGGTCCTGAAATAGTCACCA
TGGGGGAAAATGATCCGCCTGCTGTTGAAGCCCCCTTCTCATTCCGATCGCTTTTTTGGCCTTG
ATGATTTGAAAATAAGTCCTGTTGCACCAGATGCAGATGCTGTTGCTGCACAGATCCTGTCAC
TGCTGCCATTGAAGTTTTTTCCAATCATCGTCATTGGGATCATTGCATTGATATTAGCACTGG
CCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGAAGTACAGATGTCGCTCATCCTTTAAGT
GTATCGAGCTGATAGCTCGATGTGACGGAGTCTCGGATTGCAAAGACGGGGAGGACGAGTACC
GCTGTGTCCGGGTGGGTGGTCAGAATGCCGTGCTCCAGGTGTTACAGCTGCTTCGTGGAAGA
CCATGTGCTCCGATGACTGGAAGGGTCACTACGCAAATGTTGCCTGTGCCAACTGGGTTTTCC
CAAGCTATGTGAGTTCAGATAACCTCAGAGTGAGCTCGCTGGAGGGGGCAGTTCCGGGAGGAGT
TTGTGTCCATCGATCACCTCTTGCCAGATGACAAGGTGACTGCATTACACCACTCAGTATATG
TGAGGGAGGGATGTGCCTCTGGCCACGTGGTTACCTTGCACTGCACAGCCTGTGGTCATAGAA
GGGGCTACAGCTCACGCATCGTGGGTGGAAACATGTCCTTGCTCTCGCAGTGGCCCTGGCAGG
CCAGCCTTCAGTTCCAGGGCTACCACCTGTGCGGGGGCTCTGTCAACACGCCCTGTGGATCA
TCACTGCTGCACACTGTGTTTATGACTTGTACCTCCCCAAGTCATGGACCATCCAGGTGGGTC
TAGTTTTCCCTGTTGGACAATCCAGCCCCATCCCACTGGTGGAGAAGATTGTCTACCACAGCA
AGTACAAGCCAAAGAGGGCTGGGCAATGACATCGCCCTTATGAAGCTGGCCGGGGCCACTCACGT
TCAATGAAATGATCCAGCCTGTGTGCCTGCCAACTCTGAAGAGAACTTCCCCGATGGAAAAG
TGTGCTGGACGTCAGGATGGGGGGCCACAGAGGATGGAGGTGACGCCTCCCCGTCTCTGAACC
ACGCGGGCCGTCCCTTTGATTTCCAACAAGATCTGCAACCACAGGGACGTGTACGGTGGCATCA
TCTCCCCCTCCATGCTCTGCGCGGGCTACCTGACGGGTGGCGTGGACAGCTGCCAGGGGGACA
GCGGGGGGGCCCCTGGTGTGTCAAGAGAGGAGGCTGTGGAAGTTAGTGGGAGCGACCAGCTTTG
GCATCGGCTGCGCAGAGGTGAACAAGCCTGGGGTGTACACCCGTGTCACCTCCTTCTGGACT
GGATCCACGAGCAGATGGAGAGAGACCTAAAAACCT**TGA**AGAGGAAGGGGACAAGTAGCCACCT
GAGTTCCCTGAGGTGATGAAGACAGCCCGATCCTCCCCCTGGACTCCCGTGTAGGAACCTGCACA
CGAGCAGACACCCTTGAGCTCTGAGTTCCGGCACCAAGTAGCAGGCCCGAAAGAGGCACCCTT
CCATCTGATTCCAGCACAACCTTCAAGCTGCTTTTTTGTTTTTTGTTTTTTTGAGGTGGAGTCT
CGCTCTGTTGCCCAGGCTGGAGTGCAGTGGCGAAATCCCTGCTCACTGCAGCCTCCGCTTCCC
TGTTTCAAGCGATTCTCTTGCCCTCAGCTTCCCCAGTAGCTGGGACCACAGGTGCCCGCCACCA
CACCCAATAATTTTTGTATTTTGTAGTAGAGACAGGGTTTTACCATGTTGGCCAGGCTGCTCT
CAAACCCCTGACCTCAAATGATGTGCCTGCTTCAGCCTCCCACAGTGTGGGATTACAGGCAT
GGGCCACCACGCCTAGCCTCACGCTCCTTTCTGATCTTCACTAAGAACAAAAGAAGCAGCAAC
TTGCAAGGGCGGCCTTTCCCACTGGTCCATCTGGTTTTCTCTCCAGGGTCTTGCAAAATTCCT
GACGAGATAAGCAGTTATGTGACCTCACGTGCAAAGCCACCAACAGCCACTCAGAAAAGACGC
ACCAGCCCAGAAGTGCAGAACTGCAGTCACTGCACGTTTTTCATCTCTAGGGACCAGAACCAAA
CCCACCCTTTCTACTTCCAAGACTTATTTTCACATGTGGGGAGGTTAATCTAGGAATGACTCG
TTTAAGGCCTATTTTCATGATTTCTTTGTAGCATTTGGTGCTTGACGTATTATGTCTTTGA
TTCCAAATAATATGTTTCCTTCCCTCATTGTCTGGCGTGTCTGCGTGGACTGGTGACGTGAAT
CAAAATCATCCACTGAAA

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FIGURE 64

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45234
><subunit 1 of 1, 453 aa, 1 stop
><MW: 49334, pI: 6.32, NX(S/T): 1
MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALILAL
AIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVQVFTAASWK
TMCSDDWKGYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSDHLLPDDKVLTALHHSVY
VREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVITPLWI
ITAAHCVDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHSHYKPKRLGNDIALMKLAGPLT
FNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAPPLISNKICNHRDVYGGI
ISPSMLCAGYLTGGVDSCQGDSGGPLVCQERRLWKLVGATSEFGIGCAEVNKPGRVYTRVTSFLD
WIHEQMERDLKT
```

Signal Peptide:

amino acids 1-20

Transmembrane domain:

amino acids 240-284

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FIGURE 65

CGGGCCAGCCTGGGGCGGCCGGCCAGGAACCCCGTTAAGGTGTCTTCTCTTTAGGGATGGT
GAGGTTGGAAAAAGACTCCTGTAACCCTCCTCCAGGATGAACCACCTGCCAGAAGACATGGAG
AACGCTCTCAACGGGAGCCAGAGCTCCCATGCTTCTCTGCGCAATATCCATTCCATCAACCCC
ACACAACCTCATGGCCAGGATTGAGTCCTATGAAGGAAGGGAAAAGAAAGGCATATCTGATGTC
AGGAGGACTTTCTGTTTGTGTCACCTTTGACCTCTTATTCGTAACATTACTGTGGATAATA
GAGTTAAATGTGAATGGAGGCATTGAGAACACATTAGAGAAGGAGGTGATGCAGTATGACTAC
TATTCTTCATATTTTGATATATTTCTTCTGGCAGTTTTTCGATTTAAAGTGTTAATACTTGCA
TATGCTGTGTGCAGACTGCGCCATTGGTGGGCAATAGCGTTGACAACGGCAGTGACCAGTGCC
TTTTTACTAGCAAAAGTGATCCTTTCGAAGCTTTTCTCTCAAGGGGCTTTTGGCTATGTGCTG
CCCATCATTTTCATTCATCCTTGCTGGATTGAGACGTGGTTCCTGGATTTCAAAGTGTTACCT
CAAGAAGCAGAAGAAGAAAACAGACTCCTGATAGTTCAGGATGCTTCAGAGAGGGGCAGCACTT
ATACCTGGTGGTCTTTCTGATGGTCAGTTTTATTCCCTCCTGAATCCGAAGCAGGATCTGAA
GAAGCTGAAGAAAAACAGGACAGTGAGAAACCACTTTTAGAACTATGAGTACTACTTTTGTTA
AATGTGAAAAACCCTCACAGAAAGTCATCGAGGCAAAAAGAGGCAGGCAGTGAGTCTCCCTG
TCGACAGTAAAGTTGAAATGGTGACGTCCACTGCTGGCTTTATTGAACAGCTAATAAAGATTT
ATTTATTGTAATACCTCACAAACGTTGTACCATATCCATGCACATTTAGTTGCCTGCCTGTGG
CTGGTAAGGTAATGTCATGATTCATCCTCTCTTCAGTGAGACTGAGCCTGATGTGTTAACAAA
TAGGTGAAGAAAGTCTTGTGCTGTATTCCCTAATCAAAAGACTTAATATATTGAAGTAACACTT
TTTTAGTAAGCAAGATACCTTTTTTATTTCAATTCACAGAATGGAATTTTTTTGTTCATGTCT
CAGATTTATTTGTATTTCTTTTTTAACACTCTACATTTCCCTTGTTTTTTAACTCATGCACA
TGTGCTCTTTGTACAGTTTTTAAAAAGTGTAATAAAATCTGACATGTCAATGTGGCTAGTTTTA
TTTTCTTGTTTTTGCATTATGTGTATGGCCTGAAGTGTTGGACTTGCAAAAGGGGAAGAAAGG
AATTGCGAATACATGTAAATGTCACCAGACATTTGTATTATTTTTATCATGAAATCATGTTT
TTCTCTGATTGTTCTGAAATGTTCTAAATACTCTTATTTTGAATGCACAAAATGACTTAAACC
ATTCATATCATGTTTCCTTTGCGTTCAGCCAATTTCAATTAAATGAACTAAATTAAAAA

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FIGURE 66

MNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESYEGREKKGISDVRRTFCLFVTFDL
LFVTLLWIIELNVNGGIENTLEKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAI
ALTTAVTSAFLLAKVILSKLFSQGAFGYVLPPIISFILAWIETWFLDFKVLQPQEAEEENRLLIV
QDASERAALIPGGLSDGQFYSPPESEAGSEEAEKQDSEKPLLEL

Important features of the protein:**Signal peptide:**

amino acids 1-20

Transmembrane domains:

amino acids 54-72, 100-118, 130-144, 146-166

N-myristoylation sites.

amino acids 14-20, 78-84, 79-85, 202-208, 217-223

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FIGURE 67

AATAAAGCTTCCTTAATGTTGTATATGTCTTTGAAGTACATCCGTGCATTTTTTTTTTAGCATC
CAACCATTCCTCCCTTGTAGTTCTCGCCCCCTCAAATCACCTCTCCCGTAGCCACCCGACT
AACATCTCAGTCTCTGAAAATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCTCAC
GGGGCTCAGTCTCTTTTTCTTTTGGTGCCACCAGGACGGAGCATGGAGGTCACAGTACCTGC
CACCTCAACGTCTCAATGGCTCTGACGCCCGCCTGCCCTGCACCTTCAACTCCTGCTACAC
AGTGAACCACAAACAGTTCTCCCTGAAGTGGACTTACCAGGAGTGCAACAAGTCTGAGGA
GATGTTCTCCAGTTCCGCATGAAGATCATTAACTGAAGCTGGAGCGGTTTTCAAGACCGCGT
GGAGTTCTCAGGGAACCCAGCAAGTACGATGTGTGCGGTGATGCTGAGAAAGTGCAGCCGGA
GGATGAGGGGATTTACAAGTCTACATCATGAACCCCCCTGACCGCCACCGTGGCCATGGCAA
GATCCATCTGCAGGTCTCATGGAAGAGCCCCCTGAGCGGGACTCCACGGTGGCCGTGATTGT
GGGTGCCCTCCGTGGGGGCTTCTTGCTGTGGTTCATCTTGGTGCTGATGGTGGTCAAGTGTGT
GAGGAGAAAAAAGAGCAGAAGCTGAGCACAGATGACCTGAAGACCGAGGAGGAGGGCAAGAC
GGACGGTGAAGGCAACCCGGATGATGGCGCCAAGTAGTGGGTGGCCGGCCCTGCAGCCTCCCG
TGTCCCGTCTCTCCCTCTCCGCCCTGTACAGTGACCTGCCTGCTCGCTCTTGGTGTGCTT
CCCGTGACCTAGGACCCAGGGCCACCTGGGGCCTCCTGAACCCCCGACTTCGTATCTCCCA
CCCTGCACCAAGAGTGACCCACTCTCTCCATCCGAGAACTGCCATGCTCTGGGACGTGTG
GGCCCTGGGGAGAGGAGAGAAAGGGCTCCACCTGCCAGTCCCTGGGGGAGGCAGGAGGCAC
ATGTGAGGGTCCCCAGAGAGAAGGGAGTGGGTGGGCAGGGGTAGAGGAGGGGCCGTGTCAAC
TGCCAGTGTCTGCCTGGCAGTGGCTTCAGAGAGGACCTGGTGGGGAGGGAGGGCTTTCTGT
GCTGACAGCGCTCCCTCAGGAGGGCCTTGGCCTGGCACGGCTGTGCTCCTCCCTGCTCCAG
CCCAGAGCAGCCATCAGGCTGGAGGTGACGATGAGTTCTTGAAGTGGAGGGGCATGTTAAA
GGGATGACTGTGCATTCCAGGGCACTGACGGAAAGCCAGGGCTGCAGGCAAAGCTGGACATGT
GCCCTGGCCCAGGAGGCCATGTTGGGCCCTCGTTTCCATTGCTAGTGGCCTCCTTGGGGCTCC
TGTTGGCTCCTAATCCCTTAGGACTGTGGATGAGGCCAGACTGGAAGAGCAGCTCCAGGTAGG
GGGCCATGTTTCCCAGCGGGGACCCACCAACAGAGGCCAGTTTCAAAGTCAGCTGAGGGGCTG
AGGGGTGGGGCTCCATGGTGAATGCAGGTGCTGCAGGCTCTGCCTTCTCCATGGGGTAACCA
CCCTCGCCTGGGCAGGGGCAGCCAAGGCTGGGAAATGAGGAGGCCATGCACAGGGTGGGGCAG
CTTCTTTGGGGCTTCAGTGAGAACTCTCCAGTTGCCCTTGGTGGGGTTTCCACCTGGCTTT
TGGCTACAGAGAGGGAAGGGAAAGCCTGAGGCCGGCATAAGGGGAGGCCTTGGAACTGAGCT
GCCAATGCCAGCCCTGTCCCATCTGCGGCCACGCTACTCGCTCCTCTCCCAACAACTCCCTTC
GTGGGGACAAAAGTGACAATTGTAGGCCAGGCACAGTGGCTCACGCCTGTAATCCCAGCACTT
TGGGAGGCCAAGGCGGGTGGATTACCTCCATCTGTTTAGTAGAAATGGGCAAAACCCCATCTC
TACTAAAAATACAAGAATTAGCTGGGCGTGGTGGCGTGTGCCTGTAATCCCAGCTATTTGGGA
GGCTGAGGCAGGAGAATCGCTTGAGCCCGGAAGCAGAGGTTGCAGTGAAGTGAATAGTAGTAT
AGTGCCACTGCAATTCAGCCTGGGTGACATAGAGAGACTCCATCTCAAAAAAA

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FIGURE 68

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45415

<subunit 1 of 1, 215 aa, 1 stop

<MW: 24326, pI: 6.32, NX(S/T): 4

MHRDAWLPRPAFSLTGLSLFFSLVPPGRSMEVTVPATLNVLNGSDARLPCTFNSCYTVNHKQF
SLNWTYQECNNCSEEMFLQFRMKIINLKLERFQDRVEFSGNPSKYDVSVMRLRVQPEDEGIYN
CYIMNPPDRHRGHGKIHLQVLMEEPPERDSTVAVIVGASVGGFLAVVILVLMVVKCVRRKKEQ
KLSTDDLKTEEEGKTDGEGNPDDGAK

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 161-179

Immunoglobulin-like fold:

amino acids 83-127

N-glycosylation sites.

amino acids 42-45, 66-69 and 74-77

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FIGURE 69

GGGCGCTGGTTCTGCGGCTACTGGCTGTACGGAGCAGGAGCAAGAGGTCGCCGCCAGCCTCCGCCGCCGAGCCTC
GTTTCGTGTCCCCGCCCTCGCTCCTGCAGCTACTGCTCAGAAACGCTGGGGCGCCACCCTGGCAGACTAACGAA
GCAGCTCCCTTCCCACCCCACTGCAGGTCTAATTTTGGACGCTTTGCCTGCCATTTCTTCCAGGTTGAGGGAGC
CGCAGAGGCGGAGGCTCGCGTATTCTGTCAGTCAGCACCCACGTCGCCCGCGGACGCTCGGTGCTCAGGCCCTTC
GCGAGCGGGGCTCTCCGTCTGCGGTCCCTTGTGAAGGCTCTGGGCGGCTGCAGAGGCCGCGCGTCCGGTTTGGCT
CACCTCTCCCAGGAACTTCACACTGGAGAGCCAAAAGGAGTGGAAGAGCCTGTCTTGGAGATTTTCTGGGGAA
ATCCTGAGGTCATTCAATTATGAAGTGTACCGCGCGGGAGTGGCTCAGAGTAACCACAGTGCTGTTTCATGGCTAGA
GCAATTCAGCCATGGTGGTCCCAATGCCACTTTATTGGAGAACTTTTGGAAAAATACATGGATGAGGATGGT
GAGTGGTGGATAGCCAAACAACGAGGGAAAAGGGCCATCACAGACAATGACATGCAGAGTATTTTGGACCTTCAT
AATAAATTACGAAGTCAGGTGTATCCAACAGCCTCTAATATGGAGTATATGACATGGGATGTAGAGCTGGAAAGA
TCTGCAGAATCCTGGGCTGAAAGTTGCTTGTGGGAACATGGACCTGCAAGCTTGCTTCCATCAATTGGACAGAAT
TTGGGAGCACACTGGGGAAGATATAGGCCCCGACGTTTTCATGTACAATCGTGGTATGATGAAGTGAAGACTTT
AGTACCCCATATGAACATGAATGCAACCCATATTGTCCATTCAAGGTGTTCTGGCCCTGTATGTACACATTATACA
CAGGTCGTGTGGGCAACTAGTAACAGAATCGGTTGTGCCATTAATTTGTGTCATAACATGAACATCTGGGGGCGAG
ATATGGCCCCAAGCTGTCTACCTGGTGTGCAATTACTCCCCAAGGGAACTGGTGGGGCCATGCCCCCTTACAAA
CATGGGCGGCCCTGTTCTGCTTGCCCCACTAGTTTTTGGAGGGGGCTGTAGAGAAAATCTGTGCTACAAAGAAGGG
TCAGACAGGTATTATCCCCCTCGAGAAGAGGAAACAAATGAAATAGAACGACAGCAGTCACAAGTCCATGACACC
CATGTCCGGACAAGATCAGATGATAGTAGCAGAAATGAAGTCATAAGCGCACAGCAAATGTCCAAATTTGTTTCT
TGTGAAGTAAGATTAAGAGATCAGTGCAAGGAACAACCTGCAATAGGTACGAATGTCCTGCTGGCTGTTTGGAT
AGTAAAGCTAAAGTTATTGGCAGTGTACATTATGAAATGCAATCCAGCATCTGTAGAGCTGCAATTCATTATGGT
ATAATAGACAATGATGGTGGCTGGGTAGATATCACTAGACAAGGAAGAAAGCATTATTTTCATCAAGTCCAATAGA
AATGGTATTCAAACAATTGGCAAATATCAGTCTGCTAATTCCTTCACAGTCTCTAAAGTAACAGTTCAGGCTGTG
ACTTGTGAACAACCTGTGGAACAGCTCTGTCCATTTTCATAAGCCTGCTTCACATTGCCCCAAGAGTATACGTCCCT
CGTAACTGTATGCAAGCAAATCCACATTATGCTCGTGTAAATGGAACTCGAGTTTATTCTGATCTGTCCAGTATC
TGCAGAGCAGCAGTACATGCTGGAGTGGTTCGAAATCACGGTGGTTATGTTGATGTAATGCCTGTGGACAAAAGA
AAGACCTACATTGCTTCTTTTTCAGAAATGGAATCTTCTCAGAAAGTTTACAGAATCCTCCAGGAGGAAAGGCATT
AGAGTGTGTTGCTGTTGTGTGAAGTGAATACTTGGAAAGAGGACCATAAAGACTATTCCAAATGCAATATTTCTGA
ATTTTGTATAAACTGTAACTTACTGTACAGAGTACATCACTATTTTCAGCCCCAAAAGGTGCCAAATGCATA
TAAATCTTGATAAACAAAGTCTATAAAATAAAACATGGGACATTAGCTTTGGGAAAAGTAATGAAAATATAATGG
TTTTAGAAATCCTGTGTTAAATATTGCTATATTTTCTAGCAGTTATTTCTACAGTTAATTACATAGTCATGATT
GTTCTACGTTTCATATATTATATGGTGCCTTGTATATGCCACTAATAAAATGAATCTAAACATTGAATGTGAATG
GCCCTCAGAAAATCATCTAGTGCATTTAAAAATAATCGACTCTAAACTGAAAGAAACCTTATCACATTTTCCCC
AGTTCAATGCTATGCCATTACCAACTCCAAATAATCTCAAATAATTTTCCACTTAATAACTGTAAAGTTTTTTTC
TGTTAATTTAGGCATATAGAATATTAAATCTGATATTGCACTTCTTATTTTATATAAAATAATCCTTTAATATC
CAAATGAATCTGTAAATGTTTGATTCTTGGGAATGGCCTTAAAAATAAATGTAATAAAGTCAGAGTGGTGGT
ATGAAAACATTCCTAGTGATCATGTAGTAAATGTAGGGTTAAGCATGGACAGCCAGAGCTTTCTATGTACTGTTA
AAATTGAGGTCACATATTTTCTTTTGTATCCTGGCAAATACTCCTGCAGGCCAGGAAGTATAATAGCAAAAAGTT
GAACAAAGATGAACAAATGTATTACATTACCATTGCCACTGATTTTTTTTAAATGGTAAATGACCTTGATATAA
ATATTGCCATATCATGGTACCTATAATGGTGATATATTTGTTTCTATGAAAAATGTATTGTGCTTTGATACTAAA
AATCTGTAAATGTAGTTTTGGTAATTTTTTTCTGCTGGTGGATTACATATTAAATTTTTTCTGCTGGTGGGA
TAAACATTAAATTAATCATGTTTCAAAAAAAAAAAAAA

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FIGURE 70

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45417

<subunit 1 of 1, 500 aa, 1 stop

<MW: 56888, pI: 8.53, NX(S/T): 2

MKCTAREWLRVTTVLFMARAI PAMVVPNATLLEKLLEKYMDEDGEWWIAKQRGKRAITDNDMQ
SILDLHNKLR SQVYPTASNMEYMTWDVELERSAESWAESCLWEHGPASLLPSIGQNLGAHWGR
YRPPTFHVQSWYDEVKDFSYPYEHECNPYCPFRCSGPVCTHYTQV VWATSNRIGCAINLCHNM
NIWGQIWP KAVYLV CNYS PKGNWWGHAPYKHGRPCSACPPSFGGGCRENL CYKEGSDRYYPFR
EETNEIERQQSQVHDTHVRTRSDSSRNEVIS AQQMSQIVSCEVRLRDQCKGTT CNRYECPA
GCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITRQGRKHYFIKSNRNGIQTIGKY
QSANSFTVSKVTVQAVTCETTVEQLCPFHKPA SHCPRVYCPRNCMQANPHYARVIGTRVYSDL
SSICRAAVHAGVVRNHGGYVDVMPVDKRKTYIASFQNGIFSESLQNPPGGKA FRVFAVV

Important features:**Signal peptide:**

amino acids 1-20

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 protein

amino acids 165-186, 196-218, 134-146, 96-108 and 58-77

N-glycosylation site

amino acids 28-31

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FIGURE 71

CAGCCCCGCGCGCCGGCCGAGTCGCTGAGCCGCGGCTGCCGGACGGGACGGGACCGGCTAGGC
TGGGCGCGCCCCCGGGCCCCGCGTGGGC**ATG**GGGCGCACTGGCCCCGGGCGCTGCTGCTGCCT
CTGCTGGCCCAGTGGCTCCTGCGCGCCGCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTGCCC
CTCCGGGTGGCCGCGGCCACGAACCGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCCTGCC
GAGCGCCACGCCGACGGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGGGCGCC
GCCAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGACTCTGGCCGCGGCTACTACCTGGAG
ATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAGTAACTTT
GCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGTCTAGCACA
TACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACGGGCTTCGTT
GGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAACATTGCCACT
ATTTTTGAATCAGAGAATTTCTTTTGCCTGGGATTAAATGGAATGGAATACTTGGCCTAGCT
TATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCCCTGGTGACACAA
GCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCCCGTTGCTGGATCT
GGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGTATAAAGGAGACATC
TGGTATAACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTGAAATTGGAAATTGGA
GGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGCCATCGTGGACAGTGGC
ACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGGAAAGCTGTGGCCCGCGCA
TCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAGCTGGCGTGCTGGACGAAT
TCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCTGAGAGACGAGAACTCCAGC
AGGTCATTCCGTATCACAATCCTGCCTCAGCTTTACATTTCAGCCCATGATGGGGGCCGGCCTG
AATTATGAATGTTACCGATTTCGGCATTTCCTCCATCCACAAATGCGCTGGTGATCGGTGCCACG
GTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAAGAGGGTGGGCTTCGCAGCGAGC
CCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTTCCGGGCCTTTCTCAACAGAGGAT
GTAGCCAGCAACTGTGTCCTCCGCTCAGTCTTTGAGCGAGCCCATTTTGTGGATTGTGTCTAT
GCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTTAATCGTCCTGCTGCTGCTGCCGTTT
CGGTGTCAGCGTCGCCCCGTGACCCTGAGGTCTCAATGATGAGTCCTCTCTGGTCAGACAT
CGCTGGAA**TGA**ATAGCCAGGCCTGACCTCAAGCAACCATGAACTCAGCTATTAAGAAAATCA
CATTTCCAGGGCAGCAGCCGGGATCGATGGTGGCGCTTCTCCTGTGCCACCCGTCTTCAAT
CTCTGTTCTGCTCCCAGATGCCTTCTAGATTCACTGTCTTTTGATTCTTGATTTTCAAGCTTT
CAAATCCTCCCTACTTCCAAGAAAAATAATTAAAAAAAACCTTCATTCTAA

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FIGURE 72

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45493
><subunit 1 of 1, 518 aa, 1 stop
><MW: 56180, pI: 5.08, NX(S/T): 2
MGALARALLLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGGPGTPAERHADGLALA
LEPALASPAGAAANFLAMVDNLQGDSSGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHSYI
DTYFDTERSSTYRSKGFDTVYKYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFESENFLLP
GIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGSLVLG
GIEPSLYKGGDIWYTPIKEEWYYQIEILKLEIGGQSLNLDREYNADKAIVDSTLLRLPQKV
FDAVVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISIIYLRDENSSRSFRITILPQ
LYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCAEIAGAAV
SEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCGAILLVLLVLLLLPFRQRRPRDPE
VVNDESSLVRHRWK
```

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 466-494

N-glycosylation sites.

amino acids 170-173 and 366-369

Leucine zipper pattern.

amino acids 10-31 and 197-118

Eukaryotic and viral aspartyl proteases

amino acids 109-118, 252-261 and 298-310

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FIGURE 73

GCCGCGGCGAGAGCGCGCCAGCCCCGCCGCGATGCCGCGCGCCAGGACGCCTCCTCCCGCTGCTGGCCCCGGC
CGGCGGCCCTGACTGCGCTGCTGCTGCTGCTGCTGGGCCATGGCGGCGCGGGCGCTGGGGCGCCCGGGCCAGG
AGGCGGCGGCGGCGGCGGCGGACGGGCCCCCGCGGCGAGACGGCGAGGACGGACAGGACCCGCACAGCAAGCACC
TGTACACGGCCGACATGTTACGCGACGGGATCCAGAGCGCCGCGCACTTCGT CATGTTCTTCGCGCCCTGGTGTG
GACACTGCCAGCGGCTGCAGCCGACTTGAATGACCTGGGAGACAAATACAACAGCATGGAAGATGCCAAAGTCT
ATGTGGCTAAAGTGGACTGCACGGCCCACTCCGACGTGTGCTCCGCCAGGGGGTGGGAGGATACCCACCTTAA
AGCTTTTCAAGCCAGGCCAAGAAGCTGTGAAGTACCAGGGTCCTCGGGACTTCCAGACACTGGAAAACTGGATGC
TGCAGACACTGAACGAGGAGCCAGTGACACCAGAGCCGGAAGTGGAAACCGCCAGTGCCCCGAGCTCAAGCAAG
GGCTGTATGAGCTCTCAGCAAGCAACTTTGAGCTGCACGTTGCACAAGGCGACCACTTTATCAAGTTCTTCGCTC
CGTGGTGTGGTCACTGCAAAGCCCTGGCTCCAACCTGGGAGCAGCTGGCTCTGGGCCTTGAACATTCGGAACTG
TCAAGATTGGCAAGGTTGATTGTACACAGCACTATGAACTCTGCTCCGGAACACAGGTTCTGGCTATCCCACTC
TTCTCTGGTTCCGAGATGGGAAAAAGGTGGATCAGTACAAGGGAAAGCGGGATTGGAGTCACTGAGGGAGTACG
TGGAGTCGCAGCTGCAGCGCACAGAGACTGGAGCGACGGAGACCGTCACGCCCTCAGAGGCCCGGTGCTGGCAG
CTGAGCCCCGAGGCTGACAAGGGCACTGTGTTGGCACTCACTGAAAAATAACTTCGATGACACCATTGCAGAAGGAA
TAACCTTCATCAAGTTTTATGCTCCATGGTGTGGTCACTGTAAGACTCTGGCTCCTACTTGGGAGGAACTCTCTA
AAAAGGAATTCCCTGGTCTGGCGGGGTCAAGATCGCCGAAGTAGACTGCACTGCTGAACGGAATATCTGCAGCA
AGTATTCGGTACGAGGCTACCCACGTTATTGCTTTCCGAGGAGGGAAGAAAGTCAGTGAGCACAGTGGAGGCA
GAGACCTTGACTCGTTACACCGCTTTGTCCTGAGCCAAGCGAAAGACGAACCTTAGGAACACAGTTGGAGGTCAC
CTCTCCTGCCAGCTCCCGCACCCCTGCGTTTAGGAGTTCAGTCCACAGAGGCCACTGGGTTCCAGTGGTGGCT
GTTCAGAAAAGCAGAACAATACTAAGCGTGAGGTATCTTCTTGTGTGTGTGTTTTCCAAGCCAACACACTCTACAG
ATTCTTTATTAAGTTAAGTTTCTCTAAGTAAATGTGTAACATCATGGTCACTGTGTAACATTTTCAGTGGCGATA
TATCCCTTTGACCTTCTCTTGATGAAATTTACATGGTTTTCTTTGAGACTAAAATAGCGTTGAGGGAATGAAA
TTGCTGGACTATTTGTGGCTCCTGAGTTGAGTGATTTTGGTGAAAGAAAGCACATCCAAAGCATAGTTTACCTGC
CCACGAGTTCGGAAGGTGGCCTTGTGGCAGTATTGACGTTCTCTGATCTTAAGGTCACAGTTGACTCAATAC
TGTGTTGGTCCGTAGCATGGAGCAGATTGAAATGCAAAAACCCACACCTCTGGAAGATACCTTCACGGCCGCTGC
TGGAGCTTCTGTTGCTGTGAATACTTCTCTCAGTGTGAGAGGTTAGCCGTGATGAAAGCAGCGTTACTTCTGACC
GTGCCTGAGTAAGAGAATGCTGATGCCATAACTTTATGTGTGATACCTTGTCAAATCAGTTACTGTTTCAGGGGAT
CCTTCTGTTTCTCACGGGTGAAACATGTCTTTAGTTTCTCATGTTAACACGAAGCCAGAGCCACATGAACTGT
TGGATGTCTTCTTAGAAAGGGTAGGCATGGAAAATTCCACGAGGCTCATTCTCAGTATCTCATTAACTCATTTGA
AAGATTCCAGTTGTATTTGTACCTGGGGTGACAAGACCAGACAGGCTTTCCAGGCCTGGGTATCCAGGGAGGC
TCTGCAGCCCTGCTGAAGGGCCCTAACTAGAGTTCAGAGTTTCTGATTCTGTTTCTCAGTAGTCTTTTAGAGG
CTTGCTATACTTGGTCTGCTTCAAGGAGGTCGACCTTCTAATGTATGAAGAATGGGATGCATTTGATCTCAAGAC
CAAAGACAGATGTGAGTGGGCTGCTCTGGCCCTGGTGTGCACGGCTGTGGCAGCTGTTGATGCCAGTGTCTCTA
ACTCATGCTGTCTTGTGATTAAACACCTCTATCTCCCTTGGGAATAAGCACATACAGGCTTAAGCTCTAAGATA
GATAGGTGTTTGTCTTTTACCATCGAGCTACTTCCATAATAACCACTTTGCATCCAACACTCTTACCCACCT
CCCATACGCAAGGGGATGTGGATACTTGGCCCAAAGTAACTGGTGGTAGGAATCTTAGAAACAAGACCACTTATA
CTGTCTGTCTGAGGCAGAAGATAACAGCAGCATCTCGACCAGCCTCTGCCTTAAAGGAAATCTTTATTAATCAG
TATGGTTACAGATAATTCTTTTTTTAAAAAAACCCCAACCTCCTAGAGAAGCACAACTGTCAAGAGTCTTGTACA
CACAACCTCAGCTTTGCATCAGAGTCTTGTATTCCAAGAAAATCAAAGTGGTACAATTTGTTTGTTTACACTAT
GATACTTTCTAAATAAACTCTTTTTTTTTAA

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FIGURE 74

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46776
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47629, pI: 5.90, NX(S/T): 0
MPARPGRLLPLLARPAALTALLLLLGHGGGRWGARAQEAADGPPAADGEDGQDPHSK
HLYTADMFTHGIQSAAHFVMFFAPWCGHCQRLQPTWNDLGDKYNSMEDAKVYVAKVDCTAHS
VCSAQGVRGYP TLKLFKPGQEAVKYQGPRDFQTLNWM LQTLNEEPVTPEPEVEPPSAPELKQ
GLYEL SASNFELHVAQGDHFIKFFAPWCGHCKALAPTWEQLALGLEHSETVKIGKVDCTQH YE
LCSGNQVRGYPTLLWFRDGKKVDQYKGKRDLESLREYVESQLQRTETGATETVTPSEAPVLAA
EPEADKGTVLALTENNFDDTIAEGITFIKFYAPWCGHCKTLAPTWEELSKKEFPGLAGVKIAE
VDCTAERNICSKYSVRGYPTLLLFRGGKKVSEHSGGRDLDSLHRFVLSQAKDEL
```

Signal sequence:
amino acids 1-32

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FIGURE 75A

CGGACGCGTGGGCGGACGCGTGGGCAAAAGAACTCGGAGTGCCAAAGCTAAATAAGTTAGCTGAGAAAACGCACG
CAGTTTGCAGCGCTTGGCCGGGTGCGCCAACTACGCAAAGACCAAGCGGGCTCCGCGCGGACCGGCCGCGGGC
TAGGGACCCGGCTTTGGCCTTCAGGCTCCCTAGCAGCGGGGAAAAGGAATTGCTGCCCGGAGTTTCTGCGGAGGT
GGAGGGAGATCAGGAAACGGCTTCTTCTCACTTCGCGCGCTGGTGAGTGTGCGGGAGATTGGCAAACGCCTAGG
AAAGGACTGGGGAAAATAGCCCTGGGAAAGTGGAGAAGTGATCAGGAGGCCGGTCCACTACGGCAGTTTATCTG
TCTGATCAGAGCCAGACGCGACGCGTCCACTTCGCAAGTTCTTCCAGGTGTGGGGACCGCAGGACAGACGGCCGA
TCCCGCGCCCTCCGTACCAGCACTCCCAGGAGAGTCAGCCTCGCTCCCCAACGTGAGGGCGCTCTGGCCACGA
AAAGTTCTGTCCACTGTGATTCTCAATTCCTTGCTTGGTTTTTTCTCCAGAGAACTTTTGGGTGGAGATATTA
ACTTTTTTCTTTTTTTTTTCTTGGTGGAAGCTGCTCTAGGGAGGGGGAGGAGGAGGAGAAAGTGAAATGTGC
TGGAGAAGAGCGAGCCCTCCTTGTCTTCCGGAGTCCCATTCCATTAAGCCATCACTTCTGGAAGATTAAAGTTGT
CGGACATGGTGACAGCTGAGAGGAGAGGAGGATTTCTTGCCAGGTGGAGAGTCTTACCGTCTGTTGGGTGCATG
TGTGCGCCCGCAGCGGCGCGGGCGCGTGGTTCTCCGCGTGAGTCTCACCTGGGACCTGAGTGAATGGCTCCCA
GGGGCTGTCGCGGGGCATCCGCTCCGCTTCTCCACAGGCCTGTGTCTGTCTGGAAGATGCTAGCAATGGGGG
CGCTGGCAGGATTCGGATCCTCTGCCTCCTCACTTATGGTTACCTGTCTGCGGGCCAGGCCTTAGAAGAGGAGG
AAGAAGGGGCCCTTACTAGCTCAAGCTGGAGAGAACTAGAGCCAGCACAACCTCCACCTCCAGCCCCATCTCA
TTTTCATCTAGCGGATGATCAGGGATTTAGAGATGTGGGTACCACGGATCTGAGATTAACACCTACTCTTG
ACAAGCTCGCTGCCGAAGGAGTTAAACTGGAGAATACTATGTCCAGCCTATTTGCACACCATCCAGGAGTCAGT
TTATTACTGGAAAGTATCAGATACACACCGGACTTCAACATCTATCATAAGACCTACCAACCCAACTGTTTAC
CTCTGGACAATGCCACCCTACCTCAGAACTGAAGGAGGTTGGATATTCAACGCATATGGTCGGAAAATGGCACT
TGGGTTTTTAACAGAAAAGATGCATGCCACCAGAAGAGGATTTGATACCTTTTTTGGTTCCCTTTTGGGAAGTG
GGGATTACTATACACACTACAAATGTGACAGTCTGGGATGTGTGGCTATGACTTGTATGAAACGACAATGCTG
CCTGGGACTATGACAATGGCATATACTCCACACAGATGTACACTCAGAGAGTACAGCAAATCTTAGCTTCCATA
ACCCACAAAGCCTATATTTTTATATACTGCCTATCAAGCTGTTTCATTCACCACTGCAAGCTCCTGGCAGGTATT
TCGAACACTACCGATCCATTATCAACATAAACAGGAGAAGATATGCTGCCATGCTTCTGCTTAGTGAACAA
TCAACACAGTGAACATTGGCTCTAAAGACTTATGGTTTCTATAACAACAGCATTATCATTTACTCTTCAGATAATG
GTGGCCAGCCTACGGCAGGAGGGAGTAAGTGGCTCTCAGAGGTAGCAAAGGAACATATTGGGAAGGAGGGATCC
GGGCTGTAGGCTTTGTGCATAGCCCACTTCTGAAAAACAAGGGAACAGTGTGTAAGGAACCTGTGCACATCACTG
ACTGGTACCCCACTCTCATTTCACTGGCTGAAGGACAGATTGATGAGGACATTCAACTAGATGGCTATGATATCT
GGGAGACCATAAGTGAGGGTCTTCGCTCACCCGAGTAGATATTTGCATAACATTGACCCCTATACACCAAGGC
AAAAATGGCTCCTGGGCAGCAGGCTATGGGATCTGGAACACTGCAATCCAGTCAGGCATCAGAGTCAGCACTG
GAAATTGCTTACAGGAAATCCTGGCTACAGCGACTGGGTCCCCCTCAGTCTTTAGCAACCTGGGACCGAACC
GTGGCACAATGAACGGATCACCTTGTCAACTGGCAAAAGTGTATGGCTTTCAACATCACAGCCGACCCATATGA
GAGGGTGACCTATCTAACAGGTATCCAGGAATCGTGAAGAAGCTCTACGAGGCTCTCACAGTTCAACAAAC
TGCAGTGCCGTCAGGTATCCCCCAAAGACCCAGAAAGTAACCTAGGCTCAATGGAGGGGTCTGGGGACCATG
GTATAAAGAGGAAACCAAGAAAAAGCAAGCAAAATCAGGCTGAGAAAAAGCAAAAGAAAAAGCAAAAAA
GAAGAAGAAACAGCAGAAAGCAGTCTCAGGTAAACCGCAAAATTTGGCTCGATAATATCGCTGGCCTAAGCGTCA
GGCTTGTTTTTCATGCTGTGCCACTCCAGAGACTTCTGCCACCTGGCGCCACACTGAAACCTGCTCTGCTCAGT
CCAAGGTGCTACTCTTGTCAAGCCACACTTAGAGAGAGTGGAGATGTTTATTTCTCTCGCTCCTTTAGAAAACGTG
GTGAGTCTGAGTCCACTGCTGTGCTTCAGTCAACTGACCAACACTGCTTTGAATTATAGGAGGAGAACATA
ACCTACCATCCGCAAGCATGCTAATTTGATGGAAGTTACAGGGTAGCATGATTAACCTACCTTTGATAAATTAC
AGTCAAAGATTGTGTACCTCAAAGGCCTTGAAGAATATATTTCTTGGTGAATTTTTGTATGTCTGTATATGA
CACTTGGGTTTTTTAATTAATCTATTTTATATATAAATATATGTTTCTTTTCTGTGAAAGCTGTTTTCT
CACATGTGAACAGCTTGACCTCATTTTACCATGCGGTGAGGGAATGGCAAATAAGAATGTTTGAGCACACTGCCC
ACAATGAATGTAACATTTTTCTAAACACTTTACTAGAAGAACATTTAGTATAAAAAACCTAATTTATTTTACA
GAAAAATATTTTGTGTTTTTATAAAAAGTTATGCAATGACTTTTATTTTTATTTCTGCATACCATTAGAAGA
ATTTTATTTTCAATTTCTCAAATATCAAGCACTGTAATACTATAAATTAATGTAATACTGTGTGAATTCAGACTA
TAAAAACATCATTAGAAAACCTTATAATCGTCATTGTTCAATCAAGATTTTGAATGTAATAAGATGAATATAT
ATTACTTGGAAATTCATGTTTGTGCAAGTGTGAGACAACCTTTATGTTTCTATCATAAACTATTTATGTATCTT
AATTATTAATGATTACTTTATGGCACTAGAAAATTTACTGTGGCTTTTCTGATCTAAGTTCTAGCTTAAAT
GTATCATTTGCTCTAAAAAATAAAAAATCTTTACTAATAGGCAATGGAAGGAATGGTTTGTCTAACACCCACAGTAA
TATAATATGATTTTACAGATAGATGCTTCCCTTGGCTATGACATGGAGAAAGATTTTCCCATATAATAAATACTAA
TATTTATATTAGGTTGGTGCAAACTAGTTGCGGTTTTTCCCATTAAGTAATAACCTTACTCTATACAAAGT
GGACACTGTGGGGAGATACAGAGAAATGGAAGATACGGATCCTGCCTGGAGTAGGTAACCTTGCTTGGAAACCC
ACATGCAACGTGATGAGGAGAAATTAAGGAGTATTATCAGTAATGAAGTTTATCATGGGTGATCAATGAGCATA
GATTGGTGTGGATCCTGTAGACCCTGGTGTCTTTGAAGTGCCCTCTCCTAATGCAGAGGCCTTGAAGCTTAC

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FIGURE 75B

[illegible]

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FIGURE 76

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48296
><subunit 1 of 1, 515 aa, 1 stop
><MW: 56885, pI: 6.49, NX(S/T): 5
MAPRGCAGHPPPPSPQACVCPGKMLAMGALAGFWILCLLTGYLSWGQALEEEEEEGALLAQAGEKLEPSTTSTSQ
PHLIFILADDQGFRDVGYPHGSEIKTPTLDKLAAGVVKLENYYVQPICTPSRSQFITGKYQIHTGLQHSIIRPTQP
NCLPLDNATLPQKLKEVGYSTHMGKWHLGFNKECMPTRRGFDTFFGSLLGSGDYTHYKCDSPGMCQGYDLYEN
DNAAWDYDNGIYSTQMYTORVQQILASHNPTKPIFLYTAYQAVHSPLQAPGRYFEHYRSIININRRRYAAMLSC
DEAINNVTLALKTYGFYNNSSIIYSSDNGGQPTAGGSNWPLRGSKGTYWEGGIRAVGFVHSPLLKNKGTVCHEL
HITDWYPTLISLAEGQIDEDIQLDGYDIWETISEGLRSPRVDILHNIDPYTPRQKMAPGQQAMGSGTLQSSQPSE
CSTGNCLQEILATATGSPLSLSATWDRTGGTMNGSPCQLAKVYGFSTSQPTHMRGWTYLTGIQES
```

Important Features:**Signal Peptide:**

amino acids 1-37

Sulfatases signature 1.

amino acids 120-132

Sulfatases signature 2.

amino acids 168-177

Tyrosine kinase phosphorylation site.

amino acids 163-169

N-glycosylation sites.

amino acids 157-160, 306-309 and 318-321

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FIGURE 77

AAAAAAGCTCACTAAAGTTTCTATTAGAGCGAATACGGTAGATTTCATCCCCTTTTGAAGAACAGTACTGTGGA
GCTATTTAAGAGATAAAAACGAAATATCCTTTCTGGGAGTTCAAGATTGTGCAGTAATTGGTTAGGACTCTGAGC
GCCGCTGTTACCAATCGGGGAGAGAAAAGCGGAGATCCTGCTCGCCTTGCACGCGCCTGAAGCACAAAGCAGAT
AGCTAGGAATGAACCATCCCTGGGAGTATGTGGAACAACGGAGGAGCTCTGACTTCCCAACTGTCCCATTCTAT
GGGCGAAGGAACTGCTCCTGACTTCAGTGGTTAAGGGCAGAATTGAAAATAATTCTGGAGGAAGATAAGAAATGAT
TCCTGCGCGACTGCACCGGGACTACAAAGGGCTTGTCTGCTGGGAATCCTCCTGGGGACTCTGTGGGAGACCGG
ATGCACCCAGATACGCTATTAGTTCGGGAAGAGCTGGAGAAAGGCTCTAGGCTGGGCGACATCTCCAGGGACCT
GGGGCTGGAGCCCCGGGAGCTCGCGGAGCGCGGAGTCCGCATCATCCCCAGAGGTAGGACGCAGCTTTTCGCCCT
GAATCCGCGCAGCGGCAGCTTGGTCACGGCGGGCAGGATAGACCGGGAGGAGCTCTGTATGGGGGCCATCAAGTG
TCAATTAATCTAGACATTCTGATGGAGGATAAAGTGAAAATATATGGAGTAGAAGTAGAAGTAAGGGACATTAA
CGACAATGCGCCTTACTTTTCGTGAAAGTGAATTAGAAAATAAAAATTAGTGAAAATGCAGCCACTGAGATGCGGTT
CCCTCTACCCACCGCCTGGGATCCGGATATCGGGAAGAACTCTCTGCAGAGCTACGAGCTCAGCCCGAACACTCA
CTTCTCCCTCATCGTGCAAAATGGAGCCGACGGTAGTAAGTACCCGAATTGGTGCTGAAACGCGCCCTGGACCG
CGAAGAAAAGGCTGCTCACCACCTGGTCCTTACGGCCTCCGACGGGGCGGACCCGGTGCGCACAGGCACCGCGCG
CATCCGCGTGATGGTTCTGGATGCGAACGACAACGCACCCAGCGTTTGTCTAGCCCCGAGTACCGCGCGAGCGTTCC
GGAGAATCTGGCCTTGGGCACGCAGCTGCTTGTAGTCAACGCTACCGACCTGACGAAGGAGTCAATGCGGAAGT
GAGGTATTCTTCCGGTATGTGGACGACAAGGCGGCCCAAGTTTTCAAAGTATGTAATTGAGGACAAATATC
AACAATAGGGGAGTTGGACCACGAGGAGTCAAGATTCTACCAGATGGAAGTGCAAGCAATGGATAATGCAGGATA
TTCTGCGCGAGCCAAAGTCTGATCACTGTTCTGGACGTGAACGACAATGCCCCAGAAGTGGTCTCACCTCTCT
CGCCAGCTCGGTTCCCGAAAACCTCTCCAGAGGGACATTAATTGCCCTTTTAAATGTAAATGACCAAGATTCTGA
GGAAAACGGACAGGTGATCTGTTTCATCCAAGGAAATCTGCCCTTTAAATTAGAAAAATCTTACGGAAATTACTA
TAGTTTAGTACAGACATAGTCTTGGATAGGGAACAGGTTCTTAGCTACAACATCACAGTGACCGCCACTGACCG
GGGAACCCCGCCCTTATCCACGGAACCTCATATCTCGCTGAACGTGGCAGACACCAACGACAACCCCGCGTCTT
CCCTCAGGCCTCCTATTCGGCTTATATCCAGAGAACAATCCAGAGGAGTTTCCCTCGTCTCTGTGACCGCCCA
CGACCCCGACTGTGAAGAGAACGCCCAGATCACTTATTCCTGGCTGAGAACACCATCCAAGGGGCAAGCCTATC
GTCTACGTGTCCATCAACTCCGACACTGGGGTACTGTATGCGCTGAGCTCCTTCGACTACGAGCAGTTCGAGGA
CTTGCAAGTGAAAGTGATGGCGCGGGACAACGGGCACCCGCCCTCAGCAGCAACGTGTCTGTTGAGCCTGTTCTGT
GCTGGACCAAGACAAATGCGCCGAGATCCTGTACCCCGCCCTCCCAACGGACGGTTCCACTGGCGTGGAGCT
GGTCCCCGCTCCGACAGAGCCCGGTACCTGGTGACCAAGGTGGTGGCGGTGGACAGAGACTCCGCGCCAGAACGC
CTGGCTGTCTACCGTCTGCTCAAGGCCAGCGAGCCGGGACTCTTCTCGGTGGGTCTGCACACGGGCGAGGTGCG
CACGGCGCGAGCCCTGCTGGACAGAGACGCGCTCAAGCAGAGCCTCGTAGTGGCCGTCCAGGACCACGGCCAGCC
CCCTCTCTCCGCCACTGTACGCTCACCCTGGCCGTGGCCGACAGCATCCCCAAGTCTGGCGGACCTCGGCAG
CCTCGAGTCTCCAGCTAACTCTGAAACCTCAGACCTCACTCTGTACCTGGTGGTAGCGGTGGCCGCGGTCTCCTG
CGTCTTCTGGCCTTCGTCATCTTGTGCTGGCGCTCAGGCTGCGGCGCTGGCACAAAGTACGCCCTGCTGCAGGC
TTCAGGAGGCGGCTTGACAGGAGCGCCGGCGTCGCACCTTGTGGCGGTGGACGGGGTGCAGGCTTTCCTGCAGAC
CTATTCCCACGAGGTTTCCCTCACCACGGACTCGCGGAAGAGTCACTGATCTTCCCCAGCCCACTATGCAGA
CATGCTCGTCAGCCAGGAGAGCTTTGAAAAAAGCGAGCCCCCTTTGCTGTCAGGTGATTGCGTATTTTCTAAAGA
CAGTCATGGGTTAATTGAGGTGAGTTTATATCAAATCTTCTTTTCTTTTAAATTGCTCTGTCTCCCAAGC
TGGAGTGACGCGGTACGATCATAGCTCACTGCGGCCTCAAACCTCCTAGGCTCAAGCAATTATCCCACCTTTGCT
CCGGTGTAAACAGGGACTACAGGTGCAAGCCACCTACTGTCTGCCTATCTATCTATCTATCTATCTATCTAT
CTATCTATCTATCTATCTATTACTTTCTTGTACAGACGGGAGTCTCACGCCTGTAATCCCAAGTACTTTGGGAGGC
CGAGGCGGGTGGATCACCTGAGGTTGGGAGTTTGAGACCAGCTGACCAACATGGAGAAACCCGCTCTATACTAA
AAAAATACAAAATTAGCCGGGCGTGGTGGTGCATGTCTGTAATCCCAGCTACTTGGGAGGCTGAGTCAGGAGAAT
TGCTTTAACCTGGGAGGTGGAGGTGCAATGAGCTGAGATTGTGCCATTGCACTCCAGCCTGGGCAACAAGAGTG
AAACTCTATCTCA

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FIGURE 78

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48306
><subunit 1 of 1, 916 aa, 1 stop
><MW: 100204, pI: 4.92, NX(S/T): 4
MIPARLHRDYKGLVLLGILLGTLWETGCTQIRYSVPEELEKGSRVGDISRDIGLEPRELAERGVRIIPRGRTQLF
ALNPRSGSLVTAGRIDREELCMGAIKCQLNLDILMEDKVKIYGVEVEVRDINDNAPYFRESELEIKISENAATEM
RFPLPHAWDPDIGKNSLQSYELSPNTHFSLIVQNGADGSKYPELVLKRALDREEKAAHHLVLTASDGGDPVRTGT
ARIRVMVLDANDNAPAFAPQPEYRASVPENLALGTQLLVVNATDPDEGVNAEVRYSFYVDDKAAQVFKLDCNSGT
ISTIGELDHEESGFYQMEVQAMDNAGYSARAKVLITVLDVNDNAPEVVLTSLASSVPENSPRGTLIALNVNDQD
SEENGQVICFIQGNLPFKLEKSYGNYYSLVTDIVLDREQVPSYNITVTATDRGTPPLSTETHISLNVADTNDNPP
VFPQASYSAYIPENNPRGVSLVSVTAHDPDCEENAQITYSLAENTIQGASLSSYVSINSDTGVLYALSSFDYEQF
RDLQVKVMARDNGHPPLSSNVSLSLFVLDQNDNAPEILYPALPTDGSTGVELAPRSAEPGYLVTKVAVDRDSGQ
NAWLSYRLLKASEPGLFSVGLHTGEVRTARALLDRDALKQSLVVAVQDHGQPPLSATVTTLTVAVADSIPQVLADL
GSLESPANSETSDLTLYLVVAVAAVSCVFLAFVILLALLRLRRWHKSRLLQASGGGLTGAPASHFVGVDGVQAFI
QTYSHEVSLTTDSRKSHLIFPQPNYADMLVSQESFEKSEPLLLSGDSVFSKDSHGLIEVSLYQIFFLFFFNCSVS
QAGVQRYDHSSLRPQTPRLKQLSHLCLRCNRDYRCKPPTVCLSIYLSIYLSIYLSIYLLLSCTDGS LTPVIPVLW
EAEAGGSPEVGS LRPA
```

Signal sequence:

amino acids 1-30

Transmembrane domains:

amino acids 693-711, 809-823, 869-888

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FIGURE 79

AGCCGCTGCCCCGGGCGGGCGCCCGCGGCGGCACCAATGAGTCCCCGCTCGTGCCCTGCGTTGCTGCGCCTCCTC
GTCTTCGCCGCTCTTCTCAGCCGCCGCGAGCAACTGGCTGTACCTGGCCAAGCTGTCTGTCGGTGGGGAGCATCTCA
GAGGAGGAGACGTGCGAGAACTCAAGGGCCTGATCCAGAGGCAGGTGCAGATGTGCAAGCGGAACCTGGGAAGTC
ATGGACTCGGTGCGCCGCGGTGCCAGCTGGCCATTGAGGAGTGCCAGTACCAGTTCCGGAACCGGCGCTGGAAC
TGCTCCACACTCGACTCCTTGCCCGTCTTCGGCAAGGTGGTGACGCAAGGGACTCGGGAGGCGGCCTTCGTGTAC
GCCATCTCTTCGGCAGGTGTGGCCTTTGCAGTGACGCGGGCGTGCAGCAGTGGGGAGCTGGAGAAGTGCGGCTGT
GACAGGACAGTGTCATGGGGTCAGCCACAGGGCTTCCAGTGGTCAGGATGCTCTGACAACATCGCCTACGGTGTG
GCCTTCTCACAGTCGTTTGTGGATGTGCGGGAGAGAAGCAAGGGGGCCTCGTCCAGCAGAGCCCTCATGAACCTC
CACAACAATGAGGCCGGCAGGAAGGCCATCCTGACACACATGCGGGTGGAATGCAAGTGCCACGGGGTGTGAGGC
TCCTGTGAGGTAAAGACGTGCTGGCGAGCCGTGCCGCCCTTCCGCCAGGTGGGTACGCACTGAAGGAGAAGTTT
GATGGTGCCACTGAGGTGGAGCCACGCCGCGTGGGCTCCTCCAGGGCACTGGTACCACGCAACGCACAGTTCAAG
CCGCACACAGATGAGGACCTGGTGTACTTGAGCCTAGCCCCGACTTCTGTGAGCAGGACATGCGCAGCGGCGTG
CTGGGCACGAGGGGCCGCACATGCAACAAGACGTCCAAGGCCATCGACGGCTGTGAGCTGCTGTGCTGTGGCCGC
GGCTTCCACACGGCGCAGGTGGAGCTGGCTGAACGCTGCAGCTGCAAATCCACTGGTGTGCTTCGTCAAGTGC
CGGCAGTGCCAGCGGCTCGTGGAGTTGCACACGTGCCGATGACCGCCCTGCCCTAGCCCTGCGCCGGCAACCACCTA
GTGGCCCAGGGAAGGCCGATAATTTAAACAGTCTCCACCACCTACCCCAAGAGATACTGGTTGTATTTTTTGT
CTGGTTTGGTTTTTTGGTTCCTCATGTTATTTATTGCCGAAACCAGGCAGGCAACCCCAAGGGCACCAACCAGGGC
CTCCCCAAAGCCTGGGCCTTTGTGGCTGCCACTGACCAAGGGACCTTGCTCGTGCCGCTGGCTGCCCGCATGTG
GCTGCCACTGACCACTCAGTTGTTATCTGTGTCCGTTTTTCTACTTGCAGACCTAAGGTGGAGTAACAAGGAGTA
TTACCACCACATGGCTACTGACCGTGTCTCGGGGAAGAGGGGGCCTTATGGCAGGGAAAAATAGGTACCGACTTG
ATGGAAGTCACACCCTCTGGAAAAAGAACTCTTAACTCTCCAGCACACATACACATGGACTCCTGGCAGCTTGA
GCCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAGGGAACAAGCAGATACCAGGTCAAGGGCACCAAGGTTTCAAT
TCAGCCCTTACATGGACAGCTAGAGGTTGATATCTGTGGGTCTTCCAGGCAAGAAGAGGGAGATGAGAGCAAG
AGACGACTGAAGTCCCACCCTAGAACCCAGCCTGCCCCAGCCTGCCCCTGGGAAGAGGAACTTAACCACTCCCC
AGACCCACCTAGGCAGGCATATAGGCTGCCATCCTGGACCAGGGATCCCGGCTGTGCCTTTGCAGTCATGCCCGA
GTACCTTTTACAGCGCTGTTCTCCATGAACTGAAAAACACACACACACACACACACACACACACACACACAC
ACACACACACGGACACACACACACACCTGCGAGAGAGAGGGAGGAAAGGGCTGTGCCTTTGCAGTCATGCCCGAG
TCACCTTTTACAGCACTGTTCTCTC

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FIGURE 80

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48328
<subunit 1 of 1, 351 aa, 1 stop
<MW: 39052, pI: 8.97, NX(S/T): 2
MSPRSCLRSLRLLVFAVFSAAAASNWLYLAKLSSVGSISEEETCEKLKGLIQRQVQMCKRNLEVMDSVRRGAQLAI
EECQYQFRNRRWNCSTLDSLVPVFGKVVTQGTREAAFVYAISSAGVAFVTRACSSGELEKCGCDRTVHGVSPQGF
QWSGCSNDIAYGVAFSQSFVDVRERSKGASSSRALMNLHNNEAGRKAILLTHMRVECKCHGVSGSCEVKTWCRAVP
PFRQVGHALKEKFDGATEVEPRRVGSSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGRTCNKTS
KAIDGCELLCCGRGFHTAQVELAERCSCKEFWCCFVKCRQCQRLVELHTCR

Important features:**Signal peptide:**

amino acids 1-22

N-glycosylation sites.

amino acids 88-91 and 297-300

Wnt-1 family signature.

amino acids 206-215

Homologous region to Wnt-1 family proteins

amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

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FIGURE 81

CCGAGCCGGGCGCGCAGCGACGGAGCTGGGGCCGGCCTGGGACCATGGGCGTGAGTGCAATCTACGGATCAGTCT
CTGATGGTGGGTGCTTAACCTCAGTGGGGACTCCAAGATTTCCATGAAGAAAATCAGTTGTCTTCATTCAAGAAT
TGGGGTCTGGCTCAGAATTCCTGCAGCTGGTGAAGAAATCTGTTTTCTAGAAGAGGTTTAATTAATGCCTGCAGTCT
GACATGTTCCCGATTTGAGGTGAAACCATGAAGAGAAAATAGAATACTTAATAATGCTTTTCCGCAACCGCTTCT
TGCTGCTGCTGGCCCTGGCTGCGCTGCTGGCCTTTGTGAGCCTCAGCCTGCAGTTCTTCCACCTGATCCCGGTGT
CGACTCCTAAGAATGGAATGAGTAGCAAGAGTCGAAAGAGAATCATGCCCGACCCTGTGACGGAGCCCCCTGTGA
CAGACCCCGTTTATGAAGCTCTTTTGTACTGCAACATCCCCAGTGTGGCCGAGCGCAGCATGGAAGGTGATGCCC
CGCATCATTTTAAGCTGGTCTCAGTGCATGTGTTCAATCGCCACGGAGACAGGTACCCACTGTATGTCATTCCCA
AAACAAAGCGACAGAAATTGACTGCACTCTGGTGGCTAACAGGAAACCGTATCACCCAAAACCTGGAAGCTTTCA
TTAGTCACATGTCAAAAGGATCCGGAGCCTCTTTCGAAAGCCCCCTTGAACCTCCTTGCCCTCTTTACCCAAATCACC
CATGTGTGAGATGGGAGAGCTCACACAGACAGGAGTTGTGCAGCATTTGCAGAACGGTCAGCTGCTGAGGGATA
TCTATCTAAAGAAACACAACTCCTGCCAATGATTGGTCTGCAGACCAGCTCTATTTAGAGACCACTGGGAAAA
GCCGGACCTACAAAGTGGGCTGGCCTTGCTTTATGGCTTTCTCCCAGATTTTGAAGTGAAGAAGATTTATTTCA
GGCACCAGCCAAGTGGCTGTTCTGCTCTGGAAGCTGCTATTGCCCGGTAAGAAACAGTATCTGGAAAAGGAGC
AGCGTCGTGAGTACCTCCTACGTTTGAAGAACAGCCAGCTGGAGAAGACCTACGGGGAGATGGCCAAGATCGTGG
ATGTCCCCACCAAGCAGCTTAGAGCTGCCAACCCCATAGACTCCATGCTCTGCCACTTCTGCCACAATGTGAGCT
TTCCCTGTACACAGAAATGGCTGTGTTGACATGGAGCACTCAAGGTAATTAAGACCCATCAGATCGAGGATGAAA
GGGAAAGACGGGAGAAGAAATTGACTTCCGGTATTCTCTCCTGGGTGCCACCCCATCCTGAACCAACCATCG
GCCGGATGCAGCGTGCCACCGAGGGCAGGAAAGAAGAGCTCTTGGCCCTCTACTCTGCTCATGATGTCACTCTGT
CACCAGTTCTCAGTGCCTTGGGCCTTTCAGAAGCCAGGTTCCCAAGGTTTGCAGCCAGGTTGATCTTTGAGCTTT
GGCAAGACAGAGAAAAGCCAGTGAACATTCCGTCCGGATTCTTTACAATGGCGTCGATGTACATTCCACACCT
CTTTCTGCCAAGACCACCACAAGCGTTCTCCCAAGCCCATGTGCCCGCTTGAAAACCTGGTCCGCTTTGTGAAAA
GGGACATGTTTGTAGCCCTGGGTGGCAGTGGTACAAATTATTATGATGCATGTACAGGGAAGGATTCATAAAGG
TATGCAGTACAGCAGTATAGAATCCATGCCAATACAGAGCATAGGGAAAGGTCCACTTCTAGTTTTGTCTGTTAC
TAAGGGTAGAAGATTATTGCTTTTTTAAAGGCTAAATATTGTTTGTGGGAACCAAGATGGTTGGGGTTGAACAGT
AAGCACATTGCTGCAATGTGGTACGTGAATTGCTTGGTACAAAATGGCCAGTTCACAGAGGAATAGAAGGTACTT
TATCATAGCCAGACTTCGCTTAGAATGCCAGAATAATATAGTTCAAGACCTGAAGTTGCCAATCCAAGTTTGCAC
TCTTCTGGCCTGCCCCATGTTACTATGTGATGGAACCAAGCAGCACACCTCAACCAAAATTTTTTTAATCTTAGACATT
TTTACCTTGTCCTTGTTAAGAATTTCTTGAAGTGATTATCTAAAATAAAGGTTGGCAAACCTTTTTCTGTAAAGG
GCCAGATTGTAAATATTTTCAAGCTGTGTGGACCAAAAGGCCACATACAGTCTCTGTGCATACTCACTCTGT
TTCTGAAGCAGGAAAGCCACCACAGACAGTACATAAAGGAATATGTGTAGCTGGGTCCCAGGCCAGACAAAACA
GATGGTGACCAGACTTGGCCCTGGGCTGTAGTTTGTGACCCCTCATCTAAAAAATAGGCTATACTACAATTGC
ACTTCCAGCACTTTGAGAACGAGTTGAATACCAAGAATTATCAATGGTTCTCCAGTAACTTCTGCTAGAAACA
CAGAATTTGGTCTGTATCTGACACTAGAACAAAACCTTGAGGGTAAATAAACATTGAATTAGAATGAATCATAGAA
AACTGATTAGAAGAATACTTGATGTTTATGATGATTGTTGTTACAAGATAGTTTTAAGTATGTTCTAAATATTTGT
CTGCTGTAGTCTATTTGCTGTATATGCTGAAATTTTTGTATGCCATTTAGTATTTTTATAGTTTAGGAAAATATT
TTCTAAGACCAGTTTTAGATGACTCTTATTCCTGTAGTAATATTCAATTTGCTGTACCTGCTTGGTGGTTAGAAG
GAGGCTAGAAGATGAATTCAGGCACCTTTCTTCCAATAAACTAATTATGGCTCATTCCCTTTGACAAGCTGTAGA
ACTGGATTCATTTTTAAACATTTTTCATCAGTTTCAAATGGTAAATTCTGATTGATTTTTAAATGCGTTTTTGG
AGAATTTGCTATTAGGTAGTTTACAGATCTTTATAAGGTGTTTTATATATTAGAAGCAATTATAATTACATCTG
TGATTTCTGAACATAATGGTGCTAATTACAGAGAAATGGAAAGTGAAAGTGAGATTCTCTGTTGTATCGGCATTCC
AACTTTTTCTCTTTGTTTTTGTCCAGTGTTGCATTTGAATATGTCTGTTTCTATAAATAAATTTTTTAAGAATAA

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FIGURE 82

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48329
><subunit 1 of 1, 480 aa, 1 stop
><MW: 55240, pI: 9.30, NX(S/T): 2
MLFRNRFLLLLAIAALLAFVSLSLQFFHLIPVSTPKNGMSSKSRKRIMPDVTEPPVTDPVYEALLYCNIPSAE
RSMEGHAPHHFKLVSVHVFIRHGDRYPLYVIPKTKRPEIDCTLVANRKPYHPKLEAFISHMSKSGSGASFESPLNS
LPLYPNHPLCEMGELTQTGVVQHLQNGQLLRDIYLLKKHKLNPNDWSADQLYLETTGKSRTLQSGLALLYGFLPDF
DWKKIYFRHQPSALFCSGSCYCPVRNQYLEKEQRRQYLLRLKNSQLEKTYGEMAKIVDVPTKQLRAANPIDSMC
HFCHNVSPCTRNGCVDMEHFKVIKTHQIEDERERREKKLYFGYSLLGAHPILNQITIGRMQRATEGRKEELFALY
SAHDVTLSFVLSALGLSEARFPRFAARLIFELWQDREKPSEHSVRILYNGVDVTFHTSFCQDHHKRSPKPMCPLE
NLVRFVVKRDMFVALGGSGTNYDACHREGF
```

Signal sequence:
amino acids 1-18

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FIGURE 83

TCTCGCAGATAGTAAATAATCTCGGAAAGGCGAGAAAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGT
GACGTTGTGGAGATGGGGAGCGTCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCC
CCGTGTTTGCTATGCCGATGCTGTCTAGTGGAAACAACCTCCACTGTAACCTAGATTGATCTATGCACCTTTCTTG
CTGTGTTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAACCTGAATAAGATTCTTGGATTT
TGTGAGAATGAGAAAGGTGTTGTCCCTTGTAAACATTTTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTTGGT
TTGGCTATGTTCTATCTTCTTCTCTCTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTG
CACAAATGGATTTTGGTTCTTTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATTCCAGAAGGA
ACTTTTACAACCTGTGTGGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTCATCCTCATACAACCTAGTCTTACTT
ATTGATTTTGCACATTATGGAATGAATCGTGGGTTGAAAAAATGGAAGAAGGGAACCTCGAGATGTTGGTATGCA
GCCCTGTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTAGTTGCTATCGTCTGTTCTTTGTCTACTACACT
CATCCAGCCAGTTGTTTCAAAAAACAAGGCGTTCATCAGTGTCAACATGCTCCTCTGCGTTGGTGCTTCTGTAAATG
TCTATACTGCCAAAAATCCAAGAATCACAAACCAAGATCTGGTTTGTACAGTCTTCAGTAATTACAGTCTACACA
ATGATTTTGACATGGTCAGCTATGACCAATGAACCAGAAACAATTTGCAACCCAAGTCTACTAAGCATAATTGGC
TACAATACAACAAGCACTGTCCCAAAGGAAGGGCAGTCAGTCCAGTGGTGGCATGCTCAAGGAATTATAGGACTA
ATTCTCTTTTTTGTGTGTGTATTTTATCCAGCATCCGTACTTCAAACAATAGTCAGGTTAATAAACTGACTCTA
ACAAGTGATGAATCTACATTAATAGAAGATGGTGGAGCTAGAAGTGATGGATCACTGGAGGATGGGGACCATGTT
CACCGAGCTGTAGATAATGAAAGGGATGGTGTCACTTACAGTTATTCCTTCTTTCACTTCATGCTTTTCTGGCT
TCACCTTTATATCATGATGACCTTACCAACTGGTCCAGGTATGAACCTCTCGTGAGATGAAAAGTCAAGTGGCA
GCTGTCTGGGTGAAAATCTCTTCCAGTTGGATTGGCATCGTGTCTGTATGTTGGACACTCGTGGCACCAGTTGTT
CTTACAAATCGTGATTTTGAAGTGAAGTGTGATGTTTTTGTCTTCCATGTAACCTTCTCCAGTGTTCGGCATGAATTA
GATTTTACTGCTTGTCTATTTTGTATTTTCTTACCAAGTGCATTGATATGTGAAGTAGAATGAATTGCAGAGGAA
AGTTTTATGAATATGGTGATGAGTTAGTAAAAGTGGCCATTATTGGGCTTATCTCTGCTCTATAGTTGTGAAAT
GAAGAGTAAAAACAATTTGTTTGAATTTTAAATTTATATTAGACCTTAAGCTGTTTTCAGCAAGCATTAAAGC
AAATGTATGGCTGCCTTTTGAATATTTGATGTGTGCTGGCAGGATACTGCAAGAACAACCTGGTTTATTTTAAA
ATTTATAACAAGTCACTTAAATGCCAGTTGTCTGAAAAATCTTATAAGGTTTACCCTTGATACGGAATTTACA
CAGGTAGGGAGTGTTTGTGGACAATAGTGTAGGTTATGGATGGAGGTGTCGGTACTAAATGAATAACGAGTAA
ATAATCTTACTTGGGTAGAGATGGCCTTTGCCAACAAAGTGAACCTGTTTGGTTGTTTTTAACTCATGAAGTATG
GGTTCAGTGGAATGTTTGGAACTCTGAAGGATTTAGACAAGGTTTTGAAAAGGATAATCATGGGTAGAAAGGAA
GTGTTTTGAAAGTCACTTTGAAAGTTAGTTTTGGGCCAGCACGGTAGCTCACCTTGGTAATCCAGCACTTTG
GGAGCTTAAGTGGGTAGATTACTTGAAGCCAGGAATTCAGACCAGCTTGGCACATGGTGAACCTGTTCTATAAAA
ATAATCTGGCTTTGAGCATATGCTGTGGTCCAGCACTGAGAGGCTAGTGAAGATTGCTGAGCCAGAGCCAAAG
GTTGCAGTGAGCAAGTCACGTCACTGCACTCTAGCTGGCACAGAGTAAGCCAAAAAATATATATATATGAAAT
CAAGGAGGCAAAATTTTGAAGGGAAGGAAGTAACCTGCAAAACCACTAGGCTTTAGTAGGTACTTATATAAAATC
TAGTCCAGTTCTCTCATTTAAAAAATGAAGACACTGAAATACAGACTTAAATAGCTCAGATAGCTAATTAGGAA
ATTTCAAGTTGGCCAATAATAGCATTCTCTGACATTTAAAAATAATTTCTATTCAAAATACATGCATATTGAT
TTACACCTCATACTGTGATAATTAATGTGATGTGGATTGCTGGTGTCCAGCATGACCCATAAACAGGTCAGAAGA
ATGATGGAATGTTTGAATAAACTCCTGCTTATAGTATACTACACAGTTCAAAAGATGTTTAAATGCTTTTGT
ATTTACTGCCATGTAATTGAAATATATAGATTATTGTAACCTTTCAACCTGAAAATCAAGCAGTATGAGAGTTA
GTTATTTGTATGTGTCACTAGTGTCTAATGAAGCTTTTAAATCTACAATTTCTTCTTTAAAAATATTTATTAAT
GTGAATGGAATATAACAATTCAGCTTAATCCCCAACCTTATTCTGTGTGTAGACATTGTATCCACAATTTTGA
ATGGCTGTGTTTTACCTCTAAATAAATGAATTCAGAGAAAAA

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FIGURE 84

MGSVLGLCSMASWIPCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGMEEQLNKIPGFCENE
KGVVPCNILVGKYKAVYRLCFGLAMFYLLSLLMIKVKSSSDPRAAVHNGFWFFKFAAAIAIIIGAFFIPEGTFTT
VWFYVGMAGAFCFILIQVLVLLIDFAHSWNEVVEKMEEGNSRCWYAALLSATALNYLLSLVAIVLFFVYYTHPAS
CSENKAFISVNMLLCVGASVMSILPKIQESQPRSGLLQSSVITVYTMVLTWSAMTNEPETNCNPSLLSIIGYNTT
STVPKEGQSVQWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVHRAV
DNERDGVITYSYFFHEMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVVWKISSSWIGIVLYVWTLVAPLVLTNRDFD

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FIGURE 85

AACAAAGTTCAGTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGAGCTGCTGGGCAGA
GAGGGACTGTCCGGCTCCCAGATGCTGGGCCTCCTGGGGAGCACAGCCCTCGTGGGATGGATCACAGGTGCTGCT
GTGGCGGTCTGCTGCTGCTGCTGCTGCTGGCCACCTGCCTTTTCCACGGACGGCAGGACTGTGACGTGGAGAGG
AACCGTACAGCTGCAGGGGGAAACCGAGTCCGCCGGGCCCAGCCTTGGCCCTTCCGGCGGCGGGGCCACCTGGGA
ATCTTTCACCATCACCGTCATCCTGGCCACGTATCTCATGTGCCGAATGTGGGCCTCCACCACCACCACCC
CGCCACACCCCTCACCACCTCCACCACCACCACCCACCACCGCCACCATCCCCGCCACGCTCGCTGAGGGCTGC
TGTCGCCGGTGCCTGTGGACAGCAGCTGCCCTGCCCTCCCATCTGTTCCAGGACAAGTGGACCCCATGTTTCC
ATGTGGAAGGATGCATCTCTGGGGTGAACGAGGGGAACAATAGACTGGGGCTTGCTCCAGCTGCATTTGCATGGC
ATGCCCCAGTGTACTATGGCAGCAGAGAATGGAGGAACACTGGGTCTGCAGTGCTGAAGGGTTTGGGGAGTGGAG
AGCAAGGGTGCTCTTTCGGGGCTGGACAGCCCGTCTTGTGACAGTGAAGTGGAGTGGAGTGGAGTGGAGTGGAG
GTGTCTTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTCATCAGGCTGCTGCAGGCCT
CTGGCGGGCAGGGCACTGGGAGAGGCCCTGAGAATGTCCTTTTGGTTTGGAGAAGGCAGTGTGAGGCTGCACAGT
CAATTCATCGGTGCCTTAGTCCAAGAAAATAAAAACCACTAAGAAGCTTTAAAAAAAAAAAAAAAAAAAAA

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FIGURE 86

MLGLLGSTALVGWITGA AVAVLLLLLLLATCLFHGRQDCDVERNRTAAGGNRVRAQWPWFRRRGHLGIFHHHRH
PGHVSHVPNVGLHHHHHPRHTPHHLHHHHHPRHHPRHAR

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FIGURE 87

CCCACGCGTCCGTCCTAGTCCCCGGGCCAACTCGGACAGTTTGCTCATTATTGCAACGGTCAAGGCTGGCTTGT
GCCAGAACGGCGCGCGCGCGCGCACGCACACACACGGGGGGAACTTTTTTAAAAATGAAAGGCTAGAAGA
GCTCAGCGGCGGCGCGGCGCGCTGCGCGAGGGCTCCGGAGCTGACTCGCCGAGGCAGGAAATCCCTCCGGTCGCGA
CGCCCCGGCCCCGGCTCGGCGCCCCGCGTGGGATGGTGACGCGCTCGCCGCGGGCCCGAGAGCTGCTGCACTGAAG
GCCGCGACGATGGCAGCGCGCCCCGCTGCCCGTGTCCCCCGCCGCGCCCTCCTGCTCGCCCTGGCCGGTGTCT
GCTCGCGCCCTGCGAGGCCCCGAGGGGTGAGCTTATGGAACCAAGGAAGAGCTGATGAAGTTGTCACTGCCCTCTGT
TCGGAGTGGGGACCTCTGGATCCAGTGAAGAGCTTCGACTCCAAGAATCATCCAGAAGTGTGAATATTCGACT
ACAACGGGAAAGCAAAGAAGTATCATATAATCTGGAAGAAATGAAGGTCTCATTGCCAGCAGTTTCACGGAAAC
CCACTATCTGCAAGACGGTACTGATGTCTCCCTCGCTCGAAATTACACGGGTCACTGTTACTACCATGGACATGT
ACGGGGATATTCTGATTCAAGCAGTCACTCTCAGCAGGTGTTCTGGTCTCAGGGGACTTATTGTGTTTGAAAATGA
AAGCTATGTCTTAGAACCCTGAAAGTGCACCAACAGATACAACTCTTCCAGCGAAGAAGCTGAAAAGCGT
CCGGGGATCATGTGGATCACATCACAACACACCAACCTCGCTGCAAGAATGTGTTCCACCACCTCTCAGAC
ATGGGCAAGAAGGCATAAAAGAGAGACCCTCAAGGCAACTAAGTATGTGGAGCTGGTGTGCTGGCAGACAACCG
AGAGTTTCAGAGGCAAGGAAAAGATCTGGAAGAACTTAAGCAGCGATTAAAGAGATTGCTAATCACGTTGACAA
GTTTTACAGACCACTGAACATTCGGATCGTGTGGTAGGCGTGGAAAGTGTGGAATGACATGGACAAATGCTCTGT
AAGTCAGGACCCATTACACAGCCTCCATGAATTTCTGGACTGGAGGAAGATGAAGCTTCTACCTCGCAAATCCCA
TGACAATGCGCAGCTTGTCACTGGGGTTTATTTCCAAGGACCACCATCGGCATGGCCCCAATCATGAGCATGTG
CACGGCAGACCACTGCGGGGAATTGTGATGGACCATTCAGACAATCCCTTGGTGCAGCCGTGACCTGGCACA
TGAGCTGGGCCACAATTTGCGGATGAATCATGACACACTGGACAGGGGCTGTAGCTGTCAAATGGCGGTTGAGAA
AGGAGGCTGCATCATGAACGCTTCCACCGGTTACCCATTTCCCATGGTGTTCAGCAGTTGCAGCAGGAAGGACTT
GGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCCTGTTTTAACCTGCCGGAAGTCAGGGAGTCTTTGGGGGCCA
GAAGTGTGGGAACAGATTGTGGAAGAAGGAGAGAGTGTGACTGTGGGGAGCCAGAGGAATGTATGAATCGCTG
CTGCAATGCCACCACCTGTACCCTGAAGCCGACGCTGTGTGCGCACATGGGCTGTGCTGTGAAGACTGCCAGCT
GAAGCCTGCAGGAACAGCGTGCAGGGACTCCAGCACTCCTGTGACCTCCAGAGTTTCTGCACAGGGGCCAGCCC
TCACTGCCCAGCCAATGTGTACCTGCACGATGGGCACTCATGTGAGGATGTGGACGGCTACTGCTACAATGGCAT
CTGCCAGACTCACGAGCAGCAGTGTGTGACGCTCTGGGGACCAGGTGCTAAACCTGCCCTGGGATCTGCTTTGA
GAGAGTCAATCTGCAGGTGATCCTTATGGCAACTGTGGCAAAGTCTCGAAGAGTTCTTTTGCCAAATGCGAGAT
GAGAGATGCTAAATGTGGAAGAAATCCAGTGTCAAGGAGGTGCCAGCCGGCCAGTCATTGGTACCAATGCCGTTTC
CATAGAAACAAACATCCCTCTGCAGCAAGGAGGCCGATTCTGTGCCGGGGACCCACGTGTACTTGGGCGATGA
CATGCCGGACCCAGGGCTTGTGCTTGCAGGCACAAAGTGTGCAGATGGAAAAATCTGCCTGAATCGTCAATGTCA
AAATATTAGTGTCTTTGGGGTTCACGAGTGTGCAATGCAGTGCCACGGCAGAGGGGTGTGCAACAACAGGAAGAA
CTGCCACTGCGAGGCCCACTGGGCACCTCCCTTCTGTGACAAGTTTGGCTTTGGAGGAAGCACAGACAGCGGCC
CATCCGGCAAGCAGAAGCAAGGCAGGAAGCTGCAGAGTCCAACAGGGAGCGCGGCCAGGGCCAGGAGCCCGTGGG
ATCGCAGGAGCATGCGTCTACTGCCTCACTGACACTCATCTGAGCCCTCCCATGACATGGAGACCGTGACCAGTG
CTGCTGCAGAGGAGTCAAGCGTCCCCAAGGCCTCCTGTGACTGGCAGCATTGACTCTGTGGCTTTGCCATCGTT
TCCATGACAACAGACACAACACAGTTCTCGGGGCTCAGGAGGGGAAGTCCAGCCTACCAGCACGTCTGCAGAAA
CAGTGCAGGAAGGGCAGCGACTTCTGTTGAGCTTCTGCTAAACATGGACATGCTTCAGTGTCTGCTCCTGAG
AGAGTAGCAGTTTACCACTCTGGCAGGCCCCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAAGTCTGGCCTTTC
ACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTTGGGCCAGTGTCCCCTTTCCCAGTGACACCTCAGCCT
TGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTCTGATATGGCTTTTAGCATTTATATATGAAAAAT
AGCAGGGTTTTAGTTTTTAATTTATCAGAGACCCTGCCACCATTCCATCTCCATCCAAGCAAACTGAATGGCAA
TGAAACAAACTGGAGAAGAAGGTAGGAGAAAGGGCGGTGAACTCTGGCTCTTTGCTGTGGACATGCGTGACCAGC
AGTACTCAGGTTTGAGGGTTTGAGAAAGCCAGGGAAACCCACAGAGTCACCAACCCTTCATTTAACAAGTAAGAA
TGTTAAAAAGTGAAAACAATGTAAGAGCCTAATCCATCCCCCGTGGCCATTACTGCATAAAATAGAGTGCATTT
GAAAT

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FIGURE 88

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49624
><subunit 1 of 1, 735 aa, 1 stop
><MW: 80177, pI: 7.08, NX(S/T): 5
MAARPLPVSPARALLALAGALLAPCEARGVSLWNQGRADEVVVSASVRSGDLWIPVKSFD SKNHPEVLNIRLQRE
SKELIINLERNEGLIASSFTETHYLQDGTDVSLARNYTGHCYYHGHVIRGYSDSAVSLSTCSGLRGLIVFENESYV
LEPMKSATNRYKLFPAKKLKSVRGSCGSHHNTPNLAAKNVFPPPSQTWARRHKRETILKATKYVELVIVADNREFQ
RQKDLKVKQRLIEIANHVDKFYRPLNIRIVLVGVEVWDMMDKCSVSQDPFTSLHEFLDWRKMKLLPRKSHDNA
QLVSGVYFQGTITIGMAPIMSMCTADQSGGIVMDHSDNPLGAAVTLAHELGHNFGMNHDITLDRGCSCQMAVEKGGC
IMNASTGYPPFMVFSSCSRKDLETSLEKGMGVCLEFNLPEVRESFGGQKCGNRFEVEEGEEDCGEPEECMNRCCNA
TTCTLKPDCAVCAHGLCCEDCQLKPAGTACRDSSNSCDLPEFCTGASPHCPANVYLHDGHSCQDQVDGYCYNGICQT
HEQQCVTLWGPAGKAPAGICFERVNSAGDPYGNCGKVS KSSFAKCEMRDAKCGKIQCQGGASRPVIGTNAVSIET
NIPLOQGGRI LCRGTHVYLGDDMPDPGLVLAGTKCADGKICLN RQCQNISVFGVHECAMQCHGRGVCNNRKNCHC
EAHWAPPFCDFKFGFGSTDSGPIRQAEARQEAESNRERGGQGEFVGSQEHASTASLTLLI
```

Signal peptide:
amino acids 1-28

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FIGURE 89

CTGCTGCATCCGGGTGTCTGGAGGCTGTGGCCGTTTTGTTTTCTTGGCTAAAAATCGGGGGAGTGAGGCGGGCCGG
CGCGGCGCGACACCGGGCTCCGGAACCACTGCACGACGGGGCTGGACTGACCTGAAAAAAATGCTCTGGATTTCTA
GAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTA
CTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGATTTCAACCACTCA
TACCATGCCTGTGGTGTATAGCAACCATAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGT
GATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTGCTCGCATTGGCTTTTCGTTGGTTTCATGTTGGCCTTT
GGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCCCTGGA
ATTGCTGTATTTTTCCAGAATGCCTTCATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGACTTA
TGGCAGTGAACACATCTGATTTCCACAGCACAAACAGCCCTGCATGGGTTTGTGTTTTTTTTACTGCTCACTCC
CAACCTTTTGTAATGCCATTTTCTAACTTATTTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACTAAAATC
ACGAGAACACCTAAACAACAACCAAAAAATCTATTGTGGTATGCACCTTGATTAACTTATAAAATGTTAGAGGAAAC
TTTCACATGAATAATTTTTGTCAAATTTTATCATGGTATAATTTGTAATAAATAAAGAAATTACAAAAGAAATT
ATGGATTTGTCAATGTAAGTATTTGTCATATCTGAGGTCCAAAACCACAATGAAAGTGCTCTGAAGATTTAATGT
GTTTATTCAAATGTGGTCTCTTCTGTGTCAAATGTTAAATGAAATATAAACATTTTTTAGTTTTTAAATATTCC
GTGGTCAAATTTCTTCCTCACTATAATTTGGTATTTACTTTTACCAAAAATTCTGTGAACATGTAATGTAAGTGGC
TTTTGAGGGTCTCCCAAGGGGTGAGTGGACGTGTTGGAAGAGAGAAGCACCATGGTCCAGCCACCAGGCTCCCTG
TGTCCCTTCCATGGGAAGGTCTCCGCTGTGCCTCTCATTTCCAAGGGCAGGAAGATGTGACTCAGCCATGACACG
TGGTTCTGGTGGGATGCACAGTCACTCCACATCCACCACTG

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FIGURE 90

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWWIIIDA AVIYPTMKDFNHSYHACGVIATIAFLMINAVSN
GQVRGDSYSEGCLGQTGARIWLFVGFMLAFGSLIASMWILFGGYVAKEKDIVYPGIAVFFQNAFIFFGGLVFKFG
RTEDLWQ

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FIGURE 91

CGACGCCGGCGT**GATG**TGGCTTCCGCTGGTGCTGCTCCTGGCTGTGCTGCTGCTGGCCGTCTCTGCAAAGTTTA
CTTGGGACTATTCTCTGGCAGCTCCCCGAATCCTTTCTCCGAAGATGTCAAACGGCCCCCAGCGCCCTGGTAAC
TGACAAGGAGGCCAGGAAGAAGGTTCTCAAACAAGCTTTTTCAGCCCAACCAAGTGCCGGAGAAGCTGGATGTGGT
GGTAATTGGCAGTGGCTTTGGGGGCTGGCTGCAGCTGCAATCTAGCTAAAGCTGGCAAGCGAGTCTGGTGCT
GGAACAACATACCAAGGCAGGGGGCTGCTGTACATACCTTTGGAAAGAATGGCCTTGAATTTGACACAGGAATCCA
TTACATTGGGCGTATGGAAGAGGGCAGCATTTGGCCGTTTTATCTTGGACCAAGATCACTGAAGGGCAGCTGGACTG
GGCTCCCCGTGCTCTCCTTTTGACATCATGGTACTGGAAGGGCCCAATGGCCGAAAGGAGTACCCCATGTACAG
TGGAGAGAAAGCCTACATTCAGGGCCTCAAGGAGAAGTTTCCACAGGAGGAAGCTATCATTGACAAGTATATAAA
GCTGGTTAAGGTGGTATCCAGTGGAGCCCTCATGCCATCCTGTTGAAATTCCTCCCATTTGCCCGTGGTTTCAGCT
CCTCGACAGGTGTGGGCTGCTGACTCGTTTTCTCTCCATTCTTCAAGCATCCACCAGAGCCTGGCTGAGGTCTCT
GCAGCAGCTGGGGGCTCCTCTGAGCTCCAGGCAGTACTCAGCTACATCTTCCCCACTTACGGTGTCAACCCCAA
CCACAGTGCCTTTTCCATGCACGCCCTGCTGGTCAACCACTACATGAAAGGAGGCTTTTATCCCCGAGGGGGTTC
CAGTGAAATTCCTTCCACACCATCCCTGTGATTGAGCGGGCTGGGGGCGCTGTCTCACAAAGGGCCACTGTGCA
GAGTGTGTGCTGGACTCAGCTGGGAAAGCCTGTGGTGTGAGTGTGAAGAAGGGGCATGAGCTGGTGAACATCTA
TTGCCCATCGTGGTCTCCAACGCAGGACTGTTCAACACCTATGAACACCTACTGCCGGGGAACGCCGCTGCCT
GCCAGGTGTGAAGCAGCAACTGGGGACGGTGCGGCCCGGCTTAGGCATGACCTCTGTTTTCATCTGCCTGCGAGG
CACCAAGGAAGACCTGCATCTGCCGTCCACCAACTACTATGTTTACTATGACACGGACATGGACCAGGCGATGGA
GCGCTACGTCTCCATGCCAGGGAGAGGCTGCGGAACACATCCCTCTTCTCTTCTTCTCGCTTTCCCATCAGCCAA
AGATCCGACCTGGGAGGACCGATTCCAGGCCGGTCCACCATGATCATGCTCATACCCACTGCCTACGAGTGGTT
TGAGGAGTGGCAGGCGGAGCTGAAGGGAAAGCGGGGCAGTGAATGAGACCTTCAAAAACCTCTTTGTGGAAGC
CTCTATGTGAGTGGTCTTCAAACCTGTTCCACAGCTGGAGGGGAAGGTGGAGAGTGTGACTGCAGGATCCCCACT
CACCAACAGTTCTATCTGGCTGCTCCCCGAGGTGCTGTACGGGGCTGACCATGACCTGGGCCGCTGCACCC
TTGTGTGATGGCCTCCTTGAGGGCCAGAGCCCCATCCCCAACCTCTATCTGACAGGCCAGGATATCTTCACTGT
TGACTGGTGGGGGCCCTGCAAGGTGCCCTGCTGTGCAGCAGCGCCATCCTGAAGCGGAACCTGTACTCAGACCT
TAAGAATCTTGATTCTAGGATCCGGGCACAGAAGAAAAAGAATTAGTTCATCAGGGAGGAGTCAAGGAAATTTG
CCCAATGGCTGGGGCATCTCCCTTGACTTACCCATAATGTCTTTCTGCATTAGTTCCTTGCACGTATAAAGCACT
CTAATTTGGTTCTGATGCCCTGAAGAGAGGGCTAGTTTAAATCACAATTCCGAATCTGGGGCAATGGAATCACTGC
TTCCAGCTGGGGCAGGTGAGATCTTTACGCCTTTTATAACATGCCATCCCTACTAATAGGATATTGACTTGGATA
GCTTGATGTCTCATGACGAGCGGCGCTCTGCATCCCTCACCCATGCCTCCTAACTCAGTGATCAAAGCGAATATT
CCATCTGTGGATAGAACCCCTGGCAGTGTGTGAGCTCAACCTGGTGGGTTGAGTTCTGTCTCTGAGGCTTCTGCT
CTCATTCAATTTAGTGCTACGCTGCACAGTTCTACACTGTCAAGGGAAAAGGGAGACTAATGAGGCTTAACTCAAA
ACCTGGGCGTGGTTTTGGTTGCCATTCCATAGGTTTGGAGAGCTCTAGATCTCTTTTGTGCTGGGTTCACTGGCT
CTTCAGGGGACAGGAAATGCCCTGTGTCTGGCCAGTGTGGTTCTGGAGCTTTGGGGTAACAGCAGGATCCATCAGT
TAGTAGGGTGCATGTGAGATGATCATATCCAATTCATATGGAAGTCCCGGGTCTGTCTTCTTATCATCGGGGTG
GCAGCTGGTTCTCAATGTGCCAGCAGGGACTCAGTACCTGAGCCTCAATCAAGCCTTATCCACCAATACACAGG
GAAGGGTGTGAGGGGAAGGGTGACATCAGGAGTCAGGGCATGGACTGGTAAGATGAATACTTTGCTGGGCTGAA
GCAGGCTGCAGGGCATTCCAGCCAAGGGCACAGCAGGGGACAGTGCAGGGAGGTGTGGGGTAAGGGAGGGAAAGTC
ACATCAGAAAAGGGAAAGCCACGGAATGTGTGTGAAGCCCAGAAATGGCATTGTCAGTTAATTAGCACATGTGAG
GGTTAGACAGGTAGGTGAATGCAAGCTCAAGGTTTGGAAAAATGACTTTTCAGTTATGTCTTTGGTATCAGACAT
ACGAAAGGTCTCTTTGTAGTTCGTGTTAATGTAACATTAATAAATTTATTGATTCCATTGCTTTAAAAA

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FIGURE 92

MWLPLVLLLAVALLLAVLCKVYLGLFSGSSPNPFSEDKRPPAPLVTDKEARKKVLKQAFSANQVPEKLDVTVVIGS
GFGGLAAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDTGIHYIGRMEEGSIGRFILDQITEGQLDWAPLS
SPFDIMVLEGPNGRKEYPMYSGEKAYIQGLKEKFPQEEAIIDKYIKLVKVVSSGAPHAILLKFLPLPVVQLLDRC
GLLTRFSPFLQASTQSLAEVLQQLGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHMKGGFYPRGGSSEIA
FHTIPVIQRAGGAVLTATVQSVLLDSAGKACGVSVKKGHELVNIYCPIVVSNAGLFNTYEHLLPGNARCLPGVK
QQLGTVRPGLGMTSVFICLRGTEKEDLHLPSTNYVYYDTDMDQAMERYVSMFREEAAEHIPLLFFAFPSAKDPTW
EDRFPGRSTMIMLIPTAYEWFEEWQAEKKGKRGSDYETFKNSFVEASMSVVLKLFPPQLEGKVESVTAGSPLTNQF
YLAAPRGACYGADHDLGRLHPCVMASLRAQSPIPNLYLTGQDIFTCGLVGALQGALLCSSAILKRNLYSDLKNLD
SRIRAQKKKN

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FIGURE 93

GGGAAAGATGGCGGCGACTCTGGGACCCCTTGGGTCTGGGAGCAGTGGCGGCGATGTTTGTCTGGCTCGGGATGG
GTCCAGGATGTTACTCCTTCTTCTTTTGTGGGTCTGGGCAGGGGCCACAGCAAGTCTGGGGCGGGTCAAACGTT
CGAGTACTTGAAACGGGAGCACTCGCTGTCTGAAGCCCTACCAGGGTGTGGGCACAGGCAGTTCTCTCACTGTGGAA
TCTGATGGGCAATGCCATGGTGATGACCCAGTATATCCGCCTTACCCAGATATGCAAAGTAAACAGGGTGCCTT
GTGGAACCGGGTGCCATGTTTCCCTGAGAGACTGGGAGTTGCAGGTGCACTTCAAATCCATGGACAAGGAAAGAA
GAATCTGCATGGGGATGGCTTGGCAATCTGGTACACAAAGGATCGGATGCAGCCAGGGCCTGTGTTTGGAAACAT
GGACAAATTTGTGGGGCTGGGAGTATTGTAGACACCTACCCCAATGAGGAGAAGCAGCAAGAGCGGGTATTCCC
CTACATCTCAGCCATGGTGAACAACGGCTCCCTCAGCTATGATCATGAGCGGATGGGCGGCCTACAGAGCTGGG
AGGCTGCACAGCCATTGTCCGCAATCTTCATTACGACACCTTCTTGGTGATTCTCGCTACGTCAAGAGGCATTTGAC
GATAATGATGGATATTGATGGCAAGCATGAGTGGAGGACTGCATTGAAGTGGCGGAGTCCGCCTGCCCCGCGG
CTACTACTTCGGCACCTCCCTCCATCACTGGGGATCTCTCAGATAATCATGATGTCAATTTCTTGAAGTTGTTTGA
ACTGACAGTGGAGAGAACCCCAAGAGGAAAAGCTCCATCGAGATGTGTTCTTGGCCTCAGTGGACAATATGAA
GCTGCCTGAGATGACAGCTCCACTGCCGCCCTGAGTGGCCTGGCCCTCTTCTCATCGTCTTTTTCTCCCTGGT
GTTTTCTGTATTTGCCATAGTCATTGGTATCACTCTACAACAAATGGCAGGAACAGAGCCGAAAGCGCTTCTA
CTGAGCCCTCCTGCTGCCACCACTTTTGTGACTGTCAACCATGAGGTATGGAAGGAGCAGGCAGTGGCCTGAGCA
TGCAGCCTGGAGAGTGTCTTGTCTCTAGCAGCTGGTGGGGACTATATTTCTGCTACTGGAGTTTTGAATGCAGG
GACCCCGCATTTCCCATGGTTGTGCATGGGGACATCTAACTCTGGTCTGGGAAGCCACCCACCCAGGGCAATGCT
GCTGTGATGTGCCTTTCCCTGCAGTCCCTCCATGTGGGAGCAGAGGTGTGAAGAGAATTTACGTGGTTGTGATGC
CAAATCACAGAACAGAATTTATAGCCCAGGCTGCCGTGTTGTTTGACTCAGAAGGCCCTTCTACTTCAGTTTT
GAATCCACAAAGAATTAATACTGGTAACACCACAGGCTTTCTGACCATCCATTGTTGGGTTTTGCATTTGACC
CAACCCTCTGCCTACCTGAGGAGCTTTCTTTGGAAACCAGGATGGAACTTCTTCCCTGCCTTACCTTCCTTTCA
CTCCATTCAATTGCTCTCTGTGTGCAACCTGAGCTGGGAAAGGCATTTGGATGCCTCTCTGTTGGGGCCTGGGG
CTGCAGAACACACCTGCGTTTCACTGGCCTTCATTAGGTGGCCCTAGGGAGATGGCTTTCTGCTTTGGATCACTG
TTCCCTAGCATGGGTCTTGGGTCTATTGGCATGTCCATGGCCTTCCCAATCAAGTCTCTTCAGGCCCTCAGTGAA
GTTTGGCTAAAGGTTGGTGTAAAAATCAAGAGAAGCCTGGAAGACATCATGGATGCCATGGATTAGCTGTGCAAC
TGACCAGCTCCAGGTTTGATCAAACCAAAAGCAACATTTGTCATGTGGTCTGACCATGTGGAGATGTTTCTGGAC
TTGCTAGAGCCTGCTTAGCTGCATGTTTTGTAGTTACGATTTTTTGAATCCCACTTTGAGTGCTGAAAGTGTAAG
GAAGCTTTCTTCTTACACCTTGGGCTTGGATATTGCCAGAGAAGAAATTTGGCTTTTTTTTTCTTAATGGACAA
GAGACAGTTGCTGTTCTCATGTTCCAAGTCTGAGAGCAACAGACCCTCATCATCTGTGCCTGGAAGAGTTCACTG
TCATTGAGCAGCACAGCCTGAGTGTGGCCTCTGTCAACCCTTATTCCACTGCCTTATTTGACAAGGGGTACAT
GCTGCTCACCTTACTGCCCTGGGATTAAATCAGTTACAGGCCAGAGTCTCCTTGGAGGGCCTGGAAGTCTGAGTC
CTCCTATGAACCTCTGTAGCCTAAATGAAATTTCTTAAATCACCGATGGAACCAAAAAAAAAAAAAAAAAAGGGCG
GCCGCGACTCTAGAGTCGACCTGCAGTAGGGATAACAGGGTAATAAGCTTGGCCGCATGG

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FIGURE 94

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50911
><subunit 1 of 1, 348 aa, 1 stop
><MW: 39711, pI: 8.70, NX(S/T): 1
MAATLGPLGSWQQWRRCLISARDGSRMLLLLLLLGSGQGPPQVGAGQTFEYLKREHSLSKPYQGVGTGSSSLWNLM
GNAMVMTQYIRLTPDMQSKQGALWNRVPCFLRDWELQVHFKIHGQKKNLHGDGLAIWYTKDRMQPGPVFGNMDK
FVGLGVFVDITYPNEEKQQERVFPYISAMVNNGSLSYDHERDGRPTLGGCTAIVRNLYDTFLVIRYVKRHLTIM
MDIDGKHEWRDCIEVPGVRLPRGYFYTSSITGDLSDNHDVISLKLFEITVERTPEEEKLHRDVFLLPSVDNMKLP
EMTAPLPPLSGLALFLIVFFSLVFSVFIVIGIILYNKWQEQRKREY
```

Signal sequence:
amino acids 1-38

Transmembrane domain:
amino acids 310-329

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FIGURE 95

CCTGTGTTAAGCTGAGGTTTCCCCTAGATCTCGTATATCCCCAACACATACCTCCACGCACACACATCCCCAAGA
ACCTCGAGCTCACACCAACAGACACACGCGCGCATACACACTCGCTCTCGCTTGTCCATCTCCCTCCCGGGGGAG
CCGGCGCGCGCTCCCACCTTTGCCGCACACTCCGGCGAGCCCGCAGCGCTCCAGGATTCTGCGGCTCGGA
ACTCGGATTGCAGCTCTGAACCCCCATGGTGGTTTTTTTAAACACTTCTTTTCCCTTCTTTCCTCGTTTGATTGC
ACCGTTTCCATCTGGGGGCTAGAGGAGCAAGGCAGCAGCCTTCCCAGCCAGCCCTTGTGGCTTGCATCGTCCA
TCTGGCTTATAAAAGTTTGTCTGAGCGCAGTCCAGAGGGCTGCGCTGCTCGTCCCTCGGCTGGCAGAAGGGGGTG
ACGCTGGGCAGCGGCGAGGAGCGCGCGCTGCTTGGCGGGCTTTCGGCTTGAGGGGCAAGGTGAAGAGCGCAC
CGGCCGTGGGGTTTACCGAGCTGGATTGTATGTTGCACCATGCTTCTTGGATCGGGGCTGTGATTCTTCCCCT
CTTGGGGCTGCTGCTCTCCCTCCCGCGGGGGCGGATGTGAAGGCTCGGAGCTGCGGAGAGGTCCGCCAGGCGTA
CGGTGCCAAGGGATTACGCCCTGGCGGACATCCCCTACCAGGAGATCGCAGGGGAACACTTAAGAATCTGTCTCA
GGAATATACATGCTGCACCACAGAAATGGAAGACAAGTTAAGCCAACAAAGCAAACCTCGAATTTGAAAACCTTGT
GGAAGAGACAAGCCATTTTGTGCGCACCACCTTTTGTGTCCAGGCATAAGAAATTTGACGAATTTTCCGAGAGCT
CCTGGAGAATGCAGAAAAGTCACTAAATGATATGTTTGTACGGACCTATGGCATGCTGTACATGCAGAATTCAGA
AGTCTTCCAGGACCTCTTACAGAGCTGAAAAGGTACTACACTGGGGTAAATGTGAATCTGGAGGAAATGCTCAA
TGACTTTTGGGCTCGGCTCCTGGAACGGATGTTTCAGCTGATAAACCCCTCAGTATCACTTCAGTGAAGACTACCT
GGAATGTGTGAGCAAATACACTGACCAGCTCAAGCCATTTGGAGACGTGCCCCGAAACTGAAGATTACAGTTAC
CCGCGCCTTCATTGCTGCCAGGACCTTTGTCCAGGGGCTGACTGTGGGCAGAGAAGTTGCAAACCGAGTTTCCAA
GGTCAGCCCAACCCAGGGTGTATCCGTGCCCTCATGAAGATGCTGTACTGCCATACTGTGCGGGGCTTCCCAC
TGTGAGGCCCTGCAACAACACTACTGTCTCAACGTGATGAAGGGCTGCTTGGCAAATCAGGCTGACCTCGACACAGA
GTGGAATCTGTTTATAGATGCAATGCTCTTGGTGGCAGAGCGACTGGAGGGGCCATTCAACATTGAGTCGGTCAT
GGACCCGATAGATGTCAAGATTTCTGAAGCCATTATGAACATGCAAGAAAACAGCATGCAGGTGTCTGCAAAGGT
CTTTCAGGGATGTGGTCAGCCCAAACCTGCTCCAGCCCTCAGATCTGCCGCTCAGCTCCTGAAAATTTTAATAC
ACGTTTCAGGCCCTACAATCCTGAGGAAAGACCAACAACCTGCTGCAGGCACAAGCTTGGACCGGCTGGTCACAGA
CATAAAAGAGAAATTGAAGCTCTCTAAAAGGTCTGGTCAGCATTACCTTACACTATCTGCAAGGACGAGAGCGT
GACAGCGGGCACGTCCAACGAGGAGGAATGCTGGAACGGGCACAGCAAAGCCAGATACTTGCCTGAGATCATGAA
TGATGGGCTCACCAACCAGATCAACAATCCCGAGGTGGATGTGGACATCACTCGGCCTGACACTTTCATCAGACA
GCAGATTATGGCTCTCCGTGTGATGACCAACAACTAAAAAACGCCCTACAATGGCAATGATGTCAATTTCCAGGA
CACAAGTGATGAATCCAGTGGCTCAGGGAGTGGCAGTGGGTGCATGGATGACGTGTGTCCCACGGAGTTTGAGTT
TGTCACCACAGAGGCCCCCGAGTGGATCCCGACCGGAGAGAGGTGGACTCTTCTGCAGCCAGCGTGGCCACTC
CCTGCTCTCCTGGTCTCTCACCTGCATTGTCTTGGCACTGCAGAGACTGTGCAGATACTTGGGTTTTTGGTCA
GATGAAACTGCATTTTAGCTATCTGAATGGCCAACTCACTTCTTTTCTTACACTCTTGGACAATGGACCATGCCA
CAAAACTTACCCTTTCTATGAGAAGAGAGCAGTAATGCAATCTGCCTCCCTTTTGTGTTTTCCCAAAGAGTACC
GGGTGCCAGACTGAAGTCTTCTCTTCTTCTCAGCTATCTGTGGGACCTTGTGTTATTCTAGAGAGAATTCTTA
CTCAAATTTTTCGTACCAGGAGATTTTCTTACCTTCATTGCTTTTATGCTGCAGAAGTAAAGGAATCTCACGTT
GTGAGGGTTTTTTTTTCTCATTTAAAT

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FIGURE 96

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50914
><subunit 1 of 1, 555 aa, 1 stop
><MW: 62736, pI: 5.36, NX(S/T): 0
MPSWIGAVILPLLGLLLSLPAGADV KARS CGEVRQAYGAKGFS LADIPYQEIAGEHLRICPQEYTCCTTEMEDKL
SQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFFRELLEN A EKSLNDMFVRTYGM LYM QNSEVFQDLFTELK RYY
TGGNVNLEEMLNDFWARLLERM FQLINPQYH FSE DY LECVSKYTDQLKPF G DVPRKLKIQVTRAFIAARTFVQGL
TVGREVANRVSKVSPTPGCIRALMKMLYCPYCRGLPTVRPCNNYCLNVMKGCLANQADLDTEWNLFIDAMLLVAE
RLEGPFNIESVMDPIDVKISEAIMNQENSMQVS AKVFQCGQPKPAPALRSARSAPENFNTRFRPYNPEERPTT
AAGTSLDRLVTDIKEKLKLSKKVWSALPYTICKDES VTAGTSNEEECWNGH SKARYLPEIMNDGLTNQINNPEVD
VDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESSGSGSGSGCMDDVCPTFEFEFVTTEAPAVDPDRR
EVDSSAAQRGHSLLSWSLTCIVLALQRLCR
```

Signal peptide:
amino acids 1-23

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FIGURE 97

GGCGGCGTCCGTGAGGGGCTCCTTTGGGCAGGGGTAGTGTGTTGGTGTCCCTGTCTTGCGTGATATTGACAAACTG
AAGCTTTCCTGCACCACTGGACTTAAGGAAGAGTGTACTCGTAGGCGGACAGCTTTAGTGGCCGGCCGGCCGCTC
TCATCCCCCGTAAGGAGCAGAGTCCTTTGTACTGACCAAGATGAGCAACATCTACATCCAGGAGCCTCCACGAA
TGGGAAGGTTTTATTGAAACTACAGCTGGAGATATTGACATAGAGTTGTGGTCCAAAGAAGCTCCTAAAGCTTG
CAGAAATTTTATCCAACCTTTGTTTGAAGCTTATTATGACAATACCATTTTTCATAGAGTTGTGCCTGGTTTCAT
AGTCCAAGGCGGAGATCCTACTGGCACAGGGAGTGGTGGAGAGTCTATCTATGGAGCGCCATTCAAAGATGAATT
TCATTACGGTTGCGTTTTAATCGGAGAGGACTGGTTGCCATGGCAAATGCTGGTTCTCATGATAATGGCAGCCA
GTTTTTCTTCACACTGGGTCGAGCAGATGAACCTTAACAATAAGCATACCATCTTTGGAAAGGTTACAGGGGATAC
AGTATATAACATGTTGCGACTGTGAGAAGTAGACATTGATGATGACGAAAGACCACATAATCCACACAAAATAAA
AAGCTGTGAGGTTTTGTTAATCCTTTTGATGACATCATTCCAAGGGAAATTAAAAGGCTGAAAAAGAGAAACC
AGAGGAGGAAGTAAAGAAATTGAAACCCAAAGGCACAAAAAATTTAGTTTACTTTTATTGGAGAGGAAGCTGA
GGAAGAAGAGGAGGAAGTAAATCGAGTTAGTCAGAGCATGAAGGGCAAAAGCAAAAGTAGTCATGACTTGCTTAA
GGATGATCCACATCTCAGTTCTGTTCCAGTTGTAGAAAGTGAAAAAGGTGATGCACCAGATTAGTTGATGATGG
AGAAGATGAAAGTGCAGAGCATGATGAATATATTGATGGTGTGAAAAAGAACCTGATGAGAGAAAGAATTGCCAA
AAAATTTAAAAAGGACACAAGTGCGAATGTTAAATCAGCTGGAGAAGGAGAAGTGGAGAAGAAATCAGTCAGCCG
CAGTGAAGAGCTCAGAAAAAGAAGCAAGACAATTAAAACGGGAACTCTTAGCAGCAAAACAAAAAAGTAGAAAA
TGCAGCAAAACAAGCAGAAAAAGAAGTGAAGAGGAAGAAGCCCCCTCCAGATGGTGTCTGTTGCCGAATACAGAAG
AGAAAAGCAAAAGTATGAAGCTTTGAGGAAGCAACAGTCAAAGAAGGGAACCTCCCGGGAAGATCAGACCCCTTGC
ACTGCTGAACAGTTTAAATCTAAACTCACTCAAGCAATTGCTGAAACACCTGAAATGACATTCTGAAACAGA
AGTAGAAGATGATGAAGGATGGATGTCACATGTACTTCAGTTTGAGGATAAAAGCAGAAAAGTGAAAGATGCAAG
CATGCAAGACTCAGATACATTTGAAATCTATGATCCTCGGAATCCAGTGAATAAAAGAAGGAGGGAAGAAAGCAA
AAAGCTGATGAGAGAGAAAAAGAAAGAAGATAAAATGAGAATAATGATAACCAGAACTTGCTGGAAATGTGCCT
ACAATGGCCTTGTAACAGCCATTGTTCCCAACAGCATCACTTAGGGGTGTGAAAAGAAGTATTTTTGAACCTGTT
GTCTGGTTTTTGAAAAACAATTATCTTTGTTTGCAAATTGTGGAATGATGTAAGCAAAATGCTTTTGGTTACTGGTA
CATGTGTTTTTTCCTAGCTGACCTTTTATATTGCTAAATCTGAAATAAATAAATTTCTTCCACAAAAA
AAAAAAAAAAAAAAAAAAAA

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FIGURE 98

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50919
><subunit 1 of 1, 472 aa, 1 stop
><MW: 53847, pI: 5.75, NX(S/T): 2
MSNIYIQEPPTNGKVLLKTTAGDIDIELWSKEAPKACRNFIQLCLEAYYDNTIFHRVVPGFIVQGGDPTGTGSGG
ESYIGAPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQFFFTLGRADELNKHTIFGKVTGDTVYNMLRLSEVDID
DDERPHNPHKIKSCEVLFPFDDIIPREIKRLKKEKPEEEVKKLKPKGTKNFSLLSFGEEAEVNRVSQSM
KGKSKSSHDLKDDPHLSSVPVVESEKGDAPDLVDDGEDESAEHDEYIDGDEKNLMRERIAKKLKKDTSANVKS
GEGEVEKKSVSRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEAPPDGAVAERYRREKQKYEALRKQOS
KKGTSREDQTLALLNQFKSKLTQAIAETPENDIPETEVEDDEGWMSHVLQFEDKSRKVKDASMQSDTFEYDPR
NPVKNRRREESKMLREKKERR
```

Important features:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 109-112 and 201-204

Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.

amino acids 49-66

Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase

amino acids 96-140, 49-89 and 22-51

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FIGURE 99

CTTTTCTGAGGAACACAGCAATGAATGGCTTTGCATCCTTGCTTCGAAGAAACCAATTTATCCTCCTGGTACTA
TTTCTTTTGCAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCCTACCGCTGAAGTCTGTGCCACACACACA
ATTTCAACAGGACCCAAAGGAGATGATGGTGAAAAAGGAGATCCAGGAGAAGAGGGAAAGCATGGCAAAGTGGGA
CGCATGGGGCCGAAAGGAATTAAAGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCC
ATTGGGAAGAAGGGTGACAAAGGGGAAAAAGGTTTGCTTGGAATACCTGGAGAAAAAGGCAAAGCAGGTACTGTC
TGTGATTGTGGAAGATACCGGAAATTTGTTGGACAACCTGGATATTAGTATTGCTCGGCTCAAGACATCTATGAAG
TTTGTCAAGAATGTGATAGCAGGGATTAGGGAAACTGAAGAGAAATTTCTACTACATCGTGCAGGAAGAGAAGAAC
TACAGGGAATCCCTAACCCACTGCAGGATTCGGGGTGGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACA
CTCATCGCTGACTATGTTGCCAAGAGTGGCTTCTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAAGGGAGGGA
CAGTACATGTCCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGCGACCCCTAT
GGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTGCCATCTTACCATGTACTTT
GTCTGTGAGTTCATCAAGAAGAAAAAGTAACTTCCCTCATCCTACGTATTTGCTATTTTCTGTGACCGTCATTA
CAGTTATTGTTATCCATCCTTTTTTTCCTGATTGTACTACATTTGATCTGAGTCAACATAGCTAGAAAATGCTAA
ACTGAGGTATGGAGCCTCCATCATCAAAAAAAAAAAAAAAAAA

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FIGURE 100

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50980
><subunit 1 of 1, 277 aa, 1 stop
><MW: 30645, pI: 7.47, NX(S/T): 2
MNGFASILLRRNQFILLVLFLLQIQSLGLDIDSRPTAEVCATHTISPGPKGDDGEKGDPEEGKHGKVGRMGPKGI
KGELGDMGDQGNIGKTGPIGKKGDKGEKGLLGIPGEKGKAGTVCDGCRYRKFGVQLDISIARLKTSMKFVKNVIA
GIRETEEFYYIIVQEEKNYRESLTHCRIRGGMLAMPKDEAANTLIADYVAKSGFFRVFIGVNDLEREGQYMSTDN
TPLQNYSNWNEGEPSDPYGHEDCVEMLSGRWNDTECHLTMYFVCEFIKKKK
```

Signal peptide:
amino acids 1-25

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FIGURE 101

GCAACCTCAGCTTCTAGTATCCAGACTCCAGCGCCGCCCGGGCGCGGACCCCAACCCCGACCCAGAGCTTCTCC
AGCGGGCGGCGCAGCGAGCGAGGCTCCCCGCCTTAACTTCCTCCGCGGGGGCCAGCCACCTTCGGGAGTCCGGGTT
GCCACCTGCAAACCTCTCCGCCTTCTGCACCTGCCACCCCTGAGCCAGCGCGGGCCCCCGAGCGAGT**CATGGCCA**
ACGCGGGGCTGCAGCTGTTGGGCTTCATTCTCGCCTTCCTGGGATGGATCGGCGCCATCGTCAGCACTGCCCTGC
CCCAGTGGAGGATTTACTCCTATGCCGGCGACAACATCGTGACCGCCAGGCCATGTACGAGGGGCTGTGGATGT
CCTGCGTGTCGCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACATTGC
AAGCAACCCGTGCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGA
AGTGTATGAAGTGCTTGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGTGCGATATTTCTTC
TTGCAGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCATGA
CCCCAGTCAATGCCAGGTACGAATTTGGTCAAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCGCCTTCTGG
GAGGTGCCCTACTTTGCTGTTCTGTCCCCGAAAAACAACCTCTTACCCAACACCAAGGCCCTATCCAAAACCTG
CACCTTCCAGCGGGAAAGACTACGTG**TGAC**CACAGAGGCAAAAGGAGAAAATCATGTTGAAACAAACCGAAAAATGG
ACATTGAGATACTATCATTAAACATTAGGACCTTAGAATTTTGGGTATTGTAATCTGAAGTATGGTATTACAAAAC
AAACAAACAAACAAAAACCCATGTGTTAAATACTCAGTGCTAAACATGGCTTAATCTTATTTTATCTTCTTTC
CTCAATATAGGAGGAAGATTTTCCATTTGTATTACTGCTTCCCATTTAGTAATCATACTCAAATGGGGGAAGG
GGTGCTCCTTAAATATATATAGATATGTATATATACATGTTTTTCTATTAAAAATAGACAGTAAAATACTATTCT
CATTATGTTGATACTAGCATACTTAAATATCTCTAAATAGGTAAATGTATTTAATTCCATATTGATGAAGATG
TTTATTGGTATATTTTCTTTTTCGTCCTTATATACATATGTAACAGTCAAATATCATTTACTCTTCTTCATTAGC
TTTGGGTGCCTTTGCCACAAGACCTAGCCTAATTTACCAAGGATGAATCTTTCAATTCTTCATGCGTGCCCTTT
TCATATACTTATTTTATTTTACCATAATCTTATAGCACTTGCATCGTTATTAAGCCCTTATTTGTTTTGTGTT
TCATTGGTCTCTATCTCCTGAATCTAACACATTTATAGCCTACATTTTAGTTTCTAAAGCCAAGAAGAAATTTAT
TACAAATCAGAACTTTGGAGGCAAATCTTTCTGCATGACCAAAGTGATAAATTCCTGTTGACCTTCCACACAAT
CCCTGTACTCTGACCCATAGCACTCTTGTTTGCTTTGAAAATATTTGTCCAATTGAGTAGCTGCATGCTGTTCCC
CCAGGTGTTGTAACACAACCTTTATGATTGAATTTTTAAGCTACTTATTCATAGTTTTATATCCCCCTAAACTAC
CTTTTTGTTCCCATTCCTTAATTGTATTGTTTTCCCAAGTGTAATTATCATGCGTTTTATATCTTCTTAATAAG
GTGTGGTCTGTTTGTCTGAACAAAGTGCTAGACTTCTGGAGTGATAATCTGGTGACAAATATCTCTCTGTAGC
TGTAAGCAAGTCACTTAATCTTTCTACCTCTTTTTCTATCTGCCAAATTGAGATAATGATACTTAACCAAGTAG
AAGAGGTAGTGTAATATTAATTAGTTTATATTACTCTTATTCTTTGAACATGAACATGCCTATGTAGTGCTT
TATTTGCTCAGCTGGCTGAGACACTGAAGAAGTCACTGAACAAAACCTACACACGTACCTTCATGTGATTCACTG
CCTTCCTCTCTCTACCAGTCTATTTCCACTGAACAAAACCTACACACATACCTTCATGTGGTTCAGTGCCTTCCT
CTCTCTACCAGTCTATTTCCACTGAACAAAACCTACGCACATACCTTCATGTGGCTCAGTGCCTTCCTCTCTCTA
CCAGTCTATTTCCATTCTTTCACTGTGTCTGACATGTTTGTGCTCTGTTCCATTTTAACTGCTCTTACTTT
TCCAGTCTGTACAGAATGCTATTTCACTTGAGCAAGATGATGTAATGGAAAGGGTGTGGCACTGGTGTCTGGAG
ACCTGGATTTGAGTCTTGGTGCTATCAATCACCGTCTGTGTTTGAGCAAGGCATTTGGCTGCTGTAAGCTTATTG
CTTCATCTGTAAGCGGTGGTTTGTAAATTCCTGATCTTCCACCTCACAGTGATGTTGTGGGGATCCAGTGAGATA
GAATACATGTAAGTGTTGTTTGTAAATTTAAAAAGTGCTATACTAAGGGAAAGAATTGAGGAATTAACGCATAC
GTTTTGGTGTGCTTTTCAAATGTTTGAAAAATAAAAAAATGTTAAG

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FIGURE 102

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185
><subunit 1 of 1, 211 aa, 1 stop
><MW: 22744, pI: 8.51, NX(S/T): 1
MANAGLQLLGFI LAF LGWIGAIVSTALPQWRIYSYAGDNIVTAQAMYEG LWMSCVSQSTGQIQCKVFDSLNLSS
TLQATRALMVVGILLGVIAIFVATVGMKCMKCLEDDEVQKMRMAVIGGAIFLLAGLAILVATAWYGNRIVQEFYD
PMTFVNARYEFGQALFTGWAAASLCLLGALLCCSCPRKTTSYPTPRPYPKPAPSSGKD YV
```

Important features:**Signal peptide:**

amino acids 1-21

Transmembrane domains:

amino acids 82-102, 118-142 and 161-187

N-glycosylation site.

amino acids 72-75

PMP-22 / EMP / MP20 family proteins .

amino acids 70-111

ABC-2 type transport system integral membrane protein

amino acids 119-133

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FIGURE 103

CCCACGCGTCCGCGGACGCGTGGGCTGGACCCAGGTCTGGAGCGAATTCCAGCCTGCAGGGCTGATAAGCGAGG
CATTAGTGAGATTGAGAGAGACTTTACCCCGCGTGGTGGTTGGAGGGCGCGCAGTAGAGCAGCAGCACAGGCGC
GGGTCCCGGGAGGCGCGCTCTGCTCGCGCCGAGATGTGGAATCTCCTTCACGAAACCGACTCGGCTGTGGCCACC
GCGCGCCGCGCGCTGGCTGTGCGCTGGGGCGCTGGTGTGGCGGGTGGCTTCTTCTCCTCGGCTTCTCTTC
GGGTGGTTTATAAAATCCTCCAATGAAGCTACTAACATTACTCCAAAGCATAATATGAAAGCATTTTTGGATGAA
TTGAAAGCTGAGAACATCAAGAAGTTCTTACATAATTTTACACAGATACCACATTTAGCAGGAACAGAACAAAAC
TTTCAGCTTGCAAAGCAAATTCATCCCAGTGGAAGAATTTGGCCTGGATTCTGTTGAGCTAGCTCATTATGAT
GTCCTGTTGTCCTACCCAAATAAGACTCATCCCACTACATCTCAATAATTAATGAAGATGGAATGAGATTTTC
AACACATCATTTATTTGAACCACCTCCTCCAGGATATGAAAATGTTTCGGATATTGTACCACCTTTCAGTGCTTTC
TCTCCTCAAGGAATGCCAGAGGGCGATCTAGTGTATGTTAACTATGCACGAACTGAAGACTTCTTTAAATTGGAA
CGGGACATGAAAATCAATTGCTCTGGGAAAATTGTAATTGCCAGATATGGGAAAGTTTTCAGAGGAAATAAGGTT
AAAAATGCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTACTCCGACCCTGCTGACTACTTTGCTCCTGGGGTG
AAGTCCATATCCAGACGGTTGGAATCTTCTGGAGGTGGTGTCCAGCGTGGAAATATCCTAAATCTGAATGGTGCA
GGAGACCCTCTCACACCAGGTTACCCAGCAAATGAATATGCTTATAGGCGTGGAATTGCAGAGGCTGTTGGTCTT
CCAAGTATTCTGTTTCATCCAATTGGATACCTATGATGCACAGAAGCTCCTAGAAAAAATGGGTGGCTCAGCACC
CCAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGGCTTTACTGGAAAATTTTCTACA
CAAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGACGAGAATTTACAATGTGATAGGTACTCTCAGAGGA
GCAGTGGAACCAGACAGATATGTCATTCTGGGAGGTCAACGGGACTCATGGGTGTTTGGTGGTATTGACCCTCAG
AGTGGAGCAGCTGTTGTTTCATGAAATTGTGAGGAGCTTTGGAACACTGAAAAGGAAGGGTGGAGACCTAGAAGA
ACAATTTTGTGTTGCAAGCTGGGATGCAGAAGAATTTGGTCTTCTTGGTTCTACTGAGTGGGCAGAGGAGAATTCA
AGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTGACTCATCTATAGAAGGAACTACACTCTGAGAGTT
GATTGTACACCGCTGATGTACAGCTTGGTACACAACCTAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAA
GGCAAATCTCTTTATGAAAGTTGGACTAAAAAAGTCTTCCCCAGAGTTCAGTGGCATGCCAGGATAAGCAAA
TTGGGATCTGGAAATGATTTTGAGGTGTTCTTCCAACGACTTGGAATTGCTTCAGGCAGAGCACGGTATACTAAA
AATTTGGGAAACAAACAAATTCAGCGGCTATCCACTGTATCACAGTGTCTATGAAACATATGAGTTGGTGGAAAAG
TTTTATGATCCAATGTTTAAATATCACCTCACTGTGGCCCAGGTTTCAGAGAGGGATGGTGGTTTGGCTAGCCAAT
TCCATAGTGCTCCCTTTTGGATTGTGCGAGATTATGCTGTAGTTTTTAAGAAAGTATGCTGACAAAATCTACAGTATT
TCTATGAAACATCCACAGGAAATGAAGACATACAGTGTATCATTTGATTCACTTTTTTCTGCAGTAAAGAATTTT
ACAGAAATTGCTTCCAAGTTTCAGTGAGAGACTCCAGGACTTTGACAAAAGCAACCCAATAGTATTAAGAATGATG
AATGATCAACTCATGTTTCTGGAAAGAGCATTATTTGATCCATTAGGGTTACCAGACAGGCCTTTTTATAGGCAT
GTCATCTATGCTCCAAGCAGCCACAACAAGTATGCAGGGGAGTCATTCCCAGGAATTTATGATGCTCTGTTTGAT
ATTGAAAGCAAAGTGGACCTTCCAAGGCCTGGGGAGAAGTGAAGAGACAGATTTATGTTGCAGCCTTCACAGTG
CAGGCAGCTGCAGAGACTTTGAGTGAAGTAGCCTAAGAGGATTTTTTAGAGAATCCGTATTGAATTTGTGTGGTA
TGTCACTCAGAAAGAATCGTAATGGGTATATTGATAAATTTTAAATTTGGTATATTGAAATAAAGTTGAATATT
ATATATAA

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FIGURE 104

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA52756
><subunit 1 of 1, 750 aa, 1 stop
><MW: 84305, pI: 6.93, NX(S/T): 10
MWNLHETDSAVATARRPRWLCAGALVLAGGFFLLGFLFGWFIKSSNEATNITPKHNMKAFLDELKAENIKKFLH
NFTQIPHLAGTEQNFQLAKQIQSQWKEFGLDSVELAHYDVLLSYPNKTHPNYISIINEDGNEIFNTSLFEPPPPPG
YENVSDIVPPFSAFSPQGMPEGDLVYVNYARTEDFFKLERDMKINCSGKIVIARYGKVFRGNKVNAQLAGAKGV
ILYSDPADYFAPGVKSYPDGWNLPGGGVQQRGNILNLNGAGDPLTPGYPANAYARRGIAEAVGLPSIPVHPIGYY
DAQKLEKMGGSAPPDSSWRGSLKVPYNVGPFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRGAVEPDRYVILG
GHRDSWVFGGIDPQSGAAVVHEIVRSFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEWAEENSRLQERGVAYI
NADSSIEGNYTLRVDCTPLMYSLVHNLTKELKSPDEGFEGKSLYESWTKKSPSPEFSGMPRISKLGSGNDFEVFF
QRLGIASGRARYTKNWETNKFSGYPLYHSVYETYELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDY
AVVLRKYADKIYSISMKHPQEMKTYSVSFDLSFAVKNFTEIASKFSERLQDFDKSNPIVLRMMNDQLMFLERAF
IDPLGLPDRPFYRHVIYAPSSHNKYAGESFPGIYDALFDIESKVDPKAWGEVKRQIYVAAFTVQAAAETLSEVA
```

Signal sequence:

amino acids 1-40

N-glycosylation sites.amino acids 76-80, 121-125, 140-144, 153-157, 195-199, 336-340, 459-463,
476-480, 638-642**Tyrosine kinase phosphorylation sites.**

amino acids 363-372, 605-613, 606-613, 617-626

N-myristoylation sites.amino acids 85-91, 168-174, 252-258, 256-262, 282-288, 335-341, 360-366,
427-433, 529-535, 707-713

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FIGURE 105

TGAAGAGTAATAGTTGGAATCAAAAGAGTCAACGCAATGAAGTGTATTTACTGCTGCGTTTTATGTTGGGAATT
CCTCTCCTATGGCCTTGTCTTGGAGCAACAGAAAAGTCTCAAACAAAGAAAGTCAAGCAGCCAGTGGCATCTCAT
TTGAGAGTGAAGCGTGGCTGGGTGTGGAACCAATTTTTGTACCAGAGGAAATGAATACGACTAGTCATCACATC
GGCCAGCTAAGATCTGATTTAGACAATGGAAACAATTTCTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAGT
ACTTTTATCATTGATGAAAGAACAGGTGACATATATGCCATACAGAAGCTTGATAGAGAGGAGCGATCCCTCTAC
ATCTTAAGAGCCCAGGTAATAGACATCGTACTGGAAGGGCTGTGGAACCTGAGTCTGAGTTTGTTCATCAAAGTT
TCGGATATCAATGACAATGAACCAAAATTCCTAGATGAACCTTATGAGGCCATTGTACCAGAGATGTCTCCAGAA
GGAACATTAGTTATCCAGGTGACAGCAAGTGATGCTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCCTCTAC
AGCTTACTTCAAGGCCAGCCATATTTTTCTGTTGAACCAACAACAGGAGTCATAAGAATATCTTCTAAAATGGAT
AGAGAAGTGAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTGTCTGGA
ACAACAAGTGTATTAATAAAGTTCAGATGTTAATGACAATAAGCCTATATTTAAAGAAAAGTTTATACCGCTTG
ACTGTCTCTGAATCTGACCCACTGGGACTTCTATAGGAACAATCATGGCATATGATAATGACATAGGAGAGAAT
GCAGAAATGGATTACAGCATTGAAGAGGATGATTGCGAAACATTTGACATTATTACTAATCATGAACTCAAGAA
GGAATAGTTATATTAATAAAGAAAGTGGATTTTGAGCACCAGAACCACTACGGTATTAGAGCAAAAGTTAAAAAC
CATCATGTTCCCTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCCTTTCATTAAGATCCAGGTGGAAGAT
GTTGATGAGCCTCCTCTTTTCTCCTTCCATATTATGTTTGAAGTTTTTGAAGAAACCCACAGGGATCATT
GTAGGCGTGGTGTCTGCCACAGACCCAGACAATAGGAAATCTCCTATCAGGTATTCTATTACTAGGAGCAAAGTG
TTCAATATCAATGATAATGGTACAATCACTACAAGTAACTCACTGGATCGTGAAATCAGTGCTTGGTACAACCTA
AGTATTACAGCCACAGAAAAATACAATATAGAACAGATCTCTTCGATCCCACTGTATGTGCAAGTTCTTAACATC
AATGATCATGCTCCTGAGTTCTCTCAATACTATGAGACTTATGTTTGTGAAATGCAGGCTCTGGTCAGGTAATT
CAGACTATCAGTGCAGTGGATAGAGATGAATCCATAGAAGAGCACCATTTTACTTTAATCTATCTGTAGAAGAC
ACTAACAATTCAAGTTTTACAATCATAGATAATCAAGATAACACAGCTGTCATTTTGACTAATAGAAGTGGTTTT
AACCTTCAAGAAGAACCTGTCTTCTACATCTCCATCTTAATTGCCGACAATGGAATCCCGTCACTTACAAGTACA
AACACCCCTTACCATCCATGTCTGTGACTGTGGTGACAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTGTG
CTTTCCATGGGATTCAAGACAGAAGTTATCATTGCTATTCTCATTTGCATTATGATCATATTTGGGTTTTATTTTT
TTGACTTTGGGTTTAAAAACAACGGAGAAAACAGATTCTATTTCTGAGAAAAGTGAAGATTTTCAAGAGAAATATA
TTCCAATATGATGATGAAGGGGTGGAGAAGAAGATACAGAGGCCCTTTGATATAGCAGAGCTGAGGAGTAGTACC
ATAATGCGGGAACGCAAGACTCGGAAAACCAAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTT
GGCCCCGACAGTGCCATATTCAGGAAATTCATTCTGGAAGGCTCGAAGAAGCTAATACTGATCCGTGTGCCCT
CCTTTTGATTCCCTCCAGACCTACGCTTTTGAGGGAACAGGGTCATTAGCTGGATCCCTGAGCTCCTTAGAATCA
GCAGTCTCTGATCAGGATGAAAGCTATGATTACCTTAATGAGTTGGGACCTCGCTTTAAAGATTAGCATGCATG
TTTGGTTCTGCAGTGCAGTCAAATAATTAGGGCTTTTTACCATCAAATTTTTAAAGTGCTAATGTGTATTTCGA
ACCCAATGGTAGTCTTAAAGAGTTTTGTGCCCTGGCTCTATGGCGGGGAAAGCCCTAGTCTATGGAGTTTTCTGA
TTTCCCTGGAGTAAATACTCCATGGTTATTTTAAGCTACCTACATGCTGTCATTGAACAGAGATGTGGGGAGAAA
TGTAACAATCAGCTCACAGGCATCAATACAACCAGATTTGAAGTAAATAATGTAGGAAGATATTTAAAGTAGA
TGAGAGGACACAAGATGTAGTCGATCCTTATGCGATTATATCATTATTTACTTAGGAAAGAGTAAAAATACCAA
CGAGAAAATTTAAAGGAGCAAAATTTGCAAGTCAAATAGAAATGTACAAATCGAGATAACATTTACATTTCTAT
CATATTGACATGAAAATTGAAAATGTATAGTCAGAGAAATTTTCATGAATTATTCCATGAAGTATTGTTTCCTTT
ATTTAAA

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FIGURE 106

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906
><subunit 1 of 1, 772 aa, 1 stop
><MW: 87002, pI: 4.64, NX(S/T): 8
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SFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIATGRAVEPESEFVIKVSINDNEPKFLD
EPYEAIVPEMSPEGLTVIQVTASDADDPSSGNNARLLYSLLQGQPYFSVEPTTGVRIRISSKMDRELQDEYWVITQ
AKDMIGQPGALSGTTSVLIKLSDVNDNKPIFKESLYRLTVSESAPTGTSGITIMAYDNDIGENAEMDYSIEEDDS
QTFDIITNHETQEGIVILKKKVD FEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLLPY
VFEVFEETPQGSFVGVSATDPDNRKSPIRYSITRSKVFENINDNGTITTSNSLDREISAWYNLSITATEKYNIEQ
ISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTI SAVDRDESIEHHFYFNLSVEDTNNSSFTIIDNQ
DNTAVILTNRTGFNLQEEPVFYISILIIDNGIPSLTSTNTLTIHVCDGDSGSTQTCQYQELVLSMGFKTEVIIA
ILICIMIIFGFIFLTGLKQRRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTS
AEIRSLYRQSLQVGPDSAIFRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGSLAGSLSSLESAVSDQDESYDYL
NELGPRFKRLACMFGSAVQSNN
```

Important features:**Signal peptide:**

amino acids 1-21

Transmembrane domain:

amino acids 597-617

N-glycosylation sites.

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518, 516-519 and 534-537

Cadherins extracellular repeated domain signature.

amino acids 136-146 and 244-254

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FIGURE 107

ATCTGGTTGAACTACTTAAGCTTAATTTGTTAACTCCGGTAAGTACCTAGCCACATGATTTGACTCAGAGATT
CTCTTTTGTCCACAGACAGTCATCTCAGGGGCAGAAAGAAAGAGCTCCCAAATGCTATATCTATTTCAGGGGGCTC
TCAAGAACAATGGAATATCATCTGATTTAGAAAATTTGGATGAAGATGGATATACTCAATTACACTTCGACTCT
CAAAGCAATACCAGGATAGCTGTTGTTTCAGAGAAAAGGATCGTGTGCTGCATCTCCTCCTTGGCGCCTCATTGCT
GTAATTTTGGGAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCCTGGGTACCATGGGGGTTCTTTCCAGC
CCTTGTCCTCCTAATTGGATTATATATGAGAAGAGCTGTTATCTATTTCAGCATGTCACTAAATTCCTGGGATGGA
AGTAAAAGACAATGCTGGCAACTGGGCTCTAATCTCCTAAAGATAGACAGCTCAAATGAATTGGGATTTATAGTA
AAACAAGTGTCTTCCCAACCTGATAATTCATTTTGGATAGGCCTTTCTCGGCCCCAGACTGAGGTACCATGGCTC
TGGGAGGATGGATCAACATTCTCTTAACCTTATTTTCAGATCAGAACCACAGCTACCCAAGAAAACCCATCTCCA
AATTGTGTATGGATTACAGTGTCACTCATTATGACCAACTGTGTAGTGTGCCCTCATATAGTATTTGTGAGAAG
AAGTTTTCAATGTAAGAGGAAGGGTGGAGAAGGAGAGAGAAAATATGTGAGGTAGTAAGGAGGACAGAAAACAGAA
CAGAAAAGAGTAACAGCTGAGGTCAAGATAAATGCAGAAAATGTTTAGAGAGCTTGGCCAACCTGTAATCTTAACC
AAGAAATTGAAGGGAGAGGCTGTGATTTCTGTATTTGTGACCTACAGGTAGGCTAGTATTATTTTTCTAGTTAG
TAGATCCCTAGACATGGAATCAGGGCAGCCAAGCTTGAGTTTTTATTTTTTATTTATTTATTTTATTTTATTTT
GTCTCACTTTGTTACCCAGGCTGGAGTGCAGTGGCACAACTCTCGACTCACTGCAGCTATCTCTCGCCTCAGCCCC
TCAAGTAGCTGGGACTACAGGTGCATGCCACCATGCCAGGCTAATTTTTTGGTGTTTTTTGTAGAGACTGGGTTTT
GCCATGTTGACCAAGCTGGTCTCTAACTCCTGGGCTTAAGTGATCTGCCCGCCTTGGCCTCCCAAAGTGCTGGGA
TTACAGATGTGAGCCACCACACCTGGCCCCAAGCTTGAATTTTCATTCTGCCATTGACTTGGCATTACCTTGGG
TAAGCCATAAGCGAATCTTAATTTCTGGCTCTATCAGAGTTGTTTCATGCTCAACAATGCCATTGAAGTGCACGG
TGTGTTGCCACGATTTGACCCTCAACTTCTAGCAGTATATCAGTTATGAAGTGAAGGTGAAATATATTTCTGAAT
AGCTAAATGAAGAAATGGGAAAAAATCTTCACCACAGTCAGAGCAATTTTATTATTTTCATCAGTATGATCATAA
TTATGATTATCATCTTAGTAAAAAGCAGGAACCTCCTACTTTTTCTTTATCAATTAAATAGCTCAGAGAGTACATC
TGCCATATCTCTAATAGAATCTTTTTTTTTTTTTTTTTTTTTTTTGTAGACAGAGTTTCGCTCTTGTTGCCAGGCTG
GAGTGCAACGGCAGCATCTCGGCTCACCGCAACCTCCGCCCCCTGGGTTCAAGCAATTCCTGCTCAGCCTCC
CAAGTAGCTGGGATTACAGTCAGGCACCACCACACCCGGCTAATTTTGTATTTTTTTAGTAGAGACAGGGTTTCT
CCATGTCGGTCAGGCTAGTCCCGAACTCCTGACCTCAAGTGATCTGCCTGCCTCGGCCTCCCAAGTGCTGGGATT
ACAGGCGTGAGCCACTGCACCCAGCCTAGAATCTTGTATAATATGTAATTGTAGGGAACTGCTCTCATAGGAAA
GTTTTCTGCTTTTTTAAATACAAAATACATAAAAATACATAAAATCTGATGATGAATATAAAAAAGTAACCAACC
TCATTGGAACAAGTATTAACATTTTGAATATGTTTTATTAGTTTTGTGATGTACTGTTTTACAATTTTACCAT
TTTTTTCAGTAATTACTGTAAAATGGTATTATTGGAATGAACTATATTTCTCATGTGCTGATTTGTCTTATTT
TTTTCATACTTTCCCACTGGTGCTATTTTTATTTCCAATGGATATTTCTGTATTACTAGGGAGGCATTTACAGTC
CTCTAATGTTGATTAATATGTGAAAAGAAATGTACCAATTTTACTAAATTATGCAGTTTAAATGGATGATTTT
ATGTTATGTGGATTTCAATTAATAAAAAAACTCTTATCAAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 108

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53912
<subunit 1 of 1, 201 aa, 1 stop
<MW: 22563, pI: 4.87, NX(S/T): 1
MEYHPDLENLDEEDGYTQLHFDSQSNTRIAVVSEKGSAAASPPWRLLIAVILGILCLVILVIAVVLGTMGVLSSPCP
PNWIIYEKSCYLFMSLSNSWDGSKRQCWQLGSNLLKIDSSNELGFIVKQVSSQPDNSFWIGLSRPQTEVPWLWED
GSTFSSNLFQIRTTATQENPSPNCVWIHVSVIYDQLCSVPSYSICEKKFSM

Important features:**Type II transmembrane domain:**

amino acids 45-65

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 197-200

N-myristoylation sites.

amino acids 35-40 and 151-156

Homologous region to LDL receptor

amino acids 34-67 and 70-200.

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FIGURE 109

CTGCAAGTTGTTAACGCCTAACACACAAGTATGTTAGGCTTCCACCAAAGTCTCAATATACCTGAATACGCACA
ATATCTTAACTCTTCATATTTGGTTTTGGGATCTGCTTTGAGGTCCCATCTTCATTTAAAAAAAATACAGAGAC
CTACCTACCCGTACGCATACATATATGTGTATATATATGTAAACTAGACAAAGATCGCAGATCATAAAGCAAG
CTCTGCTTTTAGTTTTCCAAGAAGATTACAAAGAATTTAGAGATGTTATTTGTCAAGATCCCTGTGCTGATTTCATGCCCT
TTGGGTTACGGTGTCTCAGTGATGCAGCCCTACCCTTTGGTTTGGGGACATTATGATTTGTGTAAGACTCAGAT
TTACACGGAAGAAGGGAAAGTTTGGGATTACATGGCCTGCCAGCCGAATCCACGGACATGACAAAATATCTGAA
AGTGAAACTCGATCCTCCGGATATTACCTGTGGAGACCCTCCTGAGACGTTCTGTGCAATGGGCAATCCCTACAT
GTGCAATAATGAGTGTGATGCGAGTACCCCTGAGCTGGCACACCCCTGAGCTGATGTTTGATTTTGAAGGAAG
ACATCCCTCCACATTTTGGCAGTCTGCCACTTGAAGGAGTATCCCAAGCCTCTCCAGGTAAACATCACTCTGTC
TTGGAGCAAACCATTGAGCTAACAGACAACATAGTTATTACCTTTGAATCTGGGCGTCCAGACCAAATGATCCT
GGAGAAGTCTCTCGATTATGGACGAACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTAGATGCTTTTCA
CATGGATCCTAAATCCGTGAAGGATTTATCACAGCATAACGGTCTTAGAAATCATTTGCACAGAAGAGTACTCAAC
AGGGTATACAACAAATAGCAAAATAATCCACTTTGAAATCAAAGACAGGTTGCGGCTTTTTGCTGGACCTCGCCT
ACGCAATATGGCTTCCCTCTACGGACAGCTGGATACAACCAAGAACTCAGAGATTTCTTTACAGTCACAGACCT
GAGGATAAGGCTGTTAAGACCAGCCGTGGGGAAATATTTGTAGATGAGCTACACTTGGCAGCTACTTTTACGC
GATCTCAGACATAAAGGTGCGAGGAAGGTGCAAGTGTAACTCTCCATGCCACTGTATGTGTATGACAACAGCAA
ATTGACATGCCAATGTGAGCACAACTACAGTCCAGACTGTGGGAAATGCAAGAAGAATTATCAGGGCCGACC
TTGGAGTCCAGGCTCCTATCTCCCATCCCCAAGGCACCTGCAAATACCTGTATCCCCAGTATTTCCAGTATTGG
TACGAATGTCTGCGACAACGAGCTCCTGCACTGCCAGAACGGAGGGACGTGCCACAACAACGTGCGCTGCCTGTG
CCCCGCCGCATACACGGGCATCCTCTGCGAGAAGCTGCGGTGCGAGGAGGCTGGCAGCTGCGGCTCCGACTCTGG
CCAGGGCGCGCCCCCGCACGGCACCCAGCGCTGCTGCTGCTGACCACGCTGCTGGGAACCGCCAGCCCCCTGGT
GTTCTAGTGTACCTCCAGCCACACCGGACGGCCCTGTGCCGTGGGGAAGCAGACACAACCCAAACATTTGCTA
CTAACATAGGAAACACACACATACAGACACCCCCACTCAGACAGTGTACAAACTAAGAAGGCCCTAACTGAACTAA
GCCATATTTATCACCCGTGGACAGCACATCCGAGTCAAGACTGTTAATTTCTGACTCCAGAGGAGTTGGCAGCTG
TTGATATTATCACTGCAAATCACATTGCCAGCTGCAGAGCATATTGTGGATTGGAAAGGCTGCGACAGCCCCCA
AACAGGAAAGACAAAAACAAACAAATCAACCGACCTAAAAACATTGGCTACTCTAGCGTGGTGCGCCCTAGTAC
GACTCCGCCCAGTGTGTGGACCAACCAATAGCATTCTTTGCTGTGAGGTGCATTGTGGGCATAAGGAAATCTGT
TACAAGCTGCCATATTGGCCTGCTTCCGTCCCTGAATCCCTTCAAACCTGTGCTTTAGTGAACGTTGCTCTGTAA
CCCTCGTTGGTTGAAAGATTTCTTTGTCTGATGTTAGTGATGCACATGTGTAACAGCCCCCTTAAAAAGCGCAAG
CCAGTCATACCCCTGTATATCTTAGCAGCACTGAGTCCAGTGCGAGCACACCCCACTATACAAGAGTGGCTATA
GGAAAAAGAAAGTGTATCTATCCTTTTGTATTCAAATGAAGTTATTTTCTTGAACACTGTAAATATGTAGATT
TTTTGTATTATTGCCAATTTGTGTTACCAGACAATCTGTTAATGTATCTAATTGCAATCAGCAAAGACTGACATT
TTATTTTGTCTCTTTCTGTTCTGTTTGTCTTCACTGTGCAGAGATTTCTCTGTAAGGGCAACGAACGTGCTGGCA
TCAAAGAATATCAGTTTACATATATAACAAGTGTAAAGATTCCACCAAAGGACATTCTAAATGTTTTCTTGT
GCTTTAACACTGGAAGATTTAAAGAATAAAAACTCCTGCATAAACGATTTAGGAATTTGTATTGCAATTTCTTA
AGATGAAAGGAACAGCCACCAAGCAGTTTCACTCACTTTACTGATTTCTGTGTGGACTGAGTACATTCAGCTG
ACGAATTTAGTTCCAGGAAGATGGATTGATGTTCACTAGCTTGGACAACCTCTGCAAAATATGAGACTATTTCC
ACTTGGGAAAAATTACAACAGCAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 110

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLKVKLDPPDITCGDP
PETFCAMGNPYMCNNECDASTPELAHPPELMFDFEGRHPSTFWQSATWKEYPKPLQVNITLSWSKTIELTDNIVI
TFESGRPDQMLEKSLDYGRWQPYQYYATDCLDAFHMDPKSVKDLSQHTVLEIICTEEYSTGYTTNSKIIHFEI
KDRFALFAGPRLRNMASLYGQLDTTKKLRDFFVTDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCN
LHATVCVYDNSKLTCECEHNTTGPDCGKCKKNYQGRPWSPGSYLPIPKGTANTCIPSISSIGTNVCDNELLHCQN
GGTCHNNVRCLCPAAYTGILCEKLRCEEAGSCGSDSGQGAPPHGTPALLLLTTLLGTASPLVF

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FIGURE 111

GCGTGCCGTCAGCTCGCCGGGCACCGCGGCCTCGCCCTCGCCCTCCGCCCTGCGCCTGCACCGCGTAGACCGAC
CCCCCCTCCAGCGCGCCACCCGGTAGAGGACCCCCGCCCGTGCCCCGACCGGTCCCCGCCCTTTTGTAAAACT
TAAAGCGGGCGCAGCATTAAACGCTTCCCGCCCCGGTGACCTCTCAGGGGTCTCCCCGCCAAAGGTGCTCCGCCGC
TAAGGAACATGGCGAAGGTGGAGCAGGTCTGAGCCTCGAGCCGCGAGCAGAGCTCAAATTCGAGGTCCCTTCA
CCGATGTTGTCACCACCAACCTAAAGCTTGGCAACCCGACAGACCGAAATGTGTGTTTTAAGGTGAAGACTACAG
CACCACGTAGGTACTGTGTGAGGCCCAACAGCGGAATCATCGATGCAGGGGCTCAATTAATGTATCTGTGATGT
TACAGCCTTTTCGATTATGATCCCAATGAGAAAAGTAAACACAAGTTTATGGTTCAGTCTATGTTTGCTCCAACTG
ACACTTCAGATATGGAAGCAGTATGGAAGGAGGCAAAACCGGAAGACCTTATGGATTCAAACTTAGATGTGTGT
TTGAATTGCCAGCAGAGAATGATAAACACATGATGTAGAAATAAATAAAATTATATCCACAACATGCATCAAAGA
CAGAAACACCAATAGTGTCTAAGTCTCTGAGTTCTTCTTTGGATGACACCGAAGTTAAGAAGGTTATGGAAGAAT
GTAAGAGGCTGCAAGGTGAAGTTCAGAGGCTACGGGAGGAGAACAGCAGTTCAAGGAAGAAGATGGACTGCCGA
TGAGGAAGACAGTGCAGAGCAACAGCCCCATTTCAGCATTAGCCCCAACTGGGAAGGAAGAAGGCCTTAGCACCC
GGCTCTTGGCTCTGGTGGTTTTGTTCTTTATCGTTGGTGAATTATTGGGAAGATTGCCTTGTAGAGGTAGCATG
CACAGGATGGTAAATTGGATTGGTGGATCCACCATATCATGGGATTTAAATTTATCATAACCATGTGTAAAAAGA
AATTAATGTATGATGACATCTCACAGGTCTTGCCCTTTAAATTACCCCTCCCTGCACACACATACACAGATACACA
CACACAAATATAATGTAACGATCTTTAGAAAGTTAAAAATGTATAGTAACTGATTGAGGGGAAAAAGAATGAT
CTTTATTAATGACAAGGGAAACCATGAGTAATGCCACAATGGCATATTGTAAATGTCATTTTAAACATTGGTAGG
CCTTGGTACATGATGCTGGATTACCTCTCTTAAATGACACCCCTTCTCGCCTGTTGGTGTGGCCCTTGGGGAG
CTGGAGCCCAGCATGCTGGGGAGTGCGGTGAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGCCCCAGGCT
GCTTTCCGTGTCTTCAGTTCGTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAA
TTGCACTGTGGCAGCATCAGACGTAATCGTCATAAGTGAGAGGCGTGTGTGACTGATTGACCCAGCGCTTTGGA
AATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAAC TG
TTATTCAGAGATGTTTAATGCATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGT
ACAGTTAATGCTGCGTGCTGCTGAACTCTGTTGGGTGAAGTGGTATTGCTGCTGGAGGGCTGTGGGCTCCTCTGT
CTCTGGAGAGTCTGGTCATGTGGAGGTGGGGTTTATTGGGATGCTGGAGAAGAGCTGCCAGGAAGTGTTTTTCT
GGGTGAGTAAATAACAACGTGTCATAGGGAGGGAAATTCTCAGTAGTGACAGTCAACTCTAGGTTACCTTTTTTAA
TGAAGAGTAGTCAGTCTTCTAGATTGTTCTTATACCACCTCTCAACCATTACTCACACTCCAGCGCCCGAGTCC
AAGTCTGAGCCTGACCTCCCCTTGGGGACCTAGCCTGGAGTCAGGACAAATGGATCGGGCTGCAGAGGGTTAGAA
GCGAGGGCACACAGCAGTTGTGGGTGGGGAGCAAGGAAGAGAGAACTCTTCAGCGAATCCTTCTAGTACTAGTT
GAGAGTTTGACTGTGAATTAATTTTATGCCATAAAAGACCAACCCAGTTCTGTTTGACTATGTAGCATCTTGAAA
AGAAAAATTATAATAAAGCCCCAAATTAAGAAAA

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FIGURE 112

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53977

<subunit 1 of 1, 243 aa, 1 stop

<MW: 27228, pI: 7.43, NX(S/T): 2

MAKVEQVLSLEPQHELKFRGPFDTDVVTNLKLGNPTRNVCFKVKTTAPRRYCVRPNNGIIDAGASINVSVMLOP
FDYDPNEKSKHKFMVQSMFAPDTSDMEAVWKEAKPEDLMDSKLRCVFELPAENDKPHDVEINKIISTASKTET
PIVSKSLSSSLDDTEVKKVMEECKRLQGEVQRLREENKQFKEEDGLRMRKTVQSNPISALAPTGKEEGLSTRLL
ALVVLFFIVGVIIGKIAL**Important features:****Transmembrane domain:**

amino acids 224-239

N-glycosylation site.

amino acids 68-71

N-myristoylation site.

amino acids 59-64, 64-69 and 235-240

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FIGURE 113

CCCACGCGTCCGGGTGACCTGGGCCGAGCCCTCCCGGTCCGGCTAAGATTGCTGAGGAGGCGCGGGTAGCTGGCA
GGCGCCGACTTCCGAAGGCCGCCGTCCGGGCGAGGTGTCCTCATGACTTCTCTTGTGGACCATGTCCGTGATCTT
TTTTGCCTGCGTGGTACGGGTAAGGGATGGACTGCCCCCTCTCAGCCTCTACTGATTTTTACCACACCCAAGATTT
TTTGGAATGGAGGAGACGGCTCAAGAGTTTAGCCTTGCGACTGGCCCAGTATCCAGGTGAGGTTCTGCAGAAGG
TTGTGACTTTAGTATACATTTTTCTTCTTTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCCAGC
AGCCATGGCCTTCTGCTTCCTGGAGACCCTGTGGTGGGAATTCACAGCTTCCTATGACACTACCTGCATTGGCCT
AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTCAGAAAGTGAAGTGGCATTTTAACTATGTAAG
TTCCTCTCAGATGGAGTGCAGCTTGAAAAAATTCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGGTTCTCACTCT
GGAGGACACAGATGTGGCAAATGGGGTGATGAATGGTCACACACCGATGCACTTGGAGCCTGCTCCTAATTTCCG
AATGGAACCACTGACAGCCCTGGGTATCCTCTCCCTCATTCTCAACATCATGTGTGCTGCCCTGAATCTCATTCG
AGGAGTTCACCTTGCAGAACATTCTTTACAGGATCCAAGGAGCTGGTCTGCTGGTTGGACCAAACCTCGTGAGC
CAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCATCCGGGAGCAGTGATGTCAAACCTTCTGCTGCTG
GGGAAATCTCATCAGCAGGGAGCCTGTGGAAAAGGGCATGTCAGTGAAATCTGGGAATGGCTGGATTCCGGAAACA
TCTGCCCATGTGTATTGATGGCAGAGCTGTGCCCACAAGCGCCTTTTATTTAGGGTAAATTAACAAATCCATT
CTATTCCTCTGACCCATGCTTAGTACATATGACCTTTAACCCTTACATTTATATGATTCTGGGGTTGCTTCAGAA
GTGTTATTTTCATGAATCATTCATATGATTTGATCCCCCAGGATTCTATTTTGTTTAATGGGCTTTTCTACTAAAA
GCATAAAATACTGAGGCTGATTTAGTCAGGGCAAACCATTTACTTTACATATTCGTTTTCAATACTTGCTGTTC
ATGTTACACAAGCTTCTTACGGTTTTCTTGTAACAATAAATATTTTGAGTAAATAATGGGTACATTTTAACAAAC
TCAGTAGTACAACCTAACTTGTATAAAAGTGTGTAAAAATGTATAGCCATTTATATCCTATGTATAAATTAAT
GAGGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTTTATTAAAAAAAAAAAAAAAAAAAAAAAG

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FIGURE 114

MSVIFACVVRVDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFSIHFSFSGDVACMAICS
CQCPAAMAFCFLETLWWEFTASYDTTCIGLASRPYAFLEFDSIIQKVWHFNYVSSSQMECSLEKIQEELKLQPP
AVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPVTALGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS

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FIGURE 115

CTCAGCGGGCGCTTCCTCGTAGCGAGCCTAGTGCGGGGTGTTTGCATTGAAACGTGAGCGCGACCCGACCTTAAAG
AGTGGGGAGCAAAGGGAGGACAGAGCCCTTTAAAACGAGGCGGGTGGTGCTGCCCTTTAAGGGCGGGCGTCC
GGACGACTGTATCTGAGCCCCAGACTGCCCGAGTTTCTGTGCGAGGCTGCGAGGAAAGGCCCTAGGCTGGGTC
TGGGTGCTTGGCGGGCGGGCGCTTCCTCCCCGCTCGTCTCCCCGGGGCCAGAGGCACCTCGGCTTCAGTCATGCT
GAGCAGAGTATGGAAGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAG
TGTATTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCTGACCCGCTTCAAGAAGCCT
GCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGCGCTCGAGCTGTGCACCTTTACCCCTG
GCAATTGCCCTGGGTGCTGTCTGCTCCTGCCCTTCTCCATCATCAGCAATGAGGTGCTGCTCTCCCTGCCCTCGG
AACTACTACATCCAGTGGCTCAACGGCTCCCTCATCCATGGCCTCTGGAACCTTGTTTTTCTCTTCCCCAACCTG
TCCCTCATCTTCTCATGCCCTTTGCATATTTCTTCACTGAGTCTGAGGGCTTTGCTGGCTCCAGAAAGGGTGTC
CTGGGCGGGTCTATGAGACAGTGGTGATGTTGATGCTCCTCACTCTGCTGGTGCTAGGTATGGTGTTGGGTGGCA
TCAGCCATTGTGGACAAGAACAAGGCCAACAGAGAGTCACTCTATGACTTTTGGGAGTACTATCTCCCTACCTC
TACTCATGCATCTCCTTCTTGGGGTCTGCTGCTCCTGGTGCTACTCCACTGGGTCTCGCCCGCATGTTCTCC
GTCACCTGGGAAGCTGCTAGTCAAGCCCCGGCTGCTGGAAGACCTGGAGGAGCAGCTGTACTGCTCAGCCTTTGAG
GAGGCAGCCCTGACCCGCGAGGATCTGTAATCCTACTTCTGCTGGCTGCCCTTAGACATGGAGCTGCTACACAGA
CAGGTCTGGCTCTGCAGACACAGAGGGTCTGCTGGAGAAGAGGCGGAAGGCTTCAGCCTGGCAACGGAACCTG
GGCTACCCCTGGCTATGCTGTGCTTGCTGGTGCTGACGGGCCTGTCTGTGCTCATTGTGGCCATCCACATCCTG
GAGCTGCTCATCGATGAGGCTGCCATGCCCGAGGCATGCAGGGTACCTCCTTAGGCCAGGTCTCCTTCTCCAAG
CTGGGCTCCTTTGGTGCCGTCAATCAGGTTGTACTCATCTTTTACCTAATGGTGCTCTCAGTTGTGGGCTTCTAT
AGCTCTCCACTCTTCCGGAGCCTGCGGCCCCAGATGGCACGACACTGCCATGACGCAGATAATTGGGAAGTGTGTC
TGTCTCCTGGTCTTAAGCTCAGCACTTCTGTCTTCTCTCGAACCCTGGGGCTCACTCGCTTTGACCTGCTGGGT
GACTTTGGACGCTTCAACTGGCTGGGCAATTTCTACATTGTGTTCTCTACAACGCAGCCTTTGCAGGCTCACC
ACACTCTGTCTGGTGAAGACCTTCACTGCAGCTGTGCGGGCAGAGCTGATCCGGGCCTTTGGGCTGGACAGACTG
CCGCTGCCCGTCTCCGGTTTCCCCAGGCATCTAGGAAGACCCAGCACCAGTGAACCTCCAGCTGGGGGTGGGAAG
GAAAAAAGTGGACACTGCCATCTGCTGCCTAGGCCTGGAGGGAAGCCCAAGGCTACTTGGACCTCAGGACCTGGA
ATCTGAGAGGGTGGGTGGCAGAGGGGAGCAGAGCCATCTGCACTATTGCATAATCTGAGCCAGAGTTTGGGACCA
GGACCTCCTGCTTTTCCATACTTAAGTGTGGCCTCAGCATGGGGTAGGGCTGGGTGACTGGGTCTAGCCCCCTGAT
CCCAAATCTGTTTACACATCAATCTGCCTCACTGCTGTTCTGGGCCATCCCCATAGCCATGTTTACATGATTGA
TGTGCAATAGGGTGGGGTAGGGGCAGGGAAGGACTGGGCCAGGGCAGGCTCGGGAGATAGATTGTCTCCCTTGC
CTCTGGCCCAGCAGAGCCTAAGCACTGTGCTATCCTGGAGGGGCTTTGGACCACCTGAAAGACCAAGGGGATAGG
GAGGAGGAGGCTTCAGCCATCAGCAATAAAGTTGATCCCAGGGAAAAAA

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FIGURE 116

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDEDATVNKIALELCTFTLAIA
LGAVLLLPFSIISNEVLLSLPRNYIQWLNGSLIHGLWNLVFLFPNLSLIFLMPFAYFFTESEGFAGSRKGV LGR
VYETVVMMLLLTLLVLGMVWVASAIVDKNKANRESLYDFWEYYPYLYSCISFLGVLLLLVCTPLGLARMFSVTG
KLLVKPRILLEDLEEQLYCSAFEEAALTRRICNPTSCWLPLDMELLHRQVLALQTVLLEKRRKASAWQRNLGYP
LAMLCLLVLTGLSVLIVAIHILELLIDEAAMPGRMQGTSLGQVSFSKLGSFGAVIQVVLIFYLMVSSVVGIFYSSP
LFRSLRPRWHDAMTQIIIGNCVCLLVLSALPVFSRTLGLTRFDLLGDFGRENWLGNFYIVFLYNAAFAGLTTLC
LVKTFTAAVRAELIRAFGLDRLPLPVSGFPQASRKTQHQ

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FIGURE 117

GAGAACAGGCCTGTCTCAGGCAGGCCCTGCGCCTCCTATGCGGAGATGCTACTGCCACTGCTGCTGTCTCGCTG
CTGGGCGGGTCCCAGGCTATGGATGGGAGATTCTGGATACGAGTGCAGGAGTCACTGATGGTGCCGGAGGGCCTG
TGCACTCTGTGCCCTGCTCTTTCTCCTACCCCGACAAGACTGGACAGGGTCTACCCAGCTTATGGCTACTGG
TTCAAAGCAGTGACTGAGACAACCAAGGGTGCTCCTGTGGCCACAAACCACAGAGTCGAGAGGTGGAAATGAGC
ACCCGGGGCCGATTCCAGCTCACTGGGGATCCCGCCAAGGGGAACTGCTCCTTGGTGATCAGAGACGCGCAGATG
CAGGATGAGTCACAGTACTTCTTTCTGGGTGGAGAGAGGAAGCTATGTGACATATAATTTTATGAACGATGGGTTT
TTTCTAAAAGTAACAGTGCTCAGCTTCACGCCCAGACCCCAGGACCACACACCCGACCTCACCTGCCATGTGGAC
TTCTCCAGAAAGGGTGTGAGCGCACAGAGGACCGTCCGACTCCGTGTGGCCTATGCCCCAGAGACCTTGTTATC
AGCATTTACGTGACAACACGCCAGCCCTGGAGCCCCAGCCCCAGGGAAATGTCCCATACCTGGAAGCCCCAAAA
GGCCAGTTCTGCGGCTCCTCTGTGCTGCTGACAGCCAGCCCCCTGCCACACTGAGCTGGGTCTGCGAGAACAGA
GTCTCTCCTCGTCCCATCCCTGGGGCCCTAGACCCCTGGGGCTGGAGCTGCCGGGGTGAAGGCTGGGGATTCA
GGGCGCTACACCTGCCGAGCGGAGAACAGGCTTGGCTCCCAGCAGCGAGCCCTGGACCTCTCTGTGCAGTATCCT
CCAGAGAACCTGAGAGTGATGGTTTCCCAAGCAAACAGGACAGTCTGGAAAACCTTGGGAACGGCAGCTCTCTC
CCAGTACTGGAGGGCCAAAGCCTGTGCCCTGGTCTGTGTACACACAGCAGCCCCCAGCCAGGCTGAGCTGGACC
CAGAGGGGACAGGTTCTGAGCCCCCTCCAGCCCTCAGACCCCGGGGTCTGGAGCTGCCTCGGGTTCAAGTGGAG
CAGGAAGGAGAGTTACCTGCCACGCTCGGCACCCACTGGGCTCCAGCACGTCTCTCAGCCTCTCCGTGCAC
TATAAGAAGGGACTCATCTCAACGGCATTCTCCAACGGAGCGTTTCTGGGAATCGGCATCACGGCTCTTCTTTTC
CTCTGCCCTGGCCCTGATCATCATGAAGATTCTACCGAAGAGACGGACTCAGACAGAAACCCGAGGCCCAGGTTT
TCCCGGCACAGCACGATCCTGGATTACATCAATGTGGTCCCGACGGCTGGCCCCCTGGCTCAGAAGCGGAATCAG
AAAGCCACACCAAACAGTCTCGGACCCCTCCTCCACCAGGTGCTCCCTCCCCAGAATCAAAGAAGAACAGAAA
AAGCAGTATCAGTTGCCCAGTTTCCCAAGACCCAAATCATCCACTCAAGCCCCAGAATCCCAGGAGAGCCAAGAG
GAGCTCCATTATGCCACGCTCAACTTCCAGGCGTCAGACCCAGGCTGAGGCCCCGATGCCCAAGGGCACCCAG
GCGGATTATGCAGAAGTCAAGTTCCAATGAGGGTCTCTTAGGCTTTAGGACTGGGACTTCGGCTAGGGAGGAAGG
TAGAGTAAGAGGTTGAAGATAACAGAGTGCAAAGTTTCTTCTCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT
CTCTTTCTCTCTCTTTTAAAAAACATCTGGCCAGGGCACAGTGGCTCACGCCCTGTAATCCAGCACTTTGGGAG
GTTGAGGTGGGCAGATCGCCTGAGGTGGGAGTTGAGAGACCAGCCTGGCCAACTTGGTGAAACCCCGTCTCTACT
AAAAATACAAAATTAGCTGGGCATGGTGGCAGGCGCCTGTAATCCTACCTACTTGGGAAGCTGAGGCAGGAGAA
TCACTTGAACCTGGGAGACGGAGGTTGCAGTGAGCCAAGATCACACCATTGCACGCCAGCCTGGGCAACAAAGCG
AGACTCCATCTCAAAAAAAAATCCTCCAAATGGGTGGGTGTCTGTAATCCAGCACTTTGGGAGGCTAAGGTG
GGTGGATTGCTTGAGCCAGGAGTTCGAGACCAGCCTGGGCAACATGGTGAAACCCCATCTCTACAAAAAATACA
AAACATAGCTGGGCTTGGTGGTGTGTGCCTGTAGTCCCAGCTGTGACACATTTAAACCAGAGCAACTCCATCTGG
AATAGGAGCTGAATAAAATGAGGCTGAGACCTACTGGGCTGCATTCTCAGACAGTGGAGGCATTCTAAGTCACAG
GATGAGACAGGAGTCCGTACAAGATACAGGTATAAAGACTTTGCTGATAAAACAGATTGCAGTAAAGAAGCCA
ACCAATCCCACCAAACCAAGTTGGCCACGAGAGTGACCTCTGGTGTCTCTACTGCTACACTCCTGACAGCAC
CATGACAGTTTACAAATGCCATGGCAACATCAGGAAGTTACCCGATATGTCCCAAAGGGGGAGGAATGAATAAT
CCACCCCTTGTTTTAGCAAATAAGCAAGAAATAACCATAAAAGTGGGCAACCAGCAGCTCTAGGCGCTGCTCTTGT
CTATGGAGTAGCCATTCTTTGTTCTTTACTTTCTTAATAAACTTGCTTTACCTTAAAAAAA

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FIGURE 118

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA54002
><subunit 1 of 1, 544 aa, 1. stop
><MW: 60268, pI: 9.53, NX(S/T): 3
MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSPYPRQDWTGSTPAYGYWFKAVTETTKGAPVAT
NHQSREVEEMSTRGRFQLTGDPKAGNCSLVIRDAQMQDESQYFFRVERGSYVTYNFMNDGFFLKVTVLSFTPRPQD
HNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVISISRDNTPALEPQQQGNVPYLEAQKGQFLRLLCAADSQPP
ATLSWVLQNRVLSSSHPWGPRPLGLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTV
LENLGNGTSLPVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHPLGS
QHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLFLCLALIIMKILPKRRTQTETPRPRFSRHSTILDYINVVPT
AGPLAQKRNQKATPNSPRTPPPPGAPSPESKKNQKKQYQLPSFPEPKSSTQAPESQESQEELHYATLNFPGVRPR
PEARMPKGTQADYAEVKFQ
```

Important features:**Signal peptide:**

amino acids 1-15

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 100-103, 297-300 and 306-309

Immunoglobulins and major histocompatibility complex proteins signature.

amino acids 365-371

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FIGURE 119

CTCGCGCAGGGATCGTCCC**ATG**GCCGGGGCTCGGAGCCGCGACCCCTTGGGGGGCCTCCGGGATTTGCTACCTTTT
TGGCTCCCTGCTCGTGAAGTCTCTTCTACGGGCTGTGCGCTTCAATCTGGACGTGATGGGTGCCTTGCSCAA
GGAGGGCGAGCCAGGCAGCCTCTTCGGCTTCTCTGTGGCCCTGCACCGGCAGTTGCAGCCCCGACCCAGAGCTG
GCTGCTGGTGGGTGCTCCCCAGGCCCTGGCTCTTCTGGGCAGCAGGCGAATCGCACTGGAGGCCTCTTCGCTTG
CCCGTTGAGCCTGGAGGAGACTGACTGCTACAGAGTGGACATCGACCAGGGAGCTGATATGCAAAAGGAAAGCAA
GGAGAACCAGTGGTTGGGAGTCAGTGTTCCGGAGCCAGGGGCCTGGGGGCAAGATTGTTACCTGTGCACACCGATA
TGAGGCAAGGCAGCGAGTGGACCAGATCCTGGAGACGCGGGATATGATTGGTCGCTGCTTTGTGCTCAGCCAGGA
CCTGGCCATCCGGGATGAGTTGGATGGTGGGAATGGAAGTTCTGTGAGGGACGCCCCCAAGGCCATGAACAATT
TGGGTTCTGCCAGCAGGGCACAGCTGCCGCCTTCTCCCTGATAGCCACTACCTCCTCTTTGGGGCCCCAGGAAC
CTATAATTGGAAGGGCACGGCCAGGGTGGAGCTCTGTGCACAGGGCTCAGCGGACCTGGCACACCTGGACGACGG
TCCCTACGAGGCGGGGAGAGAAGGAGCAGGACCCCGCCTCATCCCGTCCCTGCCAACAGCTACTTTGGCTT
CTCTATTGACTCGGGGAAAGGTCTGGTGCGTGCAGAAAGAGCTGAGCTTTGTGGCTGGAGCCCCCGCGCCAAACCA
CAAGGGTGTGTGGTCTCCTGCGCAAGGACAGCGCCAGTGCCTGGTGGCCGAGGTTATGCTGTCTGGGGAGCG
CCTGACCTCCGGCTTTGGCTACTCACTGGCTGTGGCTGACCTCAACAGTGTGGCTGGCCAGACCTGATAGTGGG
TGCCCCCTACTTCTTTGAGCGCCAAGAAGAGCTGGGGGGTGTGTGTATGTGTACTTGAACCAGGGGGGTCACTG
GGCTGGGATCTCCCTCTCCGGCTCTGCGGCTCCCTGACTCCATGTTCCGGATCAGCCTGGCTGTCTGGGGGA
CCTCAACCAAGATGGCTTTCCAGATATTGCAGTGGGTGCCCCCTTTGATGGTGATGGGAAAGTCTTCATCTACCA
TGGGAGCAGCCTGGGGGTTGTGCCAAACCTTCACAGGTGCTGGAGGGCGAGGCTGTGGGCATCAAGAGCTTCGG
CTACTCCCTGTGAGGCAGCTTGGATATGGATGGGAACCAATACCCTGACCTGCTGGTGGGCTCCCTGGCTGACAC
CGCAGTGCTCTTCAGGGCCAGACCCATCCTCCATGTCTCCATGAGGTCTCTATTGCTCCACGAAGCATCGACCT
GGAGCAGCCCAACTGTGCTGGCGGCCACTCGGTCTGTGTGGACCTAAGGGTCTGTTTCAGCTACATTGCAGTCCC
CAGCAGCTATAGCCCTACTGTGGCCCTGGACTATGTGTTAGATGCGGACACAGACCGGAGGCTCCGGGGCCAGGT
TCCCCGTGTGACCTTCTGAGCCGTAACCTGGAAGAACCACAGCACCAGGCCTCGGGCACCGTGTGGCTGAAGCA
CCAGCATGACCGAGTCTGTGGAGACGCCATGTTCCAGCTCCAGGAAAATGTCAAAGACAAGCTTCGGGGCCATTGT
AGTGACCTTGTCTACAGTCTCCAGACCCCTCGGCTCCGGCGACAGGCTCCTGGCCAGGGGCTGCCTCCAGTGGC
CCCCATCCTCAATGCCACCAGCCAGCACCAGCGGGCAGAGATCCACTTCTGAAGCAAGGCTGTGGTGAAGA
CAAGATCTGCCAGAGCAATCTGCAGCTGGTCCACGCCCGCTTCTGTACCCGGGTGAGCGACACGGAATTCCAACC
TCTGCCCCATGGATGTGGATGGAACAACAGCCCTGTTTGACTGAGTGGGCAGCCAGTCACTGGCCCTGGAGCTGAT
GGTCACCAACCTGCCATCGGACCCAGCCAGCCAGCCAGGCTGATGGGGATGATGCCCATGAAGCCAGCTCCTGGT
CATGCTTCTGACTCACTGCACTACTCAGGGGTCCGGGCCCTGGACCCCTGCGGAGAAGCCACTCTGCCTGTCCAA
TGAGAATGCCTCCCATGTTGAGTGTGAGCTGGGGAACCCATGAAGAGAGGTGCCAGGTCACCTTCTACCTCAT
CCTTAGCACCTCCGGGATCAGCATTGAGACCACGGAAGTGGAGGTAGAGCTGCTGTTGGCCACGATCAGTGAGCA
GGAGCTGCATCCAGTCTCTGCACGAGCCCGTGTCTTATTGAGCTGCCACTGTCCATTGCAGGAATGGCCATTCC
CCAGCAACTCTTCTTCTGCTGTGGTGTGGTGGGGGCGAGAGAGCCATGCAGTCTGAGCGGGATGTGGGACGAAGT
CAAGTATGAGGTCAAGGTTTCCAACCAAGGCCAGTGCCTCAGAACCCTGGGCTCTGCCTTCTCAACATCATGTG
GCCTCATGAGATTGCCAATGGGAAGTGGTTGCTGTACCCAATGCAGGTTGAGCTGGAGGGCGGGCAGGGGCCTGG
GCAGAAAGGGCTTTGCTCTCCAGGCCCAACATCCTCCACCTGGATGTGGACAGTAGGGATAGGAGGCGCGGGGA
GCTGGAGCCACCTGAGCAGCAGGAGCCTGGTGGAGCGGCAGGAGCCAGCATGTCTGGTGGCCAGTGTCTCTGC
TGAGAAGAAGAAAAACATCACCTGGACTGCGCCCGGGGCGACGGCCAACTGTGTGGTGTTCAGCTGCCCACTCTA
CAGCTTTGACCGCGGGCTGTGCTGCATGTCTGGGGCCGTCTCTGGAACAGCACCTTTCTGGAGGAGTACTCAGC
TGTGAAGTCCCTGGAAAGTGAATGTCCGGGCCAACATCACAGTGAAGTCTCCATAAAGAACTTGATGCTCCGAGA
TGCTTCCACAGTATCCAGTGTGTTACTTGGACCCATGGCTGTGGTGGCAGAAGGAGTGGCTGGTGGGT
CATCTCCTGGCTGTACTGGCTGGGCTGCTGGTGTAGCACTGCTGGTGTGCTCCTGTGGAAGATGGGATTCTT
CAAACGGGCGAAGCACCCCGAGGCCACCGTGCCCCAGTACCATGCGGTGAAGATTCTCGGGAAGACCGACAGCA
GTTCAAGGAGGAGAAGACGGGCACCATCCTGAGGAACAAGTGGGGCAGCCCCGGCGGGAGGGCCCCGATGCACA
CCCCATCCTGGCTGTGACGGGCATCCCGAGCTGGGCCCCGATGGGCATCCAGGGCCAGGCACCGCC**TAG**GTTCC
CATGTCCAGCCTGGCCTGTGGCTGCCCTCCATCCCTTCCCCAGAGATGGCTCCTTGGGATGAAGAGGGTAGAGT
GGGCTGCTGGTGTGCGATCAAGATTTGGCAGGATCGGCTTCTCAGGGGCACAGACCTCTCCACCCACAAGAAC
TCCTCCCACCAACTTCCCCTTAGAGTGTGTGAGATGAGAGTGGGTAAATCAGGGACAGGGCCATGGGTTAGGG
TGAGAAGGGCAGGGGTGCTCTGATGCAAAGGTGGGGAGAAGGGATCCTAATCCCTTCTCTCCATTACCCCTGT
GTAACAGGACCCCAAGGACCTGCCTCCCCGAAGTGCCTTAACCTAGAGGGTGGGGAGGAGGTTGTGTCACTGA
CTCAGGCTGCTCCTTCTCTAGTTTCCCTCTCATTTGACTTTAGTTTGGCTGCCATCAGTCTAGTGGTTTCGTGGT
TTCGTCTATTATTAATAAATAATTTGAGAAACAAAAA

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FIGURE 120

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737
><subunit 1 of 1, 1141 aa, 1 stop
><MW: 124671, pI: 5.82, NX(S/T): 5
MAGARSRDPWGASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHRQLQPRPQSWLLVGAP
QALALPGQQANRTGGLFACPLSLEETDCYRVDIDQGADMQKESKENQWLGVSVRSQGPQGGKIVTCAHRYEARQRV
DQILETRDMIGRCFVLSQDLAIRDELDGGEWKFCGRPQGHEQFGFCQQGTAAAFSPDSHYLLFGAPGTYNWKGT
ARVELCAQGSADLAHLDDGFPYEAGGEKEQDPRLIPVPANSYFGFSIDSGKGLVRAEELS FVAGAPRANHKGAVVI
LRKDSASRLVPEVMLSGERLTSFGYSLAVADLNSDGWPD LIVGAPYFFERQEELGGAVYVYLNQGGHWAGISPL
RLCGSPDSMFGISLAVLGDNLNQDGFDPDIAGVAPFDGDGKVFIYHGSSLGVVAKPSQVLEGEAVGIKSFYSLSGS
LDMDGNQYPDLLVGLADTAVLFRARPILHVSHEVSIAPRSIDLEQPN CAGGHSVCVDLRVCF SYTAVPSSYSPT
VALDYVLADADTDRRLRGQVPRVTFLSRNLEEPKHQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTL SYS
LQTPRLRRQAPGQGLPPVAPILNAHQ PSTQRAEIHFLKQCGEDKICQSNLQLVHARFCTRVSDTEFQPLPMDVD
GTTALFALSGQPVIGLELMVTNLPSPDPAQPQADGDDAHEAQLLVMLPDSLHYSGVRALDPAEKPLCLSNENASHV
ECELGNPMKRGAQVTFYLLISTSGIS IETTELEVELL LATISEQELHPVSARARVFIELPLSIAGMAIPQQLFFS
GVVRGERAMQSERDVGSKVKEYEVT VSNQGSRLTLGSAFLNIMWPHEIANGKWL LYPMQVELEGGQGPQKGLCS
PRPNILHLDVDSRDRRRRELEPPEQ QEPGERQEPSMSWWPVSSAEKKKNITLDCARGTANCVVFSCPLYSFDRAA
VLHVWGRLLWNSTFLEEYS AVKSLEVIVRANITVKSSIKNLMLRDASTV I PVMVYLDPM AVVAEGVPWWVILLAVL
AGLLVLALLVLLLWKMGGFKRAKHPEATVPQYHAVKI PREDRQQFK EECTGTILRNNWGSPRREGPD AHPILAAD
GHPELGPDGHPGPGTA
```

Important features:**Signal peptide:**

amino acids 1-33

Transmembrane domain:

amino acids 1040-1062

N-glycosylation sites.

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

Integrins alpha chain proteins.

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408 and 1031-1047

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FIGURE 121

GGCACGAGGCGGCGGGGCAGTCGCGGGATGCGCCCGGGAGCCACAGCCTGAGGCCCTCAGGTCTCTGCAGGTGTC
GTGGAGGAACCTAGCACCTGCCATCCTCTTCCCCAATTTGCCACTTCCAGCAGCTTTAGCCCATGAGGAGGATGT
GACCGGGACTGAGTCAGGAGCCCTCTGGAAGCATGGAGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCA
TCTTTCTGGCTTCGTTTGCAGCCTTGGTGCTGGTTTGCAGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGC
GCTATGATTCTAAGCCCATTGTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAACTGG
ACGATGTCGTTATCACCAACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATCGAAGATGCCTCGGGTC
TCATGTCCCACTGCATTGCCATCTTGAAGATTTGTCACACTCTGACAGAGAAGCTTGTGGCATGACAATGGGCT
CTGGGGCCAAGATGAAGACTTCAGCCAGTGTGAGCGACATCATTGTGGTGGCCAAGCGGATCAGCCCCAGGGTGG
ATGATGTTGTGAAGTCGATGTACCCTCCGTTGGACCCCCAACTCCTGGACGCACGGACGACTGCCCTGCTCCTGT
CTGTCAGTCACCTGGTGCTGGTGACAAGGAATGCCTGCCATCTGACGGGAGGCCTGGACTGGATTGACCAGTCTC
TGTCGGCTGCTGAGGAGCATTTGGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAGCCAGATAAAGGCCCTCCAG
GCCCTGAAGGCTTCCTGCAGGAGCAGTCTGCAATTTAGTGCCTACAGGCCAGCAGCTAGCCATGAAGGCCCTGC
CGCCATCCCTGGATGGCTCAGCTTAGCCTTCTACTTTTTCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTT
CAGCTGTGTGTGCATAGTAAAGCAGGAGATCCCCGTGAGTTTATGCCTCTTTTGCAGTTGCAAACCTGTGGCTGGT
GAGTGGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACTCTCTGCAAGAGGAGTATTGAAAACCTGGTGGAC
TGTCAGCTTTATTTAGCTCACCTAGTGTTTTCAAGAAAATTGAGCCACCGTCTAAGAAATCAAGAGGTTTACAT
TAAAATTAGAATTTCTGGCCTCTCTCGATCGGTGAGAATGTGTGGCAATTCTGATCTGCATTTTCAAGAGGAC
AATCAATTGAACTAAGTAGGGGTTTCTTCTTTTGGCAAGACTTGTAATCTCTCACCTGGCCTGTTTCATTTATT
TGTATTATCTGCCTGGTCCCTGAGGCGTCTGGGTCTCTCCTCTCCCTTGCAAGGTTTGGGTTTGAAGCTGAGGAAC
TACAAAGTTGATGATTTCTTTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCACTAGGTGGATAGTAAATTT
ATACTTATGTTTCCCTCAAAAAAAAAAAAAA

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FIGURE 122

METVVIVAIGVLATIFLASFAALVIVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPSELEDDVVITNPHIE
AILENEDWIEDASGLMSHCIAILKICHTLTEKLVAMTMGSGAKMKTSASVSDIIVVAKRISPRVDDVVKSMYPPL
DPKLLDARTTALLSVSHLVLVTRNACHLTGGLDWIDQSLSAEEHLEVLREAALASEPDKGLPGPEGFLQEQSAI

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FIGURE 123

CCCTTACATCCTCCTAGGACCCGGTCGGTAGTCGTCGCCCCAGCCCGCCGGGGGCGCAGCGCCCGAGCCGCGGCC
CTCGAGACGGGACCGAGAGCATCATGGGCAGCACTGTCCCGCGCTCCGCCTCCGTGCTGCTTCTGCTGCTGCTCC
TGCGCCGGGCGGAGCAGCCCTGCGGGGCCGAGCTCACCTTCGAGCTGCCGGACAACGCCAAGCAGTGCTTCCACG
AGGAGGTGGAGCAGGGCGTGAAGTTCTCCCTGGATTACCAGGTCATCACTGGAGGCCACTACGATGTTGACTGCT
ATGTAGAGGACCCCCAGGGGAACACCATCTACAGAGAAACGAAGAAGCAGTACGACAGCTTCACGTACCGGGCTG
AAGTCAAGGGCGTTTATCAGTTTTGCTTCAGTAATGAGTTTTCCACCTTCTCTCACAAGACCGTCTACTTTGACT
TTCAAGTGGGCGATGAGCCTCCCATTTCTCCAGACATGGGGAACAGGGTCACAGCTCTCACCCAGATGGAGTCCG
CCTGCGTGACCATCCATGAGGCTCTGAAAACGGTGATTGACTCCCAGACGCATTACCGGCTGCGGGAGGCCCAGG
ACCGGGCCCCGAGCGGAAGACCTTAATAGCCGAGTCTCTTACTGGTCTGTTGGCGAGACGATTGCCCTGTTCTGTTG
TCAGCTTCAGTCAGTGCTACTGTTGAAAAGCTTCTTCACAGAAAACGACCCATCAGCAGGGCAGTCCACTCCT
AGCCCCGGCATCCTGCTCTAGGGCCCCCTCATGCCCCAGGCTGGAGCAGCTCTCCTAGGTACAGCCTGCTGGGCT
GGGTGCGGTAGCCAGGGTGGAGGCAGAACGATGCTGCTGTGGTAGCCCTTTGCCTTTTCATGCCCATGCTTGATT
CTTGACCTCAGCAGCTGAAGTCTCAGAGACCAGTAATCAGAAGGCATCCGACTGCATTAAGTGTGCAGCGCTG
AAAAGACATTTACAACCTAGGCCAGGGATTAGCCACTGTGGGAGGCTGGACAGGCAATGGTTCAGTGGCCTGGCTG
TTGGCAGGAACCCAAGTGCCCAGGCCTCTTGGGCAGCTTAGGGCCCTGCCTCTGTTTCATGATGCATGGGTCAT
TTGTCTTGGGTGTCTATCCCATATGGAGAAGAAAGGGGCTCTAAGTTCTGGCTCTTCTTTCTTTGGGGTTCTCT
GTACCTGAGGAACCAGGCCCTGGGTGACTTTGCAGATCTGCTCACCTCGGTGAGCAACAGTGTGAGCCATGCA
AGCAGGACAGAATGGTGACTGGGTGCCCTTGGTGAGCTGTGTATTTCTAGGAGGTAGAAAACGTGGGAAACTG
TGGCTAATAAAAACTAAGTGTGAGCGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 124

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56052
<subunit 1 of 1, 217 aa, 1 stop
<MW: 24777, pI: 5.55, NX(S/T): 0
MGSTVPRSASVLLLLLLLLRRAEQPCGAELTFELPDNAKQCFHEEVEQGVKFSLDYQVITG
GHYDVDCYVEDPQGNTIYRETKKQYDSFTYRAEVKGVYQFCFSNEFSTFSHKTVYFDFQV
GDEPPILPDMGNRVTALTQMESACVTIHEALKTVIDSQTHYRLREAQDRARAEDLNSRVS
YWSVGETIALFVVSFSQVLLLSFFTEKRPISRAVHS
```

Important features:**Signal peptide:**

amino acids: 1-23

Transmembrane domain:

amino acids: 187-201

N-myristoylation sites:

amino acids: 26-32, 48-54, 131-137

Tyrosine kinase phosphorylation site:

amino acids: 82-91

Glycosyl hydrolases family 25 proteins:

amino acids: 53-61

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FIGURE 125

GGCACGAGGCGCTGTCCACCCGGGGGCGTGGGAGTGAGGTACCAGATTGAGCCCATTTGGCCCCGACGCCTCTGT
TCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTTCCCTAACGGACTGCAAGATGGAGGAAGGCGGGAACCTAG
GAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGTGAGGTGCCTGGGGCATGCAAATGTGGGTGACCTTCGTCT
CAGGCTTCCTGCTTTTCCGAAGCCTTCCCCGACATACCTTCGGACTAGTGCAGAGCAAACCTCTCCCTTCTACT
TCCACATCTCCATGGGCTGTGCCTTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTTGGGCTCAGCTCACAT
TCTGGGAGGCCAGCCAGCTTTACCTGCTGTTCCCTGAGCCTTACGCTGGCCACTGTCAACGCCGCTGGCTGGAAC
CCCGCACCACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGAGCGAGGCCTGGGTGGGAGGTACCAGGCA
GCCACCAGGGTCCCGATCCCTACCGCCAGCTGCGAGAGAAGGACCCCAAGTACAGTGCTCTCCGCCAGAATTTCT
TCCGCTACCATGGGCTGTCTCTCTTTGCAATCTGGGCTGCGTCCTGAGCAATGGGCTCTGTCTCGCTGGCCTTG
CCCTGGAAATAAGGAGCCTCTAGCATGGGCCCTGCATGCTAATAAATGCTTCTTCAGAAATGAAAAAAAAAAAAA
AAAAAA

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FIGURE 126

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107

<subunit 1 of 1, 231 aa, 1 stop

<NX(S/T): 0

MEEGGNLGGLIKVMHLLVLSGAWGMQMWVTFVSGFLLFRSLPRHTFGLVQSKLFPFYFHISMGCAFINLCILASQ
HAWAQLTFWEASQLYLLFLSITLATVNARWLEPRTTAAMWALQVEKERGLGGEVPGSHQGPDPYRQLREKDPKY
SALRQNFRRYHGLSSLCNLGCVLSNGLCLAGLALEIRSL

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 86-103, 60-75

Casein kinase II phosphorylation site.

amino acids 82-86

Tyrosine kinase phosphorylation site.

amino acids 144-151

N-myristoylation site.

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 54-65

G-protein coupled receptors proteins.

amino acids 44-85

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FIGURE 127

GCTTCATTTCTCCCGACTCAGCTTCCCACCCTGGGCTTTCCGAGGTGCTTTTCGCCGCTGTCCCCACCACTGCAGC
CATGATCTCCTTAACGGACACGCAGAAAATTGGAATGGGATTAACAGGATTTGGAGTGTTTTTCTGTCTTTGG
AATGATTCTCTTTTTTGACAAAGCACTACTGGCTATTGGAAATGTTTTATTTGTAGCCGGCTTGGCTTTTGTAAAT
TGGTTTAGAAAGAACATTCAGATTCTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTCTGGGTGGTGT
ATTTGTAGTCCTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTCTCTTGTTCAGGGG
CTTCTTTCCTGTCGTTGTTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAATTTACCTGGAATTAG
ATCATTGTAGATAAAAGTTGGAGAAAGCAACAATATGGTATTAACAACAAGTGAATTTGAAGACTCATTTAAATA
TTGTGTTATTTATAAAAGTCATTTGAAGAATATTGAGCACAATAATTAATACATGAAATAGCTTGTAAATGTTCTT
TACAGGAGTTTAAACGTATAGCCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAACACAGGCTTCTA
CTCAAGTGAAGTAAGAAGAAGTCAGCAAGCAAAGTGAAGAGGTTGAAATCCATGTTAATGATGCTTAAGAACTC
TTGAAGGCTATTTGTGTTGTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAACTGTGGTGCCTGTTTCT
TTTCTTTTTATTTGAAGGCTCAGGAGCATCCATAGGCATTTGCTTTTGAAGTGTCCACTGCAATGGCAAAAA
TATTTCCAGTTGCACTGTATCTCTGGAAGTGATGCATGAATTCGATTGGATTGTGTCATTTTAAAGTATTAAAC
CAAGGAAACCCCAATTTTGATGTATGGATTACTTTTTTTTGNCCNCAGGGCC

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FIGURE 128

MISLTDQKIGMGLTGFGVFFLEFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFFQKHMKATGFFLGGV
FVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFIIRVPVLGSLNLPGIRSFVDKVGESNNMV

Important features:

Transmembrane domains:

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

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FIGURE 129

AATTCAGATTTTAAAGCCCATCTGCAGTGGAATTTTCATGAAGTAGCAAGAGGACACCATCTTCTTGATTATACAA
AGAAAGGAGTGTACCTATCACACACAGGGGGAAAAATGCTCTTTTGGGTGCTAGGCCTCCTAATCCTCTGTGGTT
TTCTGTGGACTCGTAAAGGAAAACTAAAGATTGAAGACATCACTGATAAGTACATTTTTATCACTGGATGTGACT
CGGGCTTTGGAACTTGGCAGCCAGAACTTTTGATAAAAAGGGATTTTCATGTAATCGCTGCCTGTCTGACTGAAT
CAGGATCAACAGCTTTAAAGGCAGAAACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAGAGA
ATGTCAAGAGGACTGCCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGTCTGATCAATAATGCTG
GTGTTCCCGGCGTGCTGGCTCCCACTGACTGGCTGACACTAGAGGACTACAGAGAACCTATTGAAGTGAACCTGT
TTGGACTCATCAGTGTGACACTAAATATGCTTCCTTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAATGTCTCCA
GTGTTGGAGGTCGCCTTGCAATCGTTGGAGGGGGCTATACTCCATCCAAATATGCAGTGGAAGGTTTCAATGACA
GCTTAAGACGGGACATGAAAGCTTTTGGTGTGCACGTCTCATGCATTGAACCAGGATTGTTCAAAACAACTTGG
CAGATCCAGTAAAGGTAATTGAAAAAACTCGCCATTGGGAGCAGCTGTCTCCAGACATCAACAACAATATG
GAGAAGGTTACATTGAAAAAGTCTAGACAACTGAAAGGCAATAAATCCTATGTGAACATGGACCTCTCTCCGG
TGGTAGAGTGCATGGACCACGCTCTAACAAGTCTCTTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAAA
TTTTCTGGATACCTCTGTCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAAGCAGAGCTGG
CTAATCCCAAGGCAGTGTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGAAATTGGCCGATTTCAAGAAC
ACATCTCCTTTTCAACCCCATTCCTTATCTGCTCCAACCTGGACTCATTTAGATCGTGCTTATTTGGATTGCAAA
AGGGAGTCCCACCATCGCTGGTGGTATCCCAGGGTCCCTGCTCAAGTTTTCTTTGAAAGGAGGGCTGGAATGGT
ACATCACATAGGCAAGTCTGCCCCTGTATTTAGGCTTTGCCTGCTTGGTGTGATGTAAGGGAAATTGAAAGACTT
GCCCATTCAAAATGATCTTTACCGTGGCCTGCCCCATGCTTATGGTCCCCAGCATTTACAGTAACTTGTGAATGT
TAAGTATCATCTCTTATCTAAATATTTAAAGATAAGTCAACCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAA

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FIGURE 130

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56406
><subunit 1 of 1, 319 aa, 1 stop
><MW: 35227, pI: 8.97, NX(S/T): 3
MLFWVLGILLILCGFLWTRKGLKIEDITDKYIFITGCDSGFGNLAARTFDKKGFHVIAACLTESGSTALKAETSE
RLRTVLLDVTDPENVKRTAQWVKNQVGEKGLWGLINNAGVPGVLAPTDWLTLEDYREPIEVNLFGLISVTLNMLP
LVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGFNDLRRDMKAFGVHVSCTEPGLFKTNLADPVKVEKKLA
IWEQLSPDIKQQYGEGYIEKSLDKLKGKNSYVNMDLSPVVECDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAA
LQDFLLLKQKAE LANPKAV
```

Important features of the protein:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

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FIGURE 131

AGACAGTACCTCCTCCCTAGGACTACACAAGGACTGAACCAGAAGGAAGAGGACAGAGCAAAGCCATGAACATCA
TCCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCCTACTTGGAGTCGTTGGTGAAGTTTTTCATTCTC
AGAGGAGAAAATCTGTGGCTGGGGAGATTGTTCTCATTACTGGAGCTGGGCATGGAATAGGCAGGCAGACTACTT
ATGAATTTGCAAAACGACAGAGCATATTGGTTCTGTGGGATATTAATAAGCGCGGTGTGGAGGAACTGCAGCTG
AGTGCCGAAAACTAGGCGTCACTGCGCATGCGTATGTGGTAGACTGCAGCAACAGAGAAGAGATCTATCGCTCTC
TAAATCAGGTGAAGAAAGAAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACAGTATATCCAGCCGATC
TTCTCAGCACCAAGGATGAAGAGATTACCAAGACATTTGAGGTCAACATCCTAGGACATTTTTGGATCACAAAAG
CACTTCTTCCATCGATGATGGAGAGAAATCATGGCCACATCGTCACAGTGGCTTCAGTGTGCGGCCACGAAGGGA
TTCCTTACCTCATCCCATATTGTTCCAGCAAATTTGCCGCTGTTGGCTTTCACAGAGGTCTGACATCAGAACTTC
AGGCCTTGGGAAAAACTGGTATCAAACCTCATGTCTCTGCCAGTTTTTGTGAATACTGGGTTACCAAAAAATC
CAAGCACAAAGATTATGGCCTGTATTGGAGACAGATGAAGTCGTAAGAAGTCTGATAGATGGAATACTTACCAATA
AGAAAATGATTTTTGTTCCATCGTATATCAATATCTTCTGAGACTACAGAAGTTTCTTCTGAACGCGCCTCAG
CGATTTTAAATCGTATGCAGAATATTCAATTTGAAGCAGTGGTTGGCCACAAAATCAAATGAAATTGAATAAATA
AGCTCCAGCCAGAGATGTATGCATGATAATGATATGAATAGTTTCGAATCAATGCTGCAAAGCTTTATTTACAT
TTTTTCAGTCCTGATAATATTA AAAACATTGGTTTGGCACTAGCAGCAGTCAAACGAACAAGATTAATTACCTGT
CTTCCTGTTTCTCAAGAATATTTACGTAGTTTTTCATAGGTCTGTTTTCTTTCATGCCTCTTAAAAACTTCTG
TGCTTACATAAAACATACTTAAAAGGTTTTCTTTAAGATATTTTATTTTTCCATTTAAAGGTGGACAAAAGCTACC
TCCCTAAAAGTAAATACAAAGAGAACTTATTTACACAGGGAAGGTTTAAGACTGTTCAAGTAGCATTCCAATCTG
TAGCCATGCCACAGAATATCAACAAGAACACAGAATGAGTGCACAGCTAAGAGATCAAGTTTCAGCAGGCAGCTT
TATCTCAACCTGGACATATTTTAAGATTCAGCATTGAAAGATTTCCCTAGCCTCTTCCTTTTTTCATTAGCCCAA
AACGGTGCAACTCTATTCTGGACTTTATTACTTGATTCTGTCTTCTGTATAACTCTGAAGTCCACAAAAGTGGA
CCCTCTATATTTCTCCCTTTTTATAGTCTTATAAGATACATTATGAAAGGTGACCGACTCTATTTTAAATCTCA
GAATTTTAAGTTCTAGCCCCATGATAACCTTTTTCTTTGTAATTTATGCTTTCATATATCCTTGGTCCCAGAGAT
GTTTAGACAATTTTAGGCTCAAAAATTAAAGCTAACACAGGAAAAGGAAGTGTACTGGCTATTACATAAGAAACA
ATGGACCCAAGAGAAGAA

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FIGURE 132

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409

<subunit 1 of 1, 300 aa, 1 stop

<MW: 33655, pI: 9.31, NX(S/T): 1

MNIILEILLLLITIIYSYLESIVKFFIPQRRKSVAGEIVLITGAGHGIGRQTTYEFAKRQSI LVLWDINKRGVEE
TAAECRKLGVTAHAYVVDCSNREEIYRSLNQVKEVGDTVIVVNNAGTVYPADLLSTKDEEITKTFE VNILGHFW
ITKALLPSMMERNHGHIVTVASVCGHEGIPYLI PYCSSKFAAVGFHRGLTSELQALGKTGIKTSC LCPV FVNTGF
TKNPSTRLWPVLETDEVVRSLIDGILTNNKMIFVPSYINIFLRLQKFLPERASAILNRMQNIQFEAVVG HKIKMK

Important features:**Signal peptide:**

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-33 and 58-61

Short-chain alcohol dehydrogenase family protein

amino acids 165-202, 37-49, 112-122 and 210-219

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FIGURE 133

CTGAGGCGGCGGTAGC**ATG**GAGGGGGAGAGTACGTGCGCGGTGCTCTCGGGCTTTGTGCTCGGCGCACTCGCTTT
CCAGCACCTCAACACGGACTCGGACACGGAAGSTTTTCTTCTGGGGAAGTAAAAGGTGAAGCCAAGAACAGCAT
TACTGATTCCCAAATGGATGATGTTGAAGTTGTTTATACAATTGACATTCAGAAATATATTCCATGCTATCAGCT
TTTTAGCTTTTATAATTCTTCAGGCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAA
TGTGGTAGGTTGGTACAAATTCCGTCGTCAATTCAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAAAAA
CTTGCAGGAGCATTTTTCAAACCAAGACCTTGTTTTCTGCTATTAACACCAAGTATAATAACAGAAAGCTGCTC
TACTCATCGACTGGAACATTCTTATATAAACCTCAAAAAGGACTTTTTTACAGGGTACCTTTAGTGGTTGCCAA
TCTGGGCATGTCTGAACAACCTGGGTTATAAACTGTATCAGGTTCTGTATGTCCACTGGTTTTAGCCGAGCAGT
ACAAACACACAGCTCTAAATTTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGC
TTCATTACAAGAGGAATTAAAGAGTATATGCAAAAAGTGGAAGACAGTGAACAAGCAGTAGATAAACTAGTAAA
GGATGTAAACAGATTAAAAACGAGAAATTGAGAAAAGGAGAGGAGCACAGATTCAAGGCAGCAAGAGAGAAGAACAT
CCAAAAAGACCCTCAGGAGAACATTTTTCTTTGTGAGGCAATTACGGACCTTTTTTCCAAATTCTGAATTTCTTCA
TTCATGTGTTATGTCTTTAAAAAATAGACATGTTTCTAAAAGTAGCTGTAACATAACCACCATCTCGATGTAGT
AGACAATCTGACCTTAATGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAA
GCATAAGCCTTAGACTTAGATGACAGATGGCAATTCAGAGATCTCGGTTGTTAGATACACAAGACAAACGATC
TAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCCCAGAAACAGATGAAGAAATTGA
AAAGATGAAGGGTTTTGGTGAATATTCACGGTCTCCTACATTT**TGA**TCTTTTAACTTACAAGGAGATTTTTTT
ATTTGGCTGATGGGTAAAGCCAAACATTTCTATTGTTTTTACTATGTTGAGCTACTTGACAGTAAGTTCATTTGTT
TTTACTATGTTACCTGTTTGCAGTAATACACAGATAACTCTTAGTGCATTTACTTCACAAAGTACTTTTTCAA
CATCAGATGCTTTTATTTCCAAACCTTTTTTTTACCTTTCACTAAGTTGTTGAGGGGAAGGCTTACACAGACACA
TTCTTTAGAATTGGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAATCCCAGCACTTAGGGAAGACAAGTC
AGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCCTGGGCAACGTATTGAGACCATGTCTATTAAAAAATAAA
ATGGAAAAGCAAGAATAGCCTTATTTTCAAAATATGGAAAGAAATTTATATGAAAATTTATCTGAGTCATTAAAA
TTCTCCTTAAGTGATACTTTTTTAGAAGTACATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCAAT
AAATTTGCAAAACATCATCTAAAATTTAAAAA

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FIGURE 134

MEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLGGEVKGEAKNSITDSQMDDVEVVYTTIDIQKYIPCYQLFSFY
SSGEVNEQALKKILSNVKKNVVGWYKFRRHSDQIMTFRERLHKNLQEHFSNQDLVFLLLTPSIITESCSTHRLE
HSLYKPQKGLFHRVPLVVANLGMSEQLGYKTVSGSCMSTGFSRAVQTHSSKFFEDGSLKEVHKINEMYASLQEE
LKSICKKVEDSEQAVDKLVKDVNRLKREIEKRRGAQIQAAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMS
LKNRHVSKSSCNYNHHLDVVDNLTLMVEHTDIPEASPASTPQIIKHKALDLDLDRWQFKRSRLDQTQDKRSKANTG
SSNQDKASKMSSPETDEEIEKMKGFGEYSRSPTE

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FIGURE 135

GGCACAGCCGCGCGGGGAGGGCAGAGTCAGCCGAGCCGAGTCCAGCCGGACGAGCGGACCAGCGCAGGGCAGCC
CAAGCAGCGCGCAGCGAACGCCCCGCCGCCGCCACACCCTCTGCGGTCCCCGCGGCGCCTGCCACCCTTCCCTCC
TTCCCCCGCTCCCCGCCTCGCCGGCCAGTCAGCTTGCCGGGTTGCTGCCCCGCGAAACCCGAGGTACCAGCC
CGCGCTCTGCTTCCCTGGGCCGCGCGCCCTCCACGCCCTCCTTCTCCCTGGCCCCGGCGCCTGGCACCCGGGG
ACCGTTGCCTGACGCGAGGCCAGCTCTACTTTTCGCCCCGCTCTCCTCCGCTGCTCGCTCTTCCACCAACT
CCAACCTCTTCTCCCTCCAGCTCCACTCGCTAGTCCCCGACTCCGCCAGCCCTCGGCCGCTGCCGTAGCGCCGC
TTCCCGTCCGGTCCCAAAGGTGGGAACGCTCGCCCCCGGCCCGCACCATGGCACGGTTCCGGCTGCCCCGCGCTT
CTCTGCACCCCTGGCAGTGCTCAGCGCCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAAGTTGCTCGGAAGTGCGA
CGTCTTTACGTGTCCAAAGGCTTCAACAAGAACGATGCCCCCTCCACGAGATCAACGGTGATCATTGAAGATC
TGTCCCCAGGGTTCTACCTGCTGCTCTCAAGAGATGGAGGAGAAGTACAGCCTGCAAAGTAAAGATGATTTCAA
AGTGTGTCAGCGAACAGTGCAATCATTTGCAAGCTGTCTTTGCTTACGTTACAAGAAGTTTGATGAATTCTTC
AAAGAATACTTGAATGCAGAGAAATCCCTGAATGATATGTTTGTGAAGACATATGGCCATTTATACATGCAA
AATTCTGAGCTATTTAAAGATCTCTTCGTAGAGTTGAAACGTTACTACGTGGTGGGAAATGTGAACCTGGAAGAA
ATGCTAAATGACTTCTGGGCTCGCCTCCTGGAGCGGATGTTCCGCCTGGTGAACCTCCAGTACCACCTTTACAGAT
GAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGTCCCTCGCAAATTGAAGCTC
CAGGTTACTCGTGCTTTTGTAGCAGCCGTACTTTTCGCTCAAGGCTTAGCGGTTGCGGGAGATGTCGTGAGCAAG
GTCTCCGTGGTAAACCCACAGCCAGGTGTACCCATGCCCTGTTGAAGATGATCTACTGCTCCCACTGCCGGGGT
CTCGTGACTGTGAAGCCATGTTACAATACTGCTCAAACATCATGAGAGGCTGTTTGGCCAACCAAGGGGATCTC
GATTTTGAATGGAACAATTTCATAGATGCTATGCTGATGGTGGCAGAGAGGCTAGAGGGTCCCTTCAACATTGAA
TCGGTCATGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGGATAATAGTGTTCAGTGTCT
CAGAAGGTTTCCAGGGATGTGGACCCCCAAGCCCTCCAGCTGGACGAATTTCTCGTCCATCTCTGAAAGT
GCCTTCAGTGCTCGCTTCAGACCACATCACCCCGAGGAACGCCCAACCACAGCAGCTGGCACTAGTTTGGACCGA
CTGGTTACTGTGTCAAGGAGAACTGAAACAGGCCAAGAAATTTGGTCTCCTTCCGAGCAACGTTTGCAAC
GATGAGAGGATGGCTGCAGGAAACGGCAATGAGGATGACTGTTGGAATGGGAAAGGCAAAAGCAGGTACCTGTTT
GCAGTGACAGGAAATGGATTAGCCAACAGGGCAACAACCCAGAGGTCCAGGTTGACACCAGCAAACAGACATA
CTGATCCTTCGTCAAATCATGGCTCTTCGAGTGATGACCAGCAAGATGAAGAATGCATACAATGGGAACGACGTG
GACTTCTTTGATATCAGTGATGAAAGTAGTGGAGAAGGAGTGGAGTGGCTGTGAGTATCAGCAGTGCCCTTCA
GAGTTTGACTACAATGCCACTGACCATGCTGGGAAGAGTGCCAATGAGAAAGCCGACAGTGCTGGTGTCCGTCCT
GGGGCACAGGCCTACCTCCTCACTGTCTTCTGCATCTTGTTCTGTTATGCAGAGAGAGTGGAGATTAATTTCTCA
AACTCTGAGAAAAAGTGTTCATCAAAAAGTTAAAAGGCACCAGTTATCACTTTTCTACCATCCTAGTGACTTTGC
TTTTTAAATGAATGGACAACAATGTACAGTTTTTACTATGTGGCCACTGGTTTAAAGAGTGCTGACTTTGTTTC
TCATTCAAGTTTTGGGAGGAAAAGGACTGTGCATTGAGTTGGTTCTGCTCCCCAAACCATGTTAAACGTGGCT
AACAGTGTAGGTACAGAACTATAGTTAGTTGTGATTTTATCACTCTATTATTTGTTTGTATGTTTTT
TTCTCATTTTCGTTTGTGGGTTTTTTTTTCCAACGTGTGATCTCGCTTGTCTTACAAGCAAACAGGGTCCCTT
CTTGGCACGTAACATGTACGTATTTCTGAAATATTAAATAGCTGTACAGAAGCAGGTTTTATTTATCATGTTATC
TTATTAAAGAAAAAGCCCCAAAAGC

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FIGURE 136

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQGSTCCSQEMEKEY
SLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMFVKTYGHLYMQNSELFKDLFVELKRY
VVGNNLEEMLNDFWARLLERMFLVNSQYHFTDEYLECVSKYTEQLKPFQDVPRKLLQVTRAFVAARTFAQGL
AVAGDVVSKVSVVNPTAQCTHALLKMIYCSHCRLVTVKPCYNYCSNIMRGCLANQGDLD FEWNNFIDAMLMAE
RLEGPFNIESVMDPIDVKISDAIMNQDNSVQVSQKVFQGC GPPKPLPAGRISRSISESAFSARFRPHHPEERPT
TAAGTSLDRLVTDVKEKLKQAKKFWSSLP SNVCNDERMAAGNGNEDDCWNGKGKSRYLFAVTGNGLANQGNNPEV
QVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGEGSGSGCEYQQCPSEFDYNATDHAGKSANE
KADSAGVRPGAQAYLLTVFCILFLVMQREWR

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FIGURE 137

GC GGGCTGTTGACGGCGCTGCGATGGCTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTTCTCTCAGTCGGA
CTTCTGACGCCGCCAGTGGGCGGGGCCCCCTTGGGCGCTCGCCACCACTGTAGTCATGTACCCACCGCCGCCGCC
GCCGCTCATCGGGACTTCATCTCGGTGACGCTGAGCTTTGGCGAGAGCTATGACAACAGCAAGAGTTGGCGGCG
GCGCTCGTGTGGAGGAAATGGAAGCAACTGTCGAGATTGCAGCGGAATATGATTCTCTTCTCTCTGCTTTCT
GCTTTTCTGTGGACTCCTCTTCTACATCAACTTGGCTGACCATTGGAAAGCTCTGGCTTTCAGGCTAGAGGAAGA
GCAGAAGATGAGGCCAGAAATTGCTGGGTAAAACCAGCAAATCCACCCGTCTTACCAGCTCCTCAGAAGGCGGA
CACCGACCCTGAGAACTTACCTGAGATTTCTGCACAGAAGACACAAAGACACATCCAGCGGGGACCACCTCACCT
GCAGATTAGACCCCAAGCCAAGACCTGAAGGATGGGACCCAGGAGGAGGCCACAAAAGGCAAGAAGCCCCTGT
GGATCCCCGCCCCGAAGGAGATCCGCAGAGGACAGTCATCAGCTGGAGGGGAGCGGTGATCGAGCCTGAGCAGGG
CACCGAGCTCCCTTCAAGAAGAGCAGAAGTGCCACCAAGCCTCCCCTGCCACCGGCCAGGACACAGGGCACACC
AGTGCACTCTGAATATCGCCAGAAGGGCGTGATTGACGTCTTCTGCTGCATGCATGGAAGGATAACCGCAAGTTTGC
ATGGGGCCATGACGAGCTGAAGCCTGTGTCCAGGTCTTTCAGTGAGTGGTTTGGCCTCGGTCTCACACTGATCGA
CGCGCTGGACACCATGTGGATCTTGGGTCTGAGGAAAGAATTTGAGGAAGCCAGGAAGTGGGTGTGGAAGAAGTT
ACACTTTGAAAAGGACGTGGACGTCAACCTGTTTGAAGACGATCCGCATCCTGGGGGGGCTCCTGAGTGCCTA
CCACCTGTCTGGGACAGCCTCTTCTGAGGAAAGCTGAGGATTTTGGAAATCGGCTAATGCCTGCCTTCAGAAC
ACCATCCAAGATTCTTACTCGGATGTGAACATCGGTACTGGAGTTGCCACCGGCCAGGTGGACCTCCGACAG
CACTGTGGCCGAGGTGACCAGCATTCAGCTGGAGTTCCGGGAGCTCTCCCGTCTCACAGGGGATAAGAAGTTTCA
GGAGGCAGTGGAGAAGGTGACACAGCACATCCACGGCCTGTCTGGGAAGAAGGATGGGCTGGTGCCCATGTTTCA
CAATACCCACAGTGGCCTCTTACCCACCTGGGCGTATTACGCTGGGCGCCAGGGCCGACAGCTACTATGAGTA
CCTGCTGAAGCAGTGGATCCAGGGCGGGAAGCAGGAGACACAGCTGCTGGAAGACTACGTGGAAGCCATCGAGGG
TGTCAGAACGCACCTGCTGCGGCACTCCGAGCCAGTAAGCTCACCTTTGTGGGGGAGCTTGCCACGGCCGCTT
CAGTGCCAAGATGGACCACCTGGTGTGCTTCTGCCAGGGACGCTGGCTCTGGGCGTCTACCACGGCCTGCCCGC
CAGCCACATGGAGCTGGCCAGGAGCTCATGGAGACTTGTACCAGATGAACCGGCAGATGGAGACGGGGCTGAG
TCCCGAGATCGTGCACTTCAACCTTTACCCCCAGCCGGGCGTCCGGGACGTGGAGGTCAAGCCAGCAGACAGGCA
CAACCTGCTGCGGCCAGAGACCGTGGAGAGCCTGTTCTACCTGTACCGCGTCACAGGGGACCGCAAATACCAGGA
CTGGGGCTGGGAGATTCTGCAGAGCTTCAGCCGATTACACGGGTCCCCTCGGGTGGCTATTCTTCCATCAACAA
TGTCCAGGATCCTCAGAAGCCCCGAGCCTAGGGACAAGATGGAGAGCTTCTTCTGGGGGAGACGCTCAAGTATCT
GTTCTTGCTCTTCTCCGATGACCCAAACCTGCTCAGCCTGGACGCCTACGTGTTCAACACCGAAGCCCACCTCT
GCCTATCTGGACCCCTGCCTAGGGTGGATGGCTGCTGGTGTGGGGACTTCGGGTGGGCGAGGGACCTTGCTGGG
TCTGTGGCATTTCCTAAGGGGCCACGTAGCACCGGCAACCGCCAAGTGCCCCAGGCTCTGAAGTGGCTCTGGGCT
CCTCCTCGTCTCTGCTTTAATCAGGACACCGTGAGGACAAGTGAGGCGTCAGTCTTGGTGTGATGCGGGGTGGG
CTGGGCCGCTGGAGCCTCCGCCTGCTTCTCAGAAAGACACGAATCATGACTCACGATTGCTGAAGCCTGAGCAG
GTCTCTGTGGGCCGACCAGAGGGGGGCTTCGAGGTGGTCCCTGGTACTGGGGTGACCGAGTGGACAGCCCAGGGT
GCAGCTCTGCCCCGGGCTCGTGAAGCCTCAGATGTCCCCAATCCAAGGGTCTGGAGGGGCTGCCGTGACTCCAGAG
GCCTGAGGCTCCAGGGCTGGCTCTGGTGTTTACAAGCTGGACTCAGGGATCCTCCTGGCCGCCCGCAGGGGGCT
TGGAGGGCTGGACGGCAAGTCCGTCTAGCTCACGGGCCCTCCAGTGGAATGGGTCTTTTCGGTGGAGATAAAAG
TTGATTTGCTCTAACCGCAA

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FIGURE 138

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56529
><subunit 1 of 1, 699 aa, 1 stop
><MW: 79553, pI: 7.83, NX(S/T): 0
MAACEGRRSGALGSSQSDFLTPPVGGAPWAVATTVMYPPPPPPPHRDFISVTLSFGESYDNSKSWRRRSCWRKW
KQLSRLQRNMILFLLAFLLFCGLLFYINLADHWKALAFRLLEEQKMRPEIAGLKPANPPVLPAPQKADTDPENLP
EISSQKTQRHIQRGPPHLQIRPPSQDLKDGTQEEATKRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTELPSRR
AEVPTKPPLPPARTQGTPVHLNRYRQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSEWFGGLGLTLIDALDTMWI
LGLRKEFEEARKWVSKKLHFEKDVDVNLFESTITILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKIPYS
DVNIGTGVAHPPRWTSdstVAEVTSIQLEFRELsRLTGDKKFQEAVEKVTQHIHGLSGKKDGLVPMFINTHSGLF
THLGVFTILGARADSYEYLLKQWIIQGGKQETQLLEDYVEAIEGVrTHLLRHSEPSKLTfVGELAHGRFSakMDHL
VCFLPGTLALGVYHGLPASHMELAQELMETCYQMNRQMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNLRLPET
VESLFYLYRVTGDRKYQDWGWEILQSFSRfTRVPsGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLLFSDD
PNLLSLDAYVFNTeAHPLPIWTPA
```

Important features of the protein:**Transmembrane domain:**

amino acids 21-40 and 84-105 (type II)

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FIGURE 139

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCTGACCTGAGTCATC
CCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAAGCAACTTACAGCTGCACCGACAGTTG
CGATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGCTGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGA
ATCCAGGGGTGCGCCAGAGGCCACAGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAAT
GTGAGTGCAAAGATTGGTTCCTGAGAGCCCCGAGAAGAAAATTCATGACAGTGTCTGGGCTGCCAAGAAGCAGT
GCCCCTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGAAAGCCAAACAAGCAT
CCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTTTGCTCTGCCTTTGTAGGAGCTCTGAGCGC
CCACTCTTCCAATTAAACATTCTCAGCCAAGAAGACAGTGAGCACACCTACCAGACACTCTTCTTCTCCACCTC
ACTCTCCCACTGTACCCACCCCTAAATCATTCCAGTGCTCTCAAAAAGCATGTTTTTCAAGATCATTTTGT
TGCTCTCTCTAGTGTCTTCTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCCTTACCCAGGCTTAGGCTTAATTAC
CTGAAAGATTCCAGGAACTGTAGCTTCCTAGCTAGTGTCAATTAACCTTAAATGCAATCAGGAAAGTAGCAAAC
AGAAGTCAATAAATATTTTAAATGTCAAAAAAAAAAAAAAAAAA

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FIGURE 140

MKVLISLLLLLPLMLMSMVSSSLNPGVARGHRDRGQASRRWLQEGGQECECKDWFLRAPRRKFMTVSGLPKKQC
PCDHFKNVKKTRHQRHHRKPNKHSRACQQFLKQCQLRSFALPL

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FIGURE 141

AATGGCTGTCTTAGTACTTCGCCTGACAGTTGTCCTGGGACTGCTTGTCTTATTCCTGACCTGCTATGCAGACGA
CAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCAAAGCCAGACTTCCCCAAATTCCTAAG
CCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGAGTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTTAT
GGAATTTGATGATAATGAAGGAAAACATTCATCAAAGTGAATCCTCAGGACACACCCATGTGGCTCCTGGACAA
TCCAAGAGCAGCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAACTCC
CAACGAGTTCTCAGGATTCAGGCTCTGGCTTCAACCAAACAGAACTCATTTGAACACCCTGACTGCATTTTTC
TTTAGAAAAGTTAGAATAAATATGGCGCTTTGGGATCACATAGTTGATGGAGAGGAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 142

MAVLVLRRLTVVLGLLVLFITCYADDKPKDPDDKPDGKDPKDFPKFLSLLGTEIIENAVEFILRSMSRSTGFM
EFDDNEGKHSSK

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FIGURE 143

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCTCAGAGCTGGTCTG
CCATGGGACATCCTGGTCCCCTCCTGCAGCTGCTGGTGTCTTCTTACCCTGCCCCCTGCACCTCATGGCTCTGC
TGGGCTGCTGGCAGCCCCCTGTGCAAAAGCTACTTCCCCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCA
AGATGGAGAGCAAGAAACGGGAGCTCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTAC
TGGAGCTGGGCTGCGGAACCGGAGCCAACTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACCCAA
ATCCCCACTTTGAGAAGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATATGAGCGGTTTGTGGTGG
CTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGTGGTGGTCTGCACTCTGGTGTCTGTCTCTG
TGCAGAGCCCAAGGAAGGTCTGCAGGAGGTCCGGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTTCTGGGAGC
ATGTGGCAGAACCATATGGAAGCTGGGCCTTCATGTGGCAGCAAGTTTTCGAGCCCACCTGGAAACACATTGGGG
ATGGCTGCTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCCAGTTCTCCGAAATCCAAATGGAACGAC
AGCCCCCTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTCAAACAATCTTTCCCAAGCT
CCAAGGCACTCATTGCTCCTTCCCCAGCCTCCAATTAGAACAAGCCACCCACCAGCCTATCTATCTTCCACTGA
GAGGGACCTAGCAGAATGAGAGAAGACATTGATGACACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGC
AATCTCTAACTTCAATCCCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGG
ACCCTGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCCTCCCAATGTTGTCCCTTTCTCT
CGTTCCCATGGTAAAGCTCCTCTCGCTTTCTCCTGAGGCTACACCCATGCGTCTCTAGGAACTGGTCACAAAAG
TCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCCTCTCTCCCCACTACCACCTTCTTCTGAGCTGGGGGCA
CCAGGGAGAATCAGAGATGCTGGGGATGCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTT
TAATAAATAGACGAAACCACG

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FIGURE 144

MDILVPLLQLLVLLLTLPPLHMLLGCWQPLCKSYFPYLMVLTTPKSNRKMESKKRELFSSQIKGLTGASGKVALL
ELGCGTGANFQFYPPGCRVTCCLDPNPHFEKFLTKSMAENRHLQYERFVVAPGEDMRQLADGSMDVVVCTLVLCVS
QSPRKVLQEVRRVLRPGGVLFWEHVAEPYGSWAFMWQQVFPTWKHIGDGCCLTRETWKDLENAQFSEIQMERQ
PPPLKWLVPVPHIMGKAVKQSFPSKALICSFPSLQLEQATHQPIYLPRLGT

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FIGURE 145

GTGGGATTATTTGAGTGCAAGATCGTTTCTCAGTGGTGGTGGAAAGTTGCCTCATCGCAGGCAGATGTTGGGGC
TTTGTCCGAACAGCTCCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAACTAATATTTATATGACAGAAGAAAA
AGATGTCATTCCGTAAAGTAAACATCATCATCTTGGTCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACCATA
ACTTCCTCAGCTTGAGCAGTTTGTAAAGGAATGAGGTTACAGATTGAGGAATGTAGGGCCCAACCTATAGACT
TTGTCCCAAATGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCCTGTGGTCATCGCTGCATCTGAAG
ACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATTGAGCACAACACTCGCTCCAATGTGATTTTCTACATTG
TTACTCTCAACAATACAGCAGACCATCTCCGGTCCTGGCTCAACAGTGATTCCCTGAAAAGCATCAGATACAAAA
TTGTCAATTTTGACCCTAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGGAATCCATGAAACCTT
TAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCCCAGCGCAAAGAAGGCCATATACATGGATGATGATGTAA
TTGTGCAAGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATT
GTGATTCAGCCTCTACTAAAGTTGTCATCCGTGGAGCAGGAAACCAGTACAATTACATTGGCTATCTTGACTATA
AAAAGGAAAGAATTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAACC
TGACGGAATGGAAACGACAGAATATACTAACCAACTGGAAAAATGGATGAAACTCAATGTAGAAGAGGGACTGT
ATAGCAGAACCCTGGCTGGTAGCATCACAACACCTCCTCTGCTTATCGTATTTTATCAACAGCACTCTACCATCG
ATCCTATGTGGAATGTCCGCCACCTTGGTTCCAGTGCTGGAAAACGATATTCACCTCAGTTTGTAAAGGCTGCCA
AGTTACTCCATTGGAATGGACATTTGAAGCCATGGGGAAGGACTGCTTCATATACTGATGTTTGGGAAAAATGGT
ATATTCCAGACCCCAACAGGCAATTCAACCTAATCCGAAGATATACCGAGATCTCAAACATAAAGTGAACAGAA
TTTGAAGTGAAGCAAGCATTTCTCAGGAAGTCCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTC
AATGCCTATCGGTAGCAAGCCATGGAAAAAGATGTGTCAGCTAGGTAAAGATGACAACTGCCCTGTCTGGCAGT
CAGCTTCCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTTCCTTACTACAATGCTG
AATGACTGGAAAGAAGAACTGATATGGCTAGTTTCAAGCTAGCTGGTACAGATAATTCAAACTGCTGTTGGTTTTA
ATTTTGTAACCTGTGGCCTGATCTGTAAATAAACTTACATTTTTC

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FIGURE 146

MSFRKVNIIILVLAVALFLLVLHHNFLSLSSLLRNEVTDSGIVGPQPIDFVPNALRHAVDGRQEEIPVVIAASED
RLGGAIAAINSIQHNTSRNVIFYIVTLNNTADHLRSWLNSDSLKSIRYKIVNFDPKLLEGKVKEDPDQGESMKPL
TFARFYLPILVPSAKKAIYMDDDVIVQGDILALYNTALKPGHAAAFSEDCDSASTKVVIRGAGNQYNYIGYLDYK
KERIRKLSMKASTCSFNPGVFVANLTEWKRONITNQLKWMKLNVEEGLYSRTLGSITTPLLIVFYQQHSTID
PMWNVRLGSSAGKRYSPQFVKAALLHWNGHLKPWGRTASYTDVWEKWIIPDPTGKFNLIRRYTEISNIK

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FIGURE 147

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCCAGGCTACCAGTTCCTCCAAGCA
AGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTACTCCCTATTTGCATCTGTTTTGATAA
ATGATGTTGACACCCTCCACCGAATTCCTAAGTGGAAATCATGTCGGGAAGAGATACAATCCTTGGCCTGTGTATCC
TCGCATTAGCCTTGTCTTTGGCCATGATGTTTACCTTCAGATTTCATCACCACCCTTCTGGTTCACATTTTCATTT
CATTGGTTATTTTGGGATTGTTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACCTCA
GCATAGAATTGGACACAGAAAGGGAAAATATGAAGTGCGTGCTGGGGTTTGCTATCGTATCCACAGGCATCACGG
CAGTGCTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATTGACAGTTGAGCTTTTCCAAATCACAAATA
AAGCCATCAGCAGTGCTCCCTTCCTGCTGTTCCAGCCACTGTGGACATTTGCCATCCTCATTTTCTTCTGGGTCC
TCTGGGTGGCTGTGCTGCTGAGCCTGGGAAGTGCAGGAGCTGCCCAGGTTATGGAAGGCGGCCAAGTGGAAATATA
AGCCCCCTTCGGGCATTTCGGTACATGTGGTCGTACCATTTAATTGGCCTCATCTGGACTAGTGAATTCATCCTTG
CGTGCCAGCAAATGACTATAGCTGGGGCAGTGGTTACTTGTTATTTCAACAGAAGTAAAAATGATCCTCCTGATC
ATCCCATCCTTTTCGTCTCTCTCCATTCTCTTCTTCTACCATCAAGGAACCGTTGTGAAAGGGTCATTTTTAATCT
CTGTGGTGAGGATTCCGAGAATCATTGTCTGTACATGCAAACGCACTGAAAGAACAGCAGCATGGTGCATTGT
CCAGGTACCTGTTCCGATGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATG
CATATACTACAACCTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAAATCTTGTCCAAGA
ACTCAAGTCACTTTACATCTATTAAGTGGTCTTTGGAGACTTCATAATTTTCTAGGAAAGGTGTTAGTGGTGTGTT
TCACTGTTTTTTGGAGGACTCATGGCTTTTAACTACAATCGGGCATTCAGGTGTGGGCAGTCCCTCTGTTATTGG
TAGCTTTTTTTGCCTACTTAGTAGCCCATAGTTTTTTATCTGTGTTTGAAACTGTGCTGGATGCACTTTTCTGT
GTTTTGCTGTTGATCTGGAAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTT
TCGTAAAAAGGAGCAACAAATTAAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAAGGAATGAGGAGGGAA
CAGAACTCCAGGCCATTGTGAGATAGATACCCATTTAGGTATCTGTACCTGGAAAACATTTCTTCTAAGAGCCA
TTTACAGAATAGAAGATGAGACCACTAGAGAAAAGTTAGTGAATTTTTTTTTTAAAGACCTAATAAACCCCTATTC
TTCCTCAAAA

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FIGURE 148

MSGRDTILGLCIIALALSLAMMFTFRFITTLVHIFISLVILGLLFVCGVLWWLYDYTDNLSIELDTERENMKC
VLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLLFQPLWTFAILIFFWVLWVAVLLSLGTAG
AAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFILACQQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFY
HQGTVVKGSFLISVVRIPRIIVMYMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFC
TSAKDAFKILSKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGMLMAFNYNRAFQVWAVPLLLVAFFAYLVVHSFL
SVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRNEEGTELQAIVR

FIGURE 149

[illegible]

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FIGURE 150

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINCDVKAGKIIDPEFIVKCPAGCQDPKYHVG
TDVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSLSLPRWRESFIVLESKPKKGVTPYSAL
TYSSSKSPAAQAGETTKAYQRPFIPGTTAQPVTLMQLLAVTVAVATPTTLPRPSPSAASTTSIPRQSVGHRSEQE
MDLWSTATYTSSQNRPRADPGIQRQDPSGAAPQKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDG
STSIGKRRFRIQKQLLADVAQALDIGPAGPLMGVVQYGDNPATHFNLKHTNSRDLKTAIEKITQRGGLSNVGRA
ISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAENKQYVVEPNFANKAV
CRTNGFYSLHVQSWFGLHKTLOPLVKRVCDTDRACSKTCLNSADIGFVIDGSSSVGTGNFRTVLQFVTNLTKF
EISDTDRIGAVQYTYEQRLIEFGFDKYSSKPDILNAIKRVGYWSSGTSTGAAINFALEQLFKKSKPNKRKLMILI
TDGRSYDDVRIPAMAAHLKGVITYAIGVAWAAQEELEVIATHPARDHSEFFVDEFDNLHQYVPRIIQNICTEFNSQPRN

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FIGURE 151

CAGGATGAACTGGTTGCAGTGGCTGCTGCTGCTGCGGGGGCGCTGAGAGGACACGAGCTCT**ATG**CCTTTCCGGCT
GCTCATCCCGCTCGGCCCTCCTGTGCGCGCTGCTGCCTCAGCACCATGGTGCGCCAGGTCCCGACGGCTCCGCGCC
AGATCCCGCCCACTACAGTTTTTCTCTGACTCTAATTGATGCACTGGACACCTTGCTGATTTTGGGGAATGTCTC
AGAATTCCAAAGAGTGGTTGAAGTGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCCTCTGTGTTTGA
AACAAACATTTCGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGGTGGAAGTAGAGGC
TGGATGGCCCTGTTCCGGGCCTCTCCTGAGAATGGCTGAGGAGGCGGCCCGAAAACCTCCTCCAGCCTTTCAGAC
CCCCACTGGCATGCCATATGGAACAGTGAACCTACTTTCATGGCGTGAACCCAGGAGAGACCCCTGTACCTGTAC
GGCAGGGATTGGGACCTTCATTGTTGAATTTGCCACCCTGAGCAGCCTCACTGGTGACCCGGTGTTTGAAGATGT
GGCCAGAGTGGCTTTGATGCGCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTCGGCAACCCACATTGATGTGCT
CACTGGCAAGTGGGTGGCCCAGGACGCAGGCATCGGGGCTGGCGTGGACTCCTACTTTGAGTACTTGGTGAAAGG
AGCCATCCTGCTTCAGGATAAGAAGCTCATGGCCATGTTCTAGAGTATAACAAAGCCATCCGGAACCTACACCCG
CTTCGATGACTGGTACCTGTGGGTTTCAAGTGTACAAGGGGACTGTGTCCATGCCAGTCTTCCAGTCTTGGAGGC
CTACTGGCCTGGTCTTCAGAGCCTCATTGGAGACATTGACAATGCCATGAGGACCTTCTCAACTACTACACTGT
ATGGAAGCAGTTTGGGGGGCTCCCGGAATTCTACAACATTCCTCAGGGATACACAGTGGAGAAGCGAGAGGGCTA
CCCACTTCGGCCAGAACTTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCCAACCTCCTAGAACT
CGGAAGAGATGCTGTGGAATCCATTGAAAAATCAGCAAGGTGGAGTGCGGATTTGCAACAATCAAAGATCTGCG
AGACCACAAGCTGGACAACCGCATGGAGTCGTTCTTCTGGCCGAGACTGTGAAATACCTCTACCTCCTGTTTGA
CCCAACCAACTTCATCCACAACAATGGGTCCACCTTCGACGCGGTGATCACCCCTATGGGGAGTGCATCCTGGG
GGCTGGGGGGTACATCTTCAACACAGAAGCTCACCCATCGACCTTGCCGCCCTGCACTGCTGCCAGAGGCTGAA
GGAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATTCTACTCTCTCAAACGGAGCAGGTGGAATTTTCAAG
AAACACTGTTAGTTCGGGGCCATGGGAACCTCCAGCAAGGCCAGGAACACTCTTCTCACCAGAAAACCATGACCA
GGCAAGGGAGAGGAAGCCTGCCAAACAGAAGGTCCCACTTCTCAGCTGCCCCAGTCAGCCCTTACCTCCAAGTT
GGCATTACTGGGACAGGTTTTCTAGACTCCTC**TA**ACCACTGGATAATTTTTTTATTTTTTATTTTTTTGAGGCT
AAACTATAATAAATTGCTTTTGGCTATCATAAAA

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FIGURE 152

MPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYSFSLTLIDALDTLLILGNVSEFQRVVEVLQDSVDFDIDVN
ASVFETNIRVVGGLLSAHLSSKKAGVEVEAGWPCSGPLLMAEEAARKLLPAFQTPTGMPYGTVNLLHGVNPGET
PVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFE
YLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDWYLWVQMYKGTVSMFPVFSLEAYWPGLQSLIGDIDNAMRTFL
NYYTVWKQFGGLPEFYNIPOGYTVEKREGYPLRPELIESAMYLYRATGDPITLLELGRDAVESIEKISKVECGFAT
IKDLRDHKLDRMESFFLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYIFNTEAHPIDLAALHC
CQRLKEEQWEVEDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPGTLESPENHDQARERKPAKQKVPLLSGPSQP
FTSKLALLGQVFLDSS

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FIGURE 153

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTGGGAGGGGGCAGGATGGGAGGGAAAGTGAAGAAAACA
GAAAAGGAGAGGGACAGAGGCCAGAGGACTTCTCATACTGGACAGAAACCGATCAGGC**ATG**GAACTCCCCCTTCGT
CACTCACCTGTTCTTGCCCCCTGGTGTTCCTGACAGGTCTCTGCTCCCCCTTTAACCTGGATGAACATCACCACG
CCTATTCCCAGGGCCACCAGAAGCTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGACAGCGATGGAT
GCTGGTGGGCGCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTTTATCGCTGCCCTGTAGGGGGGGC
CCACAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTACCAACTGGGAAATTCACTCTCATCCTGCTGTGAATAT
GCACCTGGGGATGTCTCTGTTAGAGACAGATGGTGATGGGGGATTCACTGGTGAGC**TAAG**GAGAGGGTGGTGGCAG
TGTCTCTGAAGGTCCATAAAAGAAAAAGAGAAGTGTGGTAAGGGAAATGGTCTGTGTGGAGGGGTCAAGGAGT
TAAAAACCTAGAAAGCAAAAGGTAGGTAATGTCAGGGAGTAGTCTTCATGCCTCCTTCAACTGGGAGCATGTTT
TGAGGGTGCCCTCCCAAGCCTGGGAGTAACTATTTCCCCCATCCCAGGCCTGTGCCCTCTCTGGTCTCGTGCT
TGTGGCAGCTCTGTCTTCAGTTCTGGGATATGTGCCCGTGTGGATGCTTCATTCCAGCCTCAGGGAAGCCTGGCA
CCCACTGCCAACGTGAGCCAGAGGAAGGCTGAGTACTTGGTTCCCAAGAGGAGATACTGGGTGGGAAAAAGATG
GGGCAAAGCGGTATGATGCCTGGCAAAGGGCCTGCATGGCTATCCTCATTGCTACCTAATGTGCTTGCAAAAGCT
CCATGTTTCCTAACAGATTCAGACTCCTGGCCAGGTGTGGTGGCCACACCTGTAATTCTAGCACTTTGGGAGGC
CAAGGTGGGCAGATCACTTGAGGTCAGGAGTTCAGACCAGCCTGGCCAACATGGTGAACTCCATCTCTACTAA
AAAAAAAAAATACAAAAATTAGCTGGGTGCGCTAGTGCATGCCTGTAATCTCATCTACTCGGGAGGCTAAGACA
GGAGACTCTCACTTCAACCCAGGAGGTGGAGGTTGCGGTGAGCCAAGATTGTGCCTCTGCACTCTAGCGTGGGTG
ACAGAGTAAGCGAGACTCCATCTCAAAAATAATAATAATAATTCAGACTCCTTATCAGGAGTCCATGATCTG
GCCTGGCACAGTAACTCATGCCTGTAATCCCAACATTTTGGGAGGCCAACGCAGGAGGATTGCTTGAGGTCTGGA
GGTTTGAGACCAGCCTGGGCAACATAGAAAGACCCCATCTCTAAATAAATGTTTTAAAAAT

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FIGURE 154

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57039
><subunit 1 of 1, 124 aa, 1 stop
><MW: 13352, pI: 5.99, NX(S/T): 1
MELPFVTHLFLPLVFLTGLCSFNLDEHHPRLFPGPPEAEFGYSVLQHVGGGQRWMLVGAPWDGPGSGDRRGDVYR
CPVGGAHNAPCAKGLGDYQLGNSSHPAVNMHLGMSLLETGDGGFMVS
```

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 70-73

N-glycosylation site.

amino acids 98-101

Integrins alpha chain proteins

amino acids 67-81

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FIGURE 155

GCGAGCTCCGGGTGCTGTGGCCCGGCCTTGGCGGGGCGGCCTCCGGCTCAGGCTGGCTGAGAGGCTCCCAGCTGC
AGCGTCCCCGCCCGCCTCCTCGGGAGCTCTGATCTCAGCTGACAGTGCCCTCGGGGACCAACAAGCCTGGCAGG
GTCTCACTTTGTTGCCAGGCTGGAGTTCAGTGCCATGATCATGGTTTACTGCAGCCTTGACCTCCTGGGTTCAA
GCGATCCTGCTGAGTAGCTGGGACTACAGGACAAAATTAGAAGATCAAAATGGAAAAATATGCTGCTTTGGTTGAT
ATTTTTACCCCTGGGTGGACCCTCATTGATGGATCTGAAATGGAATGGGATTTTATGTGGCACTTGAGAAAAGGT
ACCCCGGATTGTCAGTGAAAGGACTTTCCATCTCACCAGCCCCGCATTTGAGGCAGATGCTAAGATGATGGTAAA
TACAGTGTGTGGCATCGAATGCCAGAAAGAACTCCCACTCCCAGCCTTTCTGAATTGGAGGATTATCTTTCCCTA
TGAGACTGTCTTTGAGAAATGGCACC CGAACCTTAACCAGGGTGAAAGTTCAAGATTTGGTTCTTGAGCCGACTCA
AAATATCACCACAAAGGGAGTATCTGTTAGGAGAAAGAGACAGGTGTATGGCACCAGCAGAGGTTGAGCATCTT
GGACAAAAGGTTCTTAACCAATTTCCCTTTGAGCAGCTGTGAAGCTTTCCACGGGCTGTAGTGGCATTCTCAT
TTCCCTCAGCATGTTCTAACTGCTGCCACTGTGTTTCATGATGGAAAGGACTATGTCAAAGGGAGTAAAAAGCT
AAGGGTAGGGTTGTTGAAGATGAGGAATAAAAGTGGAGGCAAGAAACGTCGAGGTTCTAAGAGGAGCAGGAGAGA
AGCTAGTGGTGGTGACCAAAGAGAGGGTACCAGAGAGCATCTGCAGGAGAGAGCGAAGGGTGGGAGAAGAAGAAA
AAAATCTGGCCGGGGTCCAGAGGATTGCCGAAGGGAGGCCTTCCTTTGAGTGGACCCGGGTCAAGAATACCCACAT
TCCGAAGGGCTGGGCACGAGGAGGCATGGGGGACGCTACCTTGGACTATGACTATGCTCTTCTGGAGCTGAAGCG
TGCTCACAAAAAGAAATACATGGAACCTGGAATCAGCCCAACGATCAAGAAAATGCCTGGTGGAATGATCCACTT
CTCAGGATTTGATAACGATAGGGCTGATCAGTTGGTCTATCGGTTTTGCAGTGTGTCCGACGAATCCAATGATCT
CCTTTACCAATACTGCGATGCTGAGTCGGGCTCCACCGGTTCCGGGGTCTATCTGCGTCTGAAAGATCCAGACAA
AAAGAATTGGAAGCGCAAAATCATTGCGGTCTACTCAGGGCACCAGTGGGTGGATGTCCACGGGGTTGAGAAGGA
CTACAACGTTGCTGTTCCGATCACTCCCCTAAAATACGCCCAGATTTGCCTCTGGATTACCGGGAACGATGCCAA
TTGTGCTTACGGCTAACAGAGACCTGAAACAGGGCGGTGTATCATCTAAATCACAGAGAAAACCAGCTCTGCTTA
CCGTAGTGAGATCACTTCATAGGTTATGCCTGGACTTGAACCTCTGTCAATAGCATTTCACATTTTTCAAAATCA
GGAGATTTTCGTCCATTTAAAAAATGTATAGGTGCAGATATTGAAACTAGGTGGGCACTTCAATGCCAAGTATAT
ACTCTTCTTTACATGGTGATGAGTTTCATTTGTAGAAAAATTTGTTGCCTTCTTAAAAATTAGACACACTTTAA
ACCTTCAAACAGGTATTATAAATAACATGTGACTCCTTAATGGACTTATTCTCAGGGTCTACTCTAAGAAGAAAT
CTAATAGGATGCTGGTTGTGTATTAAATGTGAAATTCATAGATAAAGGTAGATGGTAAAGCAATTAGTATCAGA
ATAGAGACAGAAAGTTACAACACAGTTGTACTACTCTGAGATGGATCCATTCAGCTCATGCCCTCAATGTTTAT
ATTGTGTTATCTGTTGGGTCTGGGACATTTAGTTTAGTTTTTTGAAGAATTACAAATCAGAAGAAAAAGCAAGC
ATTATAAACAAAACATAAATACTGTTTTACTGCTTTAAGAAATAACAATTACAATGTGTATTATTTAAAAATGGGA
GAAATAGTTTGTCTATGAAATAAACCTAGTTTAGAAATAGGGAAGCTGAGACATTTTAAGATCTCAAGTTTTTA
TTTAATAATACTCAAAATATGGACTTTTCATGTATGCATAGGGAAGACACTTCACAAATTATGAATGATCATGT
GTTGAAAGCCACATTATTTTATGCTATACATTCTATGTATGAGGTGCTACATTTTAGGACAAAGAATTCTGTAA
TCTTTTTCAAGAAAGAGTCTTTTTCTCCTTGACAAAATCCAGCTTTTGTATGAGGACTATAGGGTGAATTTCTCTG
ATTAGTAATTTTAGATATGTCCTTTCTTAAAAATGAATAAAATTTATGAATATGA

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FIGURE 156

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253
<subunit 1 of 1, 413 aa, 1 stop
<MW: 47070, pI: 9.92, NX(S/T): 3
MENMLLWLIFFTPGWTLLIDGSEMEWDFMWHLRKVPRIVSERTFHLTSPAFEADAKMMVNTVCGIECQKELPTPSL
SELEDYLSYETVFENGTRTLTRVKVQDLVLEPTQNITTKGVSVRRKRQVYGTDSRFSILDKRELTNFPFSTAVKL
STGCSGILISPQHVLTAACHVDGKDYVKGSKKLRVGLLKMRNKSGGKKRRGSKRSRREASGGDQREGTREHLQE
RAKGRRRRKKSGRGQRIAEGRPSFQWTRVKNTHIPKGWARGGMGDATLDYDYALLELKRAHKKKYMELGISPTIK
KMPGGMIHFSGFDNDRADQLVYRFCSVSDSNLLYQYCDAESGSTGSGVYLRLLKDPDKKNWKKRIIAVYSGHQW
VDVHGVQKDYNVAVRITPLKYAQICLWIHGNDANCAYG
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Important features:**Signal peptide:**

amino acids 1-16

N-glycosylation sites.

amino acids 90-93, 110-113 and 193-196

Glycosaminoglycan attachment site.

amino acids 236-239

Serine proteases, trypsin family, histidine active site.

amino acids 165-170

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FIGURE 157

GGGACCCATGCGGCCGTGACCCCGGCTCCCTAGAGGCCAGCGCAGCCGAGCGGACAAAGGAGCATGTCCGCG
CCGGGGGAAGGCCCGTCCCTCCGGCCGCCATAAGGCTCCGGTCCGCGCTGGGCCCGCGCCGCGCTCCTGCCCGCCCG
GGCTCCGGGGCGGCCCGCTAGGCCAGTGCGCCGCCGTGCGCCCGCAGGCCCGGCCCGCAGC**ATGG**AGCCACCC
GGACGCCGGCGGGGCCGCGCGCAGCCGCCGTGTTGCTGCCGCTCTCGCTGTTAGCGCTGCTCGCGCTGCTGGGA
GGCGGCGGCGGGCGGCGGCCGCGCGCTGCCCGCCGGCTGCAAGCACGATGGGCGGCCCGAGGGGCTGGCAGG
GCGGCGGGCGGCCCGGAGGGCAAGGTGGTGTGCAGCAGCCCTGGAACTCGCGCAGGTCTGCCCCAGATACTCTG
CCCAACCGCACGGTCAACCCTGATTCTGAGTAACAATAAGATATCCGAGCTGAAGAATGGCTCATTTTCTGGGTTA
AGTCTCCTTGAAAGATTGACCTCCGAAACAATCTTATTAGTAGTATAGATCCAGGTGCCTTCTGGGGACTGTCA
TCTCTAAAAAGATTGGATCTGACAAACAATCGAATAGGATGTCTGAATGCAGACATATTTTCGAGGACTCACCAAT
CTGGTTCGGCTAAACCTTTTCGGGAATTTGTTTTCTTCATTATCTCAAGGAACCTTTTGATTATCTTGCGTCATTA
CGGTCTTTGGAATTCAGACTGAGTATCTTTGTGTGACTGTAACATACTGTGGATGCATCGCTGGGTAAAGGAG
AAGAACATCACGGTACGGGATACCAGGTGTGTTTATCCTAAGTCACTGCAGGCCCAACCACTCACAGGCGTGAAG
CAGGAGCTGTTGACATGCGACCCCTCCGCTTGAATTGCCGTCTTTTACATGACTCCATCTCATCGCCAAGTTGTG
TTTGAAGGAGACAGCCTTCCCTTTCCAGTGCATGGCTTCATATATTGATCAGGACATGCAAGTGTTGTGGTATCAG
GATGGGAGATAGTTGAAACCGATGAATCGCAAGGTATTTTTGTTGAAAAGAACATGATTACAACCTGCTCCTTG
ATTGCAAGTGCCCTAACCATTTCTAATATTCAGGCTGGATCTACTGGAAATTGGGGCTGTCTGTCCAGACCAAA
CGTGGGAATAATACGAGGACTGTGGATATTGTGGTATTAGAGAGTTCTGCACAGTACTGCTCCAGAGAGGGTG
GTAAACAACAAGGTGACTTCAGATGGCCCAAGACATTGGCAGGCATTACTGCATATCTGCAGTGTACGCGGAAC
ACCCATGGCAGTGGGATATATCCCGGAAACCCACAGGATGAGAGAAAAGCTTGGCGCAGATGTGATAGAGGTGGC
TTTTGGGCAGATGATGATTATTCTCGCTGTCTAGTATGCAAATGATGTCACTAGAGTTCTTTATATGTTTAATCAG
ATGCCCCCTCAATCTTACCAATGCCGTGGCAACAGCTCGACAGTTACTGGCTTACACTGTGGAAGCAGCCAACCTT
TCTGACAAAATGGATGTTATATTTGTGGCAGAAATGATTGAAAATTTGGAAGATTTACCAAGGAGGAAAAATCA
AAAGAGCTAGGTGACGTGATGGTTGACATTGCAAGTAACATCATGTTGGCTGATGAACGTGTCCTGTGGCTGGCG
CAGAGGGAAGCTAAAGCCTGCAGTAGGATTGTGCAGTGTCTTCAGCGCATTGCTACCTACCGGCTAGCCGGTGGGA
GCTCACGTTTATTCAACATATTCACCCAATATTGCTCTGGAAGCTTATGTCAATCAAGTCTACTGGCTTCACGGGG
ATGACCTGTACCGTGTTCAGAAAGTGGCAGCCTCTGATCGTACAGGACTTTCGGATTATGGGAGGCGGGATCCA
GAGGGAACCTGGATAAGCAGCTGAGCTTTAAGTGCAATGTTTCAAATACATTTTCGAGTCTGGCACTAAAGGTA
TGTTACATTCTGCAATCATTTAAGACTATTTACAGT**TAA**ATTAGAATGCTCCAAATGTTCTGCTTCGCAAAATAA
CCTTATTAAAAGATTTTTTTTTGCAGGAAGATAGGTATTATTGCTTTTGCTACTGTTTTAAAGAAAACCTAACCA
GAAGAAGTGCATTACGACTTTCAAGGGCCCTAGGCATTTTTGCCTTTGATTCCCTTTCTTCACATAAAAATATCA
GAAATTACATTTTATACTGCAGTGGTATAAATGCAAATATACTATTGTTACATGTAAAAAATTTTATTTGACT
TAAAGTTTTATTTATTTGTTTTTTGCTCCTGATTTTAAGACAATAAGATGTTTTCATGGGCCCTAAAAGTATC
ATGAGCCTTTGGCACTGCGCCTGCCAAGCCTAGTGGAGAAGTCAACCTGAGACCAGGTGTTTAAATCAAGCAAGC
TGTATATCAAAATTTTGGCAGAAAACACAAATATGTCATATATCTTTTTTAAAAAAGTATTTTATTGAAGCA
AGCAAAATGAAAGCATTTTTACTGATTTTTTAAATTTGGTGCTTTAGATATATTGACTACACTGTATTGAAGCAA
ATAGAGGAGGCCAACTCCAGCACCCCTAATGGAACCACATTTTTTTCACTTAGCTTTCTGTGGGCATGTGTAATT
GTATTCTCTCGGTTTTTAAATCTCACAGTACTTTATTTCTGTCTTGTCCCTCAATAATATCACAAACAATATTCC
AGTCATTTTAAATGGCTGCATAATAACTGATCCAACAGGTGTTAGGTGTTCTGGTTTAGTGTGAGCACTCAATAAA
TATTGAATGAATGAACGAAAAAAAAAAAAAAAAA

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FIGURE 158

MEPPGRRRRGRAQPPLLLPLSLLALLALLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGKVVCSSLELAQVLP
PDTLPNRTVTLILSNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGAFWGLSSLKRLDLTNNRIGCLNADIFR
GLTNLVRNLNSGNLFSSLSQGTFDYLASLRSLFQTEYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLQAQPV
TGVKQELLTCDPPIELPSFYMTPSHRQVVFEGDSLFPQCMASYIDQMQVLWYQDGRIVETDESQGIFVEKNMIH
NCSLIASALTISNIQAGSTGNWGCHVQTKRGNNTRTVDIVVLESSAQYCPPERVVNNKGDFRWPRTLGITAYLQ
CTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDDYSRCQYANDVTRVLYMFNQMPNLNTNAVATARQLLAYTVE
AANFSDKMDVIFVAEMIEKFGRFTKEEKSKELGDMVDIASNIMLADERVLWLAQREAKACSRIVQCLQRIATYR
LAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCTVFQKVAASDRTGLSDYGRRDPEGNLDKQLSFKCNVSNTFSSL
ALKVCYILQSFKTIYS

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 13-40 (type II)

N-glycosylation site.amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336, 433-437,
453-457, 592-596**N-myristoylation site.**amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57, 57-63, 99-105,
123-129, 142-148, 162-168, 317-323, 320-326, 384-390, 403-409, 554-560

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FIGURE 159

GGGGAATCTGCAGTAGGTCTGCCGGCGATGGAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTGGCTGCTGTTGTTTCTCCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAAATGGAAAGTATTTATTGACCAAATTAACAGGTCTTTTGGAGAATTACGAACCATGTTCAAGTCAAAACTGCAGCTGCTACCATGGTGTATAGAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCAGGAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCCTAAGAACAGACTGTACCGGGAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTTATTTTGGAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCCTCAGGTTCCCTAAATGGATGGAGCTGCCATCCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACCATGATATCATGTATCCTGCTTGGACATTTGGGAAGGGGGACCTGCTGTTTGGCCAAATTTATCCTACAGGTCTTGGACGGTGGGACCTCTTCAGAGAAGATCTGTAAGGTGAGCAGCACAGTGGCCATGGAAAAAGAAAACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAGATCCTCTCATTCTTCTGTCTCGGAAAAACCCAAAACCTTGTTGATGCAGAATACACCAAAAACCAGGCCGTAAGGTCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGTGGATCACTGCAAATACAAGTATCTGTTTAAATTTTCGAGGCTAGCTGCAAGTTTCCGGTTTAAACACCTCTTCCTGTGTGGCTCACTTGTTTTTCATGTTGGTGATGAGTGGCTAGAAATCTTCTATCCACAGCTGAAGCCATGGGTTCACTATATCCCAGTCAAAACAGATCTCTCCAATGTCCAAGAGCTGTTACAATTTGTAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGGAAGCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCTCTTGAGTGAATACTCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAGGTTATGATCAAATTATTTCCCAAAATGTTGAAAACCTGAACCTATAGTAGTCATCATAGGACCATAGTCCTCTTGTGGCAACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATATCTGCTATCAAGCCAAATACCTGGTTTTCTTATCATGCTGCACCCAGAGCAACTCTTGAGAAAGATTTAAATGTGTCTAATACACTGATATGAAGCAGTTCAACTTTTTGGATGAATAAGGACCAGAAATCGTGAGATGTGGATTTTGAACCCAACTCTACCTTTCAATTTCTTAAGACCAATCACAGCTTGTGCCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCATGTGATGATGCCCTTTGTCCCATTATTTGGAGCAGAAAATTCGTCAATTTGGAAGTAGTACAACCTATTGCTGGAATTGTGAAATTATTCAGGCGTGATCTCTGTCACTTTATTTAATGTAGGAAACCCATATGGGGTTTATGAAAAATACTTGGGGATCATCTCTGAATGGTCTAAGGAAGCGGTAGCCATGCCATGCAATGATGTAGGAGTTCTCTTTGTAAACCATAAACTCTGTTACTCAGGAGGTTTCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATTATGCAATTGGATTTCAGGTTCCCTTTTGTGCCCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAAA

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FIGURE 160

MEWWASSPLRLWLLLFLLP
SAQGRQKESGSKWKVFIDQ
INRSLENYEPCSSQNCSCY
HGVIEEDLTPFRGGISRK
MMAEVVRRKLGTHYQITKN
RLYREND CMFPSRCSGVEH
FILEVIGRLPDMEMVINVR
DYPQVPKWMEPAIPVFSF
SKTSEYHDIMYPAWTFWEG
GPAVWPIYPTGLGRWDLFR
EDLVRSAQWPWKKKNSTAY
FRGSRTSPERDPLILLS
RKNPKLVDAEYTKNQAWKS
MKDTLGKPAAKDVHLVDHC
KYKYLNFNFRGVAASFRFK
HLFLCGSLVFHVGDWLEF
FYPQLKPWVHYIPVKTDLS
NVQELLQFVKANDDVAQEIA
ERGSQFIRNHLQMDDITCY
WENLLSEYSKFLSYNVT
RRKGYDQIIPKMLKTEL

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FIGURE 161

CCGAGCACAGGAGATTGCCGTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGAAGAAATTGCCAAA
CCATGTCTTTTTTCTGTTTTTCAGAGTAGTTTACAACAGATCTGAGTGTTTTAATTAAGCATGGAATACAGAAAA
CAACAAAAAAGCTTAAGCTTTAATTTTCATCTGGAATTCACAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTT
GGCTCTTCCCGCTGGCTGCTCTATCACGTGGTGCTCTCCGACTACTCACCCGAGTGTAAGAACCCTTCGGCTCG
CGTGCTTCTGAGCTGCTGTGGATGGCCTCGGCTCTCTGGACTGTCCTTCCGAGTAGGATGTCACTGAGATCCCTC
AAATGGAGCCTCCTGCTGCTGTCACTCCTGAGTTTCTTTGTGATGTGGTACCTCAGCCTTCCCCACTACAATGTG
ATAGAACGCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTTACAGACAAGACTTTCACTTCACACTTCGA
GAGCATTCAAAGTCTCTCATCAAAATCCATTTCTGGTCATTCTGGTGACCTCCCACCCTTCAGATGTGAAAGCC
AGGCAGGCCATTAGAGTTACTTGGGGTGAAAAAAGTCTTGGTGGGGATATGAGGTTCTTACATTTTTCTTATTA
GGCCAAGAGGCTGAAAAGGAAGACAAAATGTTGGCATTGTCTTAGAGGATGAACACCTTCTTTATGGTGACATA
ATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAACCATTATGGCATTACAGGTGGGTAACGTGAG
TTTTGCCCAATGCCAAGTACGTAATGAAGACAGACACTGATGTTTTTCATCAATACTGGCAATTTAGTGAAGTAT
CTTTTAAACCTAAACCACTCAGAGAAGTTTTTTCACAGGTTATCCTCTAATTGATAATTATTCCTATAGAGGATTT
TACCAAAAAACCCATATTTCTTACCAGGAGTATCCTTTCAAGGTGTCCCTCCATACTGCAGTGGGTTGGGTTAT
ATAATGTCCAGAGATTTGGTGCCAAGGATCTATGAAATGATGGGTCACGTAAAACCCATCAAGTTTGAAGATGTT
TATGTCGGGATCTGTTTGAATTTATTAAGTGAACATTCAATTCAGAGACACAAATCTTTCTTTCTATAT
AGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATTGCAGCCCATGGCTTTTCTTCCAAGGAGATCATCACT
TTTTGGCAGGTCATGCTAAGGAACACCACATGCCATTATTAACCTTCACATTCTACAAAAAGCCTAGAAGGACAGG
ATACCTTGTGGAAAGTGTTAAATAAAGTAGGTACTGTGGAAAATTCATGGGGAGGTCAGTGTGCTGGCTTACACT
GAAGTGAAGTCAAGAAAACCCAGACTGGAGACTGGAGGGTTACACTTGTGATTTATTAGTCAGGCCCTTCAAA
GATGATATGTGGAGGAATTAATATAAGGAATTGGAGGTTTTTGCTAAAGAAATTAATAGGACCAACAATTTG
GACATGTCATTCTGTAGACTAGAATTTCTTAAAGGGTGTTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAA
AACAAATGTAGAGTTTTATTATTGAACAATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGGATTACCAAT
TTAAAAATATATGTAGTTCTGTGTCAAAAAACTTCTTCACTGAAGTTATACTGAACAAAATTTTACCTGTTTTTG
GTCATTTATAAAGTACTTCAAGATGTTGCAGTATTTACAGTTATTATTATTTAAATTAAGTTCACTTTGTGTT
TTTAAATGTTTTGACGATTTCAATACAAGATAAAAGGATAGTGAATCATTCTTACATGCAACATTTTCCAGT
TACTTAACTGATCAGTTTATTATTGATACATCACTCCATTAATGTAAAGTCATAGGTCAATTATTGCATATCAGTA
ATCTCTTGGACTTTGTAAATATTTTACTGTGGTAATATAGAGAAGAATTAAAGCAAGAAAATCTGAAA

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FIGURE 162

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPiYRQDFHFTLREHSNCSH
QNPFVLVILVTSHPSDVKARQAIRVTWGEKKSWWGYEVLTFLLGQEA EKEDKMLALSLEDEHLLYGDII RQDFLD
TYNNLTlKTI MAFRWVTEFCPN AKYVMKTD TDVFINTGNLVKYLNLNHSEKFFTGYPLIDNYSYRGFYQKTHIS
YQEYPFKVFPPYCSGLGYIMSRDLVPRIYEMMGHV KPIKFEDVYVGICLNLLKVNIHIPEDTNLFFLYRIHLDVC
QLRRVIAAHGFSSKEIITFWQVMLRNTTCHY

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FIGURE 163

CATTTCTGAACTAATCGTGTGAGAATTGACTTTGAAAAGCATTGCTTTTTACAGAAGTATATTAACTTTTTAGG
AGTAATTTCTAGTTTGGATTGTAATATGAAATAATTTAAAAGGGCTTCGCTCATATATAGGAAAATCGCATATGG
TCCTAGTATTAAATTCCTATTGCTTACTGATTTTTTTGAGTTAAGAGTTGTTATATGCTAGAAATATGAGGATGTG
AATATAAATAAGAGAAGAAAAAGAATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAAGTGGTT
TGTTTACATGCAAGCTTATAGTTGAAATATTTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTTG
TTCGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTTCAGATTCCGTTGCCAA
CTCGTCCCCATTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAATCCAGGAAATCTGCATAGAAACACTTAGGC
TTTATACCAGAAAAAGCCAACTATGAATTACTGGAAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAG
CCAAATTTAAAGCAAAGGGATTGAATCCGGATGGAACCTCCAGCCCTTCAACCCTGGGTGGATTTTCTCCAGCCT
CCAAGCCATCATCACCAGAGAAGTAAAAGCTGAAGAGAAATCACCAATCTCCATTAATGTGAAGACAGTCAAAA
AAGAACCTGAGGATAGACAACAGGCTTCCAAAAGCCCTTACAATGGTGTAAAGAAAAGACAGCAAGAGAAGTAGAA
ATAGCAGAAGTGCAAGTCGATCGAGGTCAAGAACACGATCACGTTCTAGATCACATACTCCAAGAAGACACTATA
ATAATAGGCGGAGTCGATCTGGAACATACAGCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAAGCCCTC
GAAGACATCATAATCATGGTTCTCCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAAACAGAC
ATGGTCATAAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAGCCAAGAAAC
ACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTTTGAGAGGTCCCATAAAAGCAAGC
ACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCGCTGACTTTCTCTTCTTTGAGCCTGCATCAGTTCT
TGGTTTTGCCTATCTACAGTGTGATGTATGGACTCAATCAAAAACATTAAACGCAAACCTGATTAGGATTTGATTT
CTTGAAACCCTCTAGGTCTCTAGAACACTGAGGACAGTTTCTTTTGAAAAGAACTATGTTAATTTTTTTGCACAT
TAAATGCCCTAGCAGTATCTAATTAAAAACCATGGTCAGGTTCAATTGTACTTTATTATAGTTGTGTATTGTTT
ATTGCTATAAGAACTGGAGCGTGAATTCTGTAAAAATGTATCTTATTTTTATACAGATAAAATTGCAGACACTGT
TCTATTTAAGTGGTTATTTGTTTAAATGATGGTGAATACTTTCTTAACACTGGTTTGTCTGCATGTGTAAAGATT
TTTACAAGGAAATAAAATACAAATCTTGTTTTTCTAAAAAAGT

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FIGURE 164

MNDSLRTNVFVRFPETIACACIYLAARALQIPLPTRPHWFLLFGTTEEEIQEICIETLRLYTRKKPNYELLEKE
VEKRKVALQEAKLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEKSPISINVKTVKKEPEDRQQASKSPYN
GVRKDSKRSRNSRSASRSRSTRSRSRSHTPRRHYNNRRSRSGTYSSRSRSRSHSESPPRRHHNHGSPHLKAKH
TRDDLKSSNRHGHKRKKSRSRSQSKSRDHSDAAKKHRHERGHHRDRRERSRSFERSHKSKHHGGSRSRSGHGRHR

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FIGURE 165

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGCCCCGTGATTTATTAACGTGGCTTA
ATCTGAAGGTTCTCAGTCAAATTTCTTGTGATCTACTGATTGTGGGGGCATGGCAAGGTTTGCTTAAAGGAGCTT
GGCTGGTTTTGGGCCCTTGTAGCTGACAGAAGGTGGCCAGGGAGAATGCAGCACACTGCTCGGAGAATGAAGGCGC
TTCTGTTGCTGGTCTTGCCTTGGCTCAGTCCTGCTAACTACATTGACAATGTGGGCAACCTGCACTTCCTGTATT
CAGAACTCTGTAAAGGTGCCTCCCACTACGGCCTGACCAAAGATAGGAAGAGGCGCTCACAAGATGGCTGTCCAG
ACGGCTGTGCGAGCCTCACAGCCACGGCTCCCTCCCCAGAGGTTTCTGCAGCTGCCACCATCTCCTTAATGACAG
ACGAGCCTGGCCTAGACAACCTTGCTACGTGTCTCGGCAGAGGACGGGCAGCCAGCAATCAGCCCAGTGGACT
CTGGCCGGAGCAACCGAACTAGGGCACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAAAAAATAA
ATCGAGCTTTGAGTGTTCTTTCGAAGGACAAAGAGCGGGAGTGCAAGTTGCCAACCATGCCGACCAGGGCAGGGAAA
ATTCTGAAAACACCCTGCCCCGAAGTCTTTCCAAGGTTGTACCACCTGATTCCAGATGGTGAAATTACCAGCA
TCAAGATCAATCGAGTAGATCCCACTGAAAGCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAACCCCACTGGTCC
ATATCATTATCCAACACATTATTCGTGATGGGGTGATCGCCAGAGACGGCCGGCTACTGCCAGGAGACATCATTC
TAAAGGTCAACGGGATGGACATCAGCAATGTCCCTCACAACCTACGCTGTGCGTCTCCTGCGGCAGCCCTGCCAGG
TGCTGTGGCTGACTGTGATGCGTGAACAGAAGTTCGCGCAGCAGGAACAATGGACAGGCCCCGGATGCCCTACAGC
CCCGAGATGACAGCTTTCATGTGATTCTCAACAAAAGTAGCCCCGAGGAGCAGCTTGGAATAAACTGGTGCGCA
AGGTGGATGAGCCTGGGGTTTTCATCTTCAATGTGCTGGATGGCGGTGTGGCATATCGACATGGTCAGCTTGAGG
AGAATGACCGTGTGTTAGCCATCAATGGACATGATCTTCGATATGGCAGCCAGAAAGTGCGGCTCATCTGATTTC
AGGCCAGTGAAAGACGTGTTACCTCGTGTGTCGCGCCAGGTTCCGCAGCGGAGCCCTGACATCTTTCAGGAAG
CCGGCTGGAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGGAGAGGAGCAACACTCCCAAGCCCCCTCCATCCTA
CAATTACTTGTGATGAGAAGGTGGTAAATATCCAAAAAGACCCCGGTGAATCTCTCGGCATGACCGTTCGAGGGG
GAGCATCACATAGAGAATGGGATTTGCCTATCTATGTCTCATCAGTGTGAGCCCGAGGAGTCATAAGCAGAGATG
GAAGAATAAAACAGGTGACATTTTGTGAATGTGGATGGGGTCGAACTGACAGAGGTGAGCCGGAGTGAGGCAG
TGGCATTATTGAAAAGAACATCATCTCGATAGTACTCAAAGCTTTGGAAGTCAAAGAGTATGAGCCCCAGGAAG
ACTGCAGCAGCCAGCAGCCCTGGACTCCAACCACAACATGGCCCCACCCAGTGACTGGTCCCCATCCTGGGTCA
TGTGGCTGGAATTACCACGGTGCTTGTATAACTGTAAAGATATTGTATTACGAAGAAACACAGCTGGAAGTCTGG
GCTTCTGCATTGTAGGAGGTTATGAAGAATACAATGGAAACAAACCTTTTTTTCATCAAATCCATTGTTGAAGGAA
CACCAGCATACAATGATGGAAGAATTAGATGTGGTGATATTCTTCTTGCTGTCAATGGTAGAAGTACATCAGGAA
TGATACATGCTTGCTTGCAAGACTGCTGAAAGAACTTAAAGGAAGAATTACTCTAACTATTGTTTCTTGCCCTG
GCACTTTTTTATAGAATCAATGATGGGTGAGAGGAAAACAGAAAAATCACAAATAGGCTAAGAAGTTGAAACACT
ATATTTATCTTGTGAGTTTTTATATTTAAAGAAAGAATACATTGTAAAAATGTGAGGAAAAGTATGATCATCTAA
TGAAAGCCAGTTACACCTCAGAAAATATGATTCCAAAAAATTAATACTACTAGTTTTTTTTTTCAGTGTGGAGGAT
TTCTCATTACTCTACAACATTGTTTATATTTTTTCTATTCAATAAAAAGCCCTAAAACAATAAATGATTGATT
TGTATACCCCACTGAATCAAGCTGATTTAAATTTAAATTTGGTATATGCTGAAGTCTGCCAAGGGTACATTAT
GGCCATTTTTTAATTTACAGCTAAAAATTTTTTAAATGCAATTGCTGAGAAACGTTGCTTTTCATCAAACAAGAAAT
AAATATTTTTTCAGAAGTTAAA

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FIGURE 166

MKALLLLVLPWLSPANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPCDGCASLTATAPSPEVSAATIS
LMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSRSFKKINRALSVLRRTKSGSAVANHADQ
GRESENTTAPFVFPRLYHLIPDGEITSIKINRVDPSESLSIRLVGGSETPLVHIIIQHIYRDGVIARDGRLLPG
DIILKVNMDISNVPHNYAVRLLRQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIK
LVRKVDEPGVFI FNVLDGGVAYRHGQLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSQRQRSPDI
EQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVAGGASHREWDLPYVISVEPGGVI
SRDGRIKTG DILLNVDGVELTEVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNHNMAPPSDWSP
SWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIVGGYEEYNGNKPF FIKSIVEGTPAYNDGRIRC DILLAVNGRS
TSGMIHACLARLLKELKGRITLTIVSWPGTFL

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FIGURE 167

GGGAAAGCCATTTGAAAACCCATCTATACAACTATATATTTTCATTTCTGCTGCTAGCTGCCTTGGGCCTCAC
AATTTTCATTCTGTTTTCTGACTTTCAAGTTATATACCGTGGAATGGAGTTGATCCCAACCATAACATCGTGGAG
GGTTTTAATTTTGGTGGTAGCCCTCACCCAATTCTGGTGTGGCTTTCTTTGCAGAGGATTCCACCTTCAAATCA
TGAACCTCTGGCTGTTGATCAAAAGAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAGAAGCT
AGCAGAAGACTCAACCTGGCCTCCCATAAACAGGACAGATTATTCAGGTGATGGCAAAAATGGATTCTACATCAA
CGGAGGCTATGAAAGCCATGAACAGATTCCAAAAGAAAACCTCAAATTGGGAGGCCAACCCACAGAACAGCATT
CTGGGCCAGGCTGTAAATCAGAATTGTCGTCGTACATGCTCAACAGCATTGCTTTTTTCCCCAAAATTAACACATT
GTGGAGAAGTGATGATACTCTCCCTTACCTTTCCTCTCTCCATTCAAGCATTCAAAGTATATTTTCAATGAATT
AAACCTTGCAGCAAGGGACCTTAGATAGGCTTATTCTGACTGTATGCTTTACCAATGAGAGAAAAAATGCATT
CCTGTATCATCCTTTTCAATAAACTGTATTCATTTTGAAAAAAAAAAAAAAAAAAAAA

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FIGURE 168

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHFWLLIKREFGFYSKSQYRTWQKKLAEDSTWPPINRTDY
SGDGKNGFYINGGYESHEQIPKRKLKLGQPTQHFWARL

FIGURE 169

CGCTCGGGCACACGACCGCGCGCAAGGATGGAGCTGGTTGCTGGACGCAGATTGGGGGCTCACTTTTCTTCAGCTCCT
TCTCATCTCGTCTTGCCAAGAGAGTACACAGTCATTAATGAAGCCTGCCCTGGAGCAGAGTGGGAATATCATGTG
TCGGGAGTGCTGTGAATATGATCAGATTGAGTGCCTCTGCCCGGAAAGAGGGAAGTCGTGGGTTATACCATCCC
TTGCTGCAGGAATGAGGAGAATGAGTGTGACTCCTGCCTGATCCACCAGGTTGTACCATCTTTGAAAACCTGCAA
GAGCTGCGCAAAATGGCTCATGGGGGGGTACCTTGGATGACTTCTATGTGAAGGGTTCTACTGTGCAGAGTGGCCG
AGCAGGCTGGTACGGAGGAGACTGCATGCGATGTGGCCAGGTTCTGCGAGCCCCAAAGGGTCAGATTTTGTGTGGA
AAGCTATCCCCTAAATGCTCACTGTGAATGGACCATTCACTGCTAAACCTGGGTTTGTCAATCCAACTAAGATTGG
CATGTTGAGTCTGGAGTTTGACTACATGTGCCAGTATGACTATGTTGAGGTTTCGTGATGGAGACAACCGCGATGG
CCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAGGATCCTCACTCCACGTCCT
CTTCCACTCCGATGGCTCCAAGATTTTGACGGTTTCCATGCCATTATGAGGAGATCACAGCATGCTCCTCATC
CCCTTGTTTCCATGACGGCACGTGCGTCCTTGACAAGGCTGGATCTTACAAGTGTGCCTGCTTGGCAGGCTATAC
TGGGCAGCGCTGTGAAAATCTCTTTGAAGAAAGAACTGCTCAGACCTGGGGGGCCAGTCAATGGGTACCAGAA
AATAACAGGGGGCCCTGGGCTTATCAACGGACGCCATGCTAAATTTGGCAGCTGGTGCTCTTTCTTTTGTAAACAA
CTCCTATGTTCTTAGTGGCAATGAGAAAAGAACTTGCCAGCAGAAATGGAGAGTCTGATCGGGAACAGCCCATCTG
CATAAAAGCCTGCCGAGAACCAAAGATTTCAGACCTGGTGAGAAGGAGAGTTCTTCCGATGCAGGTTTCAGTCAAG
GGAGACACCATTACACCAGCTATACTCAGCGGCCTTCAGCAAGCAGAAACTGCAGAGTGGCCCTACCAAGAAGCC
AGCCCTTCCCTTTGGAGATCTGCCCCATGGGATACCAACATCTGCATACCCAGCTCCAGTATGAGTGCATCTCACC
CTTCTACCGCGCGCTGGGCAGCAGCAGGAGGACATGTCTGAGGACTGGGAAGTGGAGTGGGCGGGGACCATCTCTG
CATCCTATCTGCGGGAAAATTTAGAACATCACTGCTCCAAAGACCCAAAGGTTGCGCTGGCCCTGGCAGGCAGC
CATCTACAGGAGGACCAGCGGGTGCATGACGGCAGCCTACACAAGGGAGCGTGGTTCTTAGTCTGCAGCGGTGC
CCTGGTGAATGAGCGCACTGTGGTGGTGGCTGCCACTGTGTTACTGACCTGGGGAAGGTCACCATGATCAAGAC
AGCAGACCTGAAAGTTGTTTTGGGGAAATTTACCGGGATGATGACCGGGATGAGAAGACCATCCAGAGCCTACA
GATTTCTGCTATCATTTCTGCATCCCAACTATGACCCCATCCTGCTTGATGCTGACATCGCCATCCTGAAGCTCCT
AGACAAGGGCCGTATCAGCACCCGAGTCAGGCCATCTGCCCTCGCTGCCAGTCGGGATCTCAGCACTTCTCTCCA
GGAGTCCCACATCACTGTGGCTGGTGGAAATGTCTGGCAGAGTGGAGGCCCTGGCTTCAAGAACGACACACT
GCGCTCTGGGGTGGTCACTGTGGTGGACTCGCTGCTGTGTGAGGAGCAGCATGAGGACCATGGGCATCCCACTGAG
TGCTACTGATAACATGTTCTGTGCCAGCTGGGAACCCACTGCCCTTCTGATATCTGCACTGCAGAGACAGGAGG
CATCGCGGCTGTGTCTTCCCGGGACGAGCATCTCTGAGCCAGCTGGCATCTGATGGGACTGGTCACTGGAG
CTATGATAAAACATGCAGCCACAGGCTCTCCACTGCCTTCACCAAGGTGCTGCCTTTTAAAGACTGGATTGAAAG
AAATATGAAATGACACCATGCTCATGCACTCCTTGAGAAGTGTTTCTGTATATCCGTCTGTACGTGTGTCAATTGCG
TGAAGCAGTGTGGGCTGAAGTGTGATTGGCTGTGAACCTGGCTGTCGCAAGGCTTCTGACTTCAGGACAA
ACTCAGTGAAGGGTGAGTAGACCTCCATTGCTGTGTAGCTGATGCCGCGTCCACTACTAGGACAGCAATGGAA
GATGCCAGGGCTTGCAAGAAGTAAGTTTCTTCAAAGAAGACCATATACAAACCTCTCCACTCCACTGACCTGGT
GGTCTTCCCAACTTTTCAATTATACGAATGCCATCAGCTTGACCAGGGAAGATCTGGGCTTCATGAGGCCCTTT
TGAGGCTCTCAAGTTCTAGAGAGCTGCCTGTGGGACAGCCAGGGCAGCAGAGCTGGGATGTGGTGCATGCCTTT
GTGTACATGGCCACAGTACAGTCTGGTCCTTTTCTTCCCATCTCTTGTACACATTTTAATAAAATAAGGGTTG
GCTTCTGAACATACAAAAAAGTAAAAAAGTAAAAAAGTAAAAAAGTAAAAAAGTAAAAAAGTAAAAAAGTAAAAA
AAAAAAGTAAAAAAGTAAAAAAGTAAAAAAGTAAAAAAGTAAAAAAGTAAAAAAGTAAAAAAGTAAAAAAGTAAAAA

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FIGURE 170

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVVGTYTIPCCRNEENE
CDSCLIHPGCTIFENCKSCRNGSWGGLDDEFFYVKGFYCAECRAGWYGGDCMRGQVLRAPKGQILLESYPLNAHC
EWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDGGQIIKRVCGNERPAPIQSIGSSSLHVLFHSDGSKN
FDGFHAIYEEITACSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCEENLLEERNCSDPGGFVNGYQKITGGPGLI
NGRHAKIGTVVSFFCENNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPQVQSRETPLHQLY
SAAFSKQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPSCIPICGKIE
NITAPKTQGLRWPWQAAYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVVAHCVTDLGKVTMIKTADLKVVLG
KFYRDDRDEKTIQSLQISAILLHPNYDPILLADIAILKLLDKARISTRVQPICLAASRDLSTSFQESHITVAG
WNVLADVRSFGFKNDTLRSGVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDICTAETGGIAAVSFPG
RASPEPRWHLMLVSWSYDKTCSHRLSTAFTKVLPFKDWIERNMK

FIGURE 171

CTGTGCTCTTTTGCTTACGCCGAGTCGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTTCCAAGTGTGGCTTA
ATCCGCTCTCCACCACCAGATCTTTCTCCGTGGATTCCCTCTGCTAAGACCGCTGCCATGCCAGTGACGGTAACCCG
CACCACCATCACAAACCACCACGACGTCACTTCGGGGCCTGGGGTCCCCCATGATCGTGGGGTCCCCTCGGGGCCCT
GACACAGCCCCCTGGGTCTCCTTCGCCTGCTGCAGCTGGTGTCTACCTCGTGGCCCTTCTCGCTGGTGGCTAGCGT
GGGCGCTCTGGACGGGTCCATGGGCAACTGGTCCATGTTCACTTGGTCTTCTGCTTCTCCGTGAGGCTGATCAT
CCTCATCGTGGAGAGTGTGCGGGCTCCAGGCCGCTTCCCTCTGCTTGGCGCAACTTCCCCATCACCTTCGCCTG
CTATGCGGGCCCTCTTCTGCCTCTCGGCCTCCATCATCTACCCACCACCTATGTCCAGTTCCTGTCCCACGGCCG
TTCGCGGGACCACGCCATCGCGCCACCTTCTTCTCCTGCATCGCGTGTGTGGCTTACGCCACCGAAGTGGCCTG
GACCGGGGCCCCGGCCCCGGCGAGATCACTGGCTATATGGCCACCGTACCCGGGCTGCTGAAGGTCTGGAGACCTT
CGTTGCCTGCATCATCTTCGCGTTTCATCAGCGACCCCAACCTGTACCGACACCAGCCGGCCCTGGAGTGGTGCCT
GGCGGTGTACGCCATCTGCTTTCATCTAGCGCCCATCGCCATCCTGCTGAACCTGGGGGAGTGACCAACAGTGCCT
ACCCATCCCCCTCCCCAGCTTCTCTGTGCGGGCTGGCCTTGTCTGTCTGTCTCCTCTATGCCACCGCCCTTGTCT
CTGGCCCCCTTACCAGTTCGATGAGAAGTATGGCGGCCAGCCTCGCGCTCGAGAGATGTAAGCTGCAGCCGCAG
CCATGCCCTACTACGTGTGTGCCTGGGACCGCCGACTGGCTGTGGCATCCTGACGCCATCAACCTACTGGCGTA
GTGGCTGACCTGGTGCACCTCTGCCACCTGGTTTTTGTCAAGGTCTTAAGACTCTCCCAAGAGGGCTCCCGTTCCC
TCTCCAACCTCTTTTGTCTTCTTGCCCGAGTTTTCTTTATGGAGTACTTCTTCTCCCTCCGCTTCTCTCTGTTTTC
ATCTTCTGTCTCCCTCCCTCCCTACCTTTTTCTTTCTTCCCAATTCTTGCACTCTAACCACTTCTTGGATGC
CTCTTCTCTCTCCCTTTCTCTTGTCTGTTTTCTTCTCTGTGTTTTGTTGCCCACATCTGTTTTACCCCTG
AGCTGTTTTCTTTTTCTTTCTTTCTTTTTTTTTTTTTTTTTTTAAGACGGATTCTCACTCTGTGGCCAGGCTG
GAGTGCAGTGGTGCGATCTCAGCTCACTGCAACCCCCGCTCCTGGGTTCAGCGGATTCTCTCCCCCAGCCTCC
CAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGACCCAGCTGTTTTCTCTTTTTCCACTCTTTTTTCTCATC
TCTTTTTCTGGTGTGCTGTGGCTTTCTTATCTGCTGTTTTGCAAGCACCTTCTCCTGTGTCTTGGGAGCCCT
GAGACTTCTTCTCTCTCTTCTGCTCCACCACTCCAAAGGTGCTGAGCTCACATCCACACCCCTTGCAAGCCGTCC
ATGCCACAGCCCCCAAGGGGCCCCATTGCCAAAGCATGCCTGCCACCCCTCGCTGTGCCTTAGTCAGTGTGTAC
GTGTGTGTGTGTGTGTGTTTTGGGGGGTGGGGGGTGGGTAGCTGGGGATTGGGCCCTCTTCTCCCAGTGGAGGAA
GGTGTGCAGTGTACTTCCCCTTTAAATTAATAAACATATATATATATATATTTGGAGGTGAGTAATTTCCAATGG
GCGGGAGGCATTAAGCACACCCCTGGGTCCCTAGGCCCGCCTGGCACTCAGCCTTGCCAGAGATTGGCTCCAG
AATTTTTGCCAGGCTTACAGAACCACTGCCTAGAGGCATCTTAAAGGAAGCAGGGGCTGGATGCCCTTTCAT
CCCAATTTATCTCTGTGGTATGAAAAAG

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FIGURE 172

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727
<subunit 1 of 1, 322 aa, 1 stop
<MW: 35274, pI: 8.57, NX(S/T): 1
MPVTVTRTTITTTTTSSSGLGSPMIVGSPRALTQPLGLLRLLQLVSTCVAFSLVASVGAWTGSMGNWSMFTWCFC
FSVTLLIILIVELCGLQARFPLSWRNFPITFACYAALFCLSASIIYPTYVQFLSHGRSRDHAIATFFSCIACVA
YATEVAWTRARPGEITGYMATVPGLLKVLETFFVACIIFAFISDPNLYQHQPALWCVAVYAICFILAAIAILLNL
GECTNVLPIPFPSFLSGLALLSVLLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILT
AINLLAYVADLVHSAHLVFVKV

Important features:**Transmembrane domains:**

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192, 205-226, 235-255 and 294-312

N-glycosylation site.

amino acids 66-69

Glycosaminoglycan attachment site.

amino acids 18-21

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FIGURE 173

GAACGTGCCACCATGCCAGCTAATTTTTGTATTTTTAGTAGAGACGGGGTTTCACCATGTTGGCCAGGCTGGTC
TTGAACTCGTGACCTCATGATCCGCTCACCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGACGC
CTGGCCAGCCTATGCATTTTTTAAGAAATTATTTCTGTATTAGGTGCTGTGCTAAACATTGGGCACCTACAGTGACCA
AAACAGACTGAATCCCCAAGAGCCAAAGACCAGTGAGGGAGACCAACAAGAAACAGGAAATGCAAAAGAGACCA
TTATTACTCACTATGACTAAGGGTCACAAATGGGGTACGTTGATGGAGAGTGATTTGTTAAGAGACTACAGAGGG
AGGACAGACTACCAAGAGGGGGGCCAGGAAAGCTCCTCTGACGAGGTGGTATTTACAGCCAACTGGAAGAATGA
GAAAGAGCTAGCCAGCCATCAGAATAGTCCAGAAGAGATGGGGAGCACTACACTCACTACACTTTGGCCTGAGAA
AATAGCATGGGATTGGAGGAGGCTGGGGGAACACCCTTCTGCCGACCTGGGCAGGAGGCATTGAGGGCTTGAGA
AAGGGCAATGGCAGTAGCAGTAGAAAGGACAGGGTAGGAGCAGGGACTTTGCAGGTGGAATCATTAGGTCTTATC
AACAGATATGGGCAAGCAAAGCCAGGGGAGAATTGATGGTAATGCTGAGGTTTGGAGCCAGGCTAGATGGGACAG
TGGTGGGTGATGCAAAGGAAAGAGGTGAGGAAGCAGGGCCAGACGTGGGGAGAAGGTGTGGGGGTTTGGTTTCCA
TCTTGCCGAGTCTGCCGGAATGTGGATGGGAAGACCAAGAGGAGGAGCAAGGGGCAGAGGGGAAGGGAATCTTAA
AGAAGTCTGGATGCCACACTCTTCTCCTTCCCTCCTCCTCCTCCTCCTCCTCAGAGGTCTCACTCGTGGTTCTTCAT
TTCTGCCCCTGCCTCCATCTCCTCTGGGTGCTGGGAAAGTGGAGGATTAGCTGAAGTTTTGCTTCTCGGGGCCCTG
TCTGAATCTCCATTGCTTTCTGGGAGGACATAATTACCTGTCTTAGCTTCTTATCATCTTACATTTCCCTGTAG
CCACTGGGACATATGTGTGTTCCTTCCCTAGCTCCTGTCTCCTCCTCATGCTTTGCTGGGTATGGGCATGTTAG
GGGGAAGGTCAATTGCTGTGAGAGGGGCACTGACTTTCTAATGGTGTTACCCAAGGTGAATGTTGGAGACACAGTC
GCGATGCTGCCAAGTCCCGGCGAGCCCTAACTATCCAGGAGATCGCTGCGCTGGCCAGGTCTCCCTGCATGGT
ATGCAGCCCCCTCCCATGTTTTCTGGCCACTTTGTCCTTTCTCCTCCCCTTTCACATCCCTTTGGAAGTGTTCCT
GTGAGTACATGCTGGGGTCTCCCCCTTTCTTCCCTTGCTCAGGTGAATCTCAGCCCCCTTCTCCCACCCAAAGGTTT
ACATGGATCCTAACTACTGCCACCCCTTCCACCTCCCTGCACCTGTGCTCCCTGGCCTGGTCTTTTACCAGGCTTC
TCCACCCCTCCCCTATCTCCAGGTATTTCCAGGTGGTGAAGGACCACGTGACCAAGCCTACCGCATGGCCAGG
GCCGAGTGGCTCACCTCATTGAGTGGAAAGGGCTGGAGCAAGCCGAGTGACTCACCTGCTGCCCTGGAATCAGCCT
TTTCTCCTATTACAGACCTCAGCGAGGGCGAACAAGAGGCTCGCTTTGCAGCAGGAGTGGCTGAGCAGTTTGCCA
TCGCGGAAGCCAAGCTCCGAGCATGGTCTTCGGTGGATGGCGAGGACTCCACTGATGACTCCTATGATGAGGACT
TTGCTGGGGGAATGGACACAGACATGGCTGGGCAGCTGCCCTGGGGCCGCACCTCCAGGACCTGTTACACGGGCC
ACCGGTTCTCCCGGCTGTGCGCCAGGGCTCCGTGGAGCCTGAGAGCGACTGCTCACAGACCGTGTCCCCAGACA
CCCTGTGCTCTAGTCTGTGCAGCCTGGAGATGGGTGTTGGGGTCCCCGGCCCGGCTGGCCTCCAGCTGCTGG
GCGATGAGCTGCTTCTCGCCAACTGCCCCCCAGCCGGGAAAGTGCCTTCCGCAGCCTGGGCCACTGGAGGGCCC
AGGACTCACTCTACAACCTCGCCCCCTCACAGAGTCTGCTTTTCCCCCGGAGGAGGAGCCAGCCCCCTGCAAGG
ACTGCCAGCCACTCTGCCACCACTAACGGGCAGCTGGGAACGGCAGCGCAAGCCTCTGACCTGGCCTCTTCTG
GGGTGGTGTCTTAGATGAGGATGAGGCAGAGCCAGAGGAACAGTGAACCCACATCATGCCTGGCAGTGGCATGCA
TCCCCCGGCTGCTGCCAGGGGCAGAGCCTCTGTGCCAAGTGTGGGCTCAAGGCTCCCAGCAGAGCTCCACAGCC
TAGAGGGCTCCTGGGAGCGCTCGCTTCTCCGTTGTGTGTTTTGCATGAAAGTGTGAGAGAGGAGGAGGGGCTG
GGCTGGGGGCGCATGTCTGCCCCCACTCCCGGGGCTTGCCGGGGGTTGCCCGGGGCTGAGGAGGCTGAGGAGT
GCTGTGGCAGACAGTGATGTTTCTTAAATGCCACACACATTTCTCCTCGGATAATGTGAACCACTA
AGGGGGTTGTGACTGGGCTGTGTGAGGGTGGGGTGGGAGGGGGCCAGCAACCCCCCACCCTCCCCATGCCTCTC
TCTTCTCTGCTTTTCTTCTCACTTCCGAGTCCATGTGCAGTGCTTGATAGAATCACCCCCACCTGGAGGGGCTGG
CTCCTGCCCTCCCGGAGCCTATGGGTTGAGCCGTCCCTCAAGGGCCCTGCCAGCTGGGCTCGTGCTGTGCTTC
ATTACCTCTCCATCGTCTCTAAATCTTCTTCTTTTCTTAAAGACAGAAGGTTTTTGGTCTGTTTTTTCAGTC
GGATCTTCTCTTCTCTGGGAGGCTTTGGAATGATGAAAGCATGTACCCCTCCACCCTTTTCTGGCCCCCTAATGG
GGCCTGGGCCCTTTCCCAACCCCTCCTAGGATGTGCGGGCAGTGCTGCTGGCGCCTCACAGCCAGCCGGGCTGCC
ATTCACGCAGAGCTCTCTGAGCGGGAGGTGGAAGAAAGGATGGCTCTGGTTGCCACAGAGCTGGGACTTCATGTT
CTTCTAGAGAGGGCCACAAGAGGGCCACAGGGGTGGCCGGGAGTTGTGAGCTGATGCCTGCTGAGAGGCAGGAAT
TGTGCCAGTGAGTGACAGTCATGAGGGAGTGCTCTTCTTGGGGAGGAAAGAGGTAGAGCCTTTCTGTCTGAAT
GAAAGGCCAAGGCTACAGTACAGGGCCCCCGCCAGCCAGGGTGTTAATGCCACGTAAGTGGAGGCCCTCTGGCAG
ATCTGCATTCCAAGGTCACTGGACTGTACGTTTTTATGTTGTGGGAAGGGTGGGTGGCTTTAGAAATTAAGGGC
CTTGTAGGCTTTGGCAGGTAAGAGGGCCCAAGGTAAGAACGAGAGCCAACGGGCACAAGCATTTCTATATATAAGT
GGCTCATTAGGTGTTTATTTTGTCTATTTAAGAATTTGTTTTATTAAATTAATATAAAAATCTTGTAAATCTC
TAAAA

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FIGURE 174

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSPFSPKPVHMDPNYCHPSTSLHLCSLAWSFTRLLHPPL
SPGISQVVKDHVTKPTAMAQGRVAHLIEWKGWSKPSDSPAALESASFSSYSDLSEGEQEAFAGVAEQFAIAEAK
LRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLGPHLQDLFTGHRFSRPVRQGSVEPESDCSQTVPDTLCSS
LCSLEDGLLGSPARLASQLLGDELLAKLPPSRESAFRSLGPLEAQDSLNSPLTESCLSPAEEEPAPCKDCQPL
CPPLTGSWERQRQASDLASSGVVSLDEDEAEPEEQ

Signal peptide:

amino acids 1-15

Casein kinase II phosphorylation site.amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232, 285-289,
324-328**Tyrosine kinase phosphorylation site.**

amino acids 44-52

N-myristoylation site.

amino acids 17-23, 26-32, 173-179

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 11-22

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FIGURE 175

GGTTCCTGGGCGCTCTGTTACACAAGCAAGATACAGCCAGCCCCACCTAATTTTGTTCCTGGCACCCCTCCTGC
TCAGTGCGACATTGTACACTTAACCCATCTGTTTTCTCTAATGCACGACAGATTCTTTTCAGACAGGACAACCTG
TGATATTTTCAGTTCCTGATTGTAAATACCTCCTAAGCCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTT
CTTCATCTGCAAAATGGGCATAATACAATCTATTCTTGCCACATCAAGGGATTGTTATTCCTTTAAAAAAAACC
AATACCAAAGAAGCCTACAATGTTGGCCTTAGCCAAAATTCTGTTGATTTCACGTTGTTTTATTCACTTCTATC
GGGGAGCCATGGAAGAAAATCAAGACATAAACACAACACAGAACATTGCAGAAAGTTTTTAAACAATGGAAAA
TAAACCTATTTCTTTGGAAAGTGAAGCAAACCTTAAACTCAGATAAAGAAAATATAACCACCTCAAATCTCAAGGC
GAGTCATTCCCCTCCTTTGAATCTACCCAACAACAGCCACGGAATAACAGATTTCTCCAGTAACTCATCAGCAGA
GCATTCTTTGGGCAGTCTAAAACCCACATCTACCATTCCACAAGCCCTCCCTTGATCCATAGCTTTGTTTCTAA
AGTGCCTTGAATGCACCTATAGCAGATGAAGATCTTTGCCCATCTCAGCACATCCCAATGCTACACCTGCTCT
GTCTTCAGAAAACCTTCACTTGGTCTTTGGTCAATGACACCGTGAAAACCTCCTGATAACAGTTCATTACAGTTAG
CATCCTCTCTTCAGAACCAACTTCTCCATCTGTGACCCCTTGATAGTGGAACCAAGTGGATGGCTTACCACAAA
CAGTGATAGCTTCACTGGGTTTACCCCTTATCAAGAAAAAACAACCTCTACAGCCTACCTTAAAATTACCAATAA
TTCAAAACTCTTTCAAATACGTGAGATCCCCAAAAGAAAATAGAAATACAGGAATAGTATTCGGGGCCATTTT
AGGTGCTATTCTGGGTGTCTCATTGCTTACTCTTGTGGGCTACTTGTGTGTGGAAAAAGGAAAACGGATTCATT
TTCCCATCGGCGACTTTATGACGACAGAAATGAACCAGTCTGCGATTAGACAATGCACCGGAACCTTATGATGT
GAGTTTTGGGAATTCTAGCTACTACAATCCAACCTTTGAATGATTAGCCATGCCAGAAAGTGAAGAAAATGCACG
TGATGGCATTTCCTATGGATGACATACCTCCACTTCGTACTTCTGTATAGAACTAACAGCAAAAAGGCGTTAAACA
GCAAGTGTCTATCTACATCCTAGCCTTTTGACAAATTCATCTTTCAAAGGTTACACAAAATTACTGTCACGTGGA
TTTTGTCAAGGAGAATCATAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCATCAAAGGTTTTCT
TTCTTACAATTTTTGGCCATCCTGAGGCATTTACTAAGTAGCCTTAATTTGTATTTTAGTAGTATTTTCTTAGT
AGAAAATATTTGTGGAATCAGATAAACTAAAAGATTTACCATTACAGCCCTGCCTCATAACTAAATAATAAAA
ATTATTCCACCAAAAAATTCTAAAACAATGAAGATGACTCTTTACTGCTCTGCCTGAAGCCCTAGTACCATAATT
CAAGATTGCATTTTCTTAAATGAAAATTGAAAGGGTGCTTTTTTAAAGAAAATTGACTTAAAGCTAAAAGAGGA
CATAGCCCAGAGTTTCTGTTATTGGGAAATTGAGGCAATAGAAATGACAGACCTGTATTCTAGTACGTTATAATT
TTCTAGATCAGCACACATGATCAGCCCACTGAGTTATGAAGCTGACAATGACTGCATTCAACGGGGCCATGGC
AGGAAAGCTGACCCTACCCAGGAAAGTAATAGCTTCTTTAAAAGCTTCAAAGGTTTTGGGAATTTTAACTTGTC
TTAATATATCTTAGGCTTCAATTATTTGGGTGCCTTAAAACTCAATGAGAATCATGGT

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FIGURE 176

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732
><subunit 1 of 1, 334 aa, 1 stop
><MW: 36294, pI: 4.98, NX(S/T): 13
MLALAKILLISTLFYSLLSGSHGKENQDINTTQNIAEVFKTMENKPISLESEANLNSDKENITTSNLKASHSPPL
NLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSFVSKVPWNAPIADEDLLPISAHPNATPALSSSENF
WSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVEPSGWLTTNSDSFTGFTPYQEKTTLQPTLKFTNNSKLF
TSDPQKENRNTGIVFGAILGAILGVSLTLVGYLLCGKRKTDSTFSHRRLYDDRNEPVLRLDNAPEPYDVSGNSS
YYNPTLNSAMPESEENARDGIPMDDIPPLRTSV
```

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 235-262

N-glycosylation site.amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159, 163-167, 218-222,
225-229, 298-302, 307-311

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FIGURE 177

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGAAGCTTTCTTGCCCT
GCAGTGAAGCAGAGAGATAGATATTATTACGTAATAAAAAACATGGGGCTTCAACCTGACTTTCCACCTTTCCCTA
CAAATTCGATTACTGTTGCTGTTGACTTTGTGCCTGACAGTGGTTGGGTGGGCCACCAGTAACTACTTCGTGGG
TGCCATTCAAGAGATTCCCTAAAGCAAAGGAGTTCATGGCTAATTTCCATAAGACCCTCATTTTGGGGAAGGGAAA
AACTCTGACTAATGAAGCATCCACGAAGAAGGTAGAACTTGACAACTGCCTTCTGTGTCTCCTTACCTCAGAGG
CCAGAGCAAGCTCATTTTCAAACCAGATCTCACTTTGGAAGAGGTACAGGCAGAAAATCCCAAAGTGTCCAGAGG
CCGGTATCGCCCTCAGGAATGTAAAGCTTTACAGAGGGTCCCATCCTCGTTCCCCACCGGAACAGAGAGAAAACA
CCTGATGTACCTGCTGGAACATCTGCATCCCTTCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCA
CCAGGCTGAAGGTAAAAAGTTTAAATCGAGCCAACTCTTGAATGTGGGCTATCTAGAAGCCCTCAAGGAAGAAA
TTGGGACTGCTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGAGGAGCA
TCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTGGATATTTTGGGGGTGTTAC
TGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCTAACAACCTACTGGGGATGGGGAGGCGAAGACGA
TGACCTCAGACTCAGGGTTGAGCTCCAAAGAAATGAAAATTTCCCGGCCCTGCCTGAAGTGGGTAAATATACAAT
GGTCTTCCACACTAGAGACAAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTACAGAGT
CTGGAGAACAGATGGGTTGAGTAGTTGTTCTTATAAATTAGTATCTGTGGAACACAATCCTTTATATATCAACAT
CACAGTGGATTTCTGGTTGGTGCATGACCCCTGGATCTTTTGGTGATGTTTGGGAAGAACTGATTCTTTGTTTGCA
ATAATTTTGGCCTAGAGACTTCAAAATAGTAGCACACATTAAAGAACCTGTTACAGCTCATTGTTGAGCTGAATTTT
TCCTTTTTGTATTTTCTTAGCAGAGCTCCTGGTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTTCTTAG
TCATTTTGATCATGAGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGA
TAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATATTATGGGATAAAA
GGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTTCTCGTCCAAGGTAGAAAGGTACGAAGA
TACAATACTGTTATTCATTTATCCTGTACAATCATCTGTGAAGTGGTGGTGTGAGGTGAGAAGGCGTCCACAAAA
GAGGGGAGAAAAGGCGACGAATCAGGACACAGTGAACCTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTCCGC
TGCAAAGGCAGCAGTAGCTGAGCTGGTTGCAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCAGGTATGCCTTC
CAGTGATGCCACCAGAGAATACATTCTCTATTAGTTTTTAAAGAGTTTTTGTAAATGATTTTGTACAAGTAGG
ATATGAATTAGCAGTTTACAAGTTTACATATTAATAATAAATATGTCTATCAAATACCTCTGTAGTAAAT
GTGAAAAAGCAAAA

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FIGURE 178

MGFNLT FHLSYKFRLLLLLLTLCITVVGWATSNYFVGAIQEIPKAKEFMANFHKTLILGKGKTLTNEASTKKVELD
NCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRVAILVPHRNREKHLMYLLEHLHPFLQR
QQLDYGIYVIHQAEKGKFNRAKLLNVGYLEALKEENWDCFI FHDVDLVPENDFNLYKCEEHPKHLVVGRNSTGYR
LRYSGYFGGVTA LSREQFFKVNGFSNNYWG WGGEDDDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAE
RMKLLHQVSRVWRTDGLSSCSYKLVSV EHNPLYINITVDFWFGA

Important features:**Signal peptide:**

amino acids 1-27

N-glycosylation sites.

amino acids 4-8, 220-224, 335-339

Xylose isomerase proteins.

amino acids 191-202

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FIGURE 179

CGTGGGCCGGGGTTCGCGCAGCGGGCTGTGGGCGCGCCCGGAGGAGCGACCGCCGCAGTTCTCGAGCTCCAGCTGC
ATTCCCTCCGCGTCCGCCCCACGCTTCTCCCGCTCCGGGCCCGCAATGCCCCAGGCAGTGTGGTTCGCGCCTCGG
CCGCATCCTCTGGCTTGCCCTGCCCTGCCCTGGGCCCGGCAGGGGTGGCCGAGGCCGTGTATGAACTCAATCT
CACCACCGATAGCCCTGCCACCACGGGAGCGGTGGTGACCATCTCGGCCAGCCTGGTGGCCAAGGACAACGGCAG
CCTGGCCCTGCCCGCTGACGCCACCTCTACCGCTTCCACTGGATCCACACCCCGCTGGTGTCTACTGGCAAGAT
GGAGAAGGGTCTCAGTCCACCATCCGTGTGGTGGGCCAGTGGCCGGGGAATTCGCGGTCTCTGTCTGGGTAC
TGCCGCTGACTGCTGGATGTGCCAGCCTGTGGCCAGGGGCTTTGTGGTCTCTCCCATCACAGAGTTCCCTCGTGGG
GGACCTTGTTGTACCCAGAACACTTCCCTACCCTGGCCAGCTCCTATCTCACTAAGACCGTCCCTGAAAGTCTC
CTTCCTCCTCCACGACCCGAGCAACTTCTCAAGACCGCCTTGTTTCTCTACAGCTGGGACTTCGGGGACGGGAC
CCAGATGGTGACTGAAGACTCCGTGGTCTATTATAACTATTCCATCATCGGGACCTTCACCGTGAAGCTCAAAGT
GGTGGCGGAGTGGGAAGAGGTGGAGCCGGATGCCACGAGGGCTGTGAAGCAGAAGACCGGGGACTTCTCCGCCTC
GCTGAAGCTGCAGGAAACCTTCGAGGCATCCAAGTGTGGGGCCACCTAATTCAGACCTTCCAAAAGATGAC
CGTGACCTTGAACCTCCTGGGGAGCCCTCCTCTGACTGTGTCTGGCGTCTCAAGCCTGAGTGCCTCCCGCTGGA
GGAAGGGGAGTGCCACCCCTGTGTCCGTGGCCAGCACAGCGTACAACCTGACCCACACCTTCAGGGACCCCTGGGGA
CTACTGCTTCAGCATCCGGGCCGAGAATATCATCAGCAAGACACATCAGTACCACAAGATCCAGGTGTGGCCCTC
CAGAATCCAGCCGGCTGTCTTTGCTTTCCCATGTGCTACACTTATCACTGTGATGTTGGCCTTCATCATGTACAT
GACCTGCGGAATGCCACTCAGCAAAAGGACATGGTGGAGAACCCGGAGCCACCCTCTGGGGTCAGGTGCTGCTG
CCAGATGTGCTGTGGGCCTTTCTGTCTGGAGACTCCATCTGAGTACCTGGAAATTGTTCTGTGAGAACACGGGCT
GCTCCCGCCCTCTATAAGTCTGTCAAACTTACACCGTGTGAGCACTCCCCCTCCCCACCCCATCTCAGTGTTA
ACTGACTGCTGACTTGGAGTTTCCAGCAGGGTGGTGTGCACCACTGACCAGGAGGGGTTCAATTTGCGTGGGGCTG
TTGGCCTGGATCATCCATCCATCTGTACAGTTCAGCCACTGCCACAAGCCCCCTCCCTCTCTGTACCCCTGACCC
CAGCCATTACCCATCTGTACAGTCCAGCCACTGACATAAGCCCCACTCGGTTACCACCCCTTGACCCCTACC
TTTGAAGAGGCTTCGTGCAGGACTTTGATGCTTGGGGTGTTCGCTGTGACTCCTAGGTGGGCCTGGCTGCCAC
TGCCCATTCCTCTCATATTGGCACATCTGCTGTCCATTGGGGGTTCAGTTTCTCTCCCCAGACAGCCCTACCT
GTGCCAGAGAGCTAGAAAGAAGGTCATAAAGGGTTAAAAATCCATAACTAAAGGTTGTACACATAGATGGGCACA
CTCACAGAGAGAAGTGTGCATGTACACACACACACACACACACACACACAGAAATATAAACACATG
CGTCACATGGGCATTTAGATGATCAGCTCTGTATCTGGTTAAGTCGGTTGCTGGGATGCACCCCTGCACTAGAGC
TGAAAGGAAATTTGACCTCCAAGCAGCCCTGACAGGTTCTGGGCCCGGGCCCTCCCTTTGTGCTTTGTCTCTGCA
GTTCTTGCGCCCTTTATAAGGCCATCCTAGTCCCTGCTGGCTGGCAGGGGCTGGATGGGGGGCAGGACTAATAC
TGAGTGATTGCAGAGTGCTTTATAAATATCACCTATTTTATCGAAACCATCTGTGAACTTTCACTGAGGAAA
AGGCCTTGACGCGGTAGAAGAGGTTGAGTCAAGGCCGGGCGCGGTGGCTCACGCCTGTAATCCAGCACTTTGGG
AGGCCGAGGCGGTGGATCACGAGATCAGGAGATCGAGACCACCTGGCTAACACGGTGAACCCCGTCTCTACT
AAAAAATACAAAAGTTAGCCGGGCGTGGTGGTGGGTGCTGTAGTCCAGCTACTCGGGAGGCTGAGGCAGGA
GAATGGTGCGAACCCGGGAGGCGGAGCTTGAGTGAGCCAGATGGCGCCACTGCACTCCAGCCTGAGTGACAGA
GCGGAGACTCTGTCTCCA

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FIGURE 180

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLALPADAHLYRFHWI
HTPLVLTGKMEKGLSSTIRVVGHVPGEFPVSVWVTAADCWMCQPVARGFVVLPITEFLVGDLVVTQNTSLPWPSS
YLTKTVLKVSFLLHDPSNFKTALFLYSWDFDGTQMVTEDSVVYYNYSIIIGTFTVKLKVVAEWEEVEPDATRAV
KQKTGDFSASLKLQETLRGIQVLGPTLIQTFQKMTVTLNFLGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYN
LTHTFRDPGDYCFSSIRAENIISKTHQYHKIQVWPSRIQPAVFAPPCATLITVMLAFIMYMTLRNATQQKDMVENP
EPPSGVRCCQMCCGPFLLLETPSEYLEIVRENHGLLPPLYKSVKTYTV

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

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FIGURE 181

CGGACGCGTGGGCGGCGGCTGCGGAACTCCCGTGGAGGGGCGGCTGGGCCCTCGGGCCTGACAG**ATGG**CAGTGGC
CACTGCGGCGGCAGTACTGGCCGCTCTGGGCGGGGCGCTGTGGCTGGCGGCCCGCCGGTTCTGTGGGGCCAGGGT
CCAGCGGCTGCGCAGAGGCGGGGACCCCGGCTCATGCACGGGAAGACTGTGCTGATCACCGGGGCGAACAGCGG
CCTGGGCGCGCCACGGCCGCGGAGCTACTGCGCCTGGGAGCGCGGGTGATCATGGGCTGCCGGGACCGCGCGG
CGCCGAGGAGGCGGCGGGTCAGCTCCGCCGCGAGCTCCGCCAGGCCGCGGAGTGCGGGCCAGAGCCTGGCGTCAG
CGGGGTGGGCGAGCTCATAGTCCGGGAGCTGGACCTCGCCTCGCTGCGCTCGGTGCGCGCCTTCTGCCAGGAAAT
GCTCCAGGAAGAGCCTAGGCTGGATGTCTTGATCAATAACGCAGGGATCTTCCAGTGCCCTTACATGAAGACTGA
AGATGGGTTTGAGATGCAGTTCGGAGTGAACCATCTGGGGCACTTTCTACTCACCAATCTTCTCCTTGGACTCCT
CAAAAGTTCAGCTCCAGCAGGATTGTGGTAGTTTCTTCCAACTTTATAAATACGGAGACATCAATTTTGATGA
CTTGAACAGTGAACAAAGCTATAATAAAAGCTTTTGTATAGCCGGAGCAAAGTGGCTAACATTCTTTTACCAG
GGAAGTAGCCCGCGCTTAGAAGGCACAAATGTCACCGTCAATGTGTTGCATCCTGGTATTGTACGGACAAATCT
GGGAGGCACATACACATTCCTGTTGGTCAAACCACTCTTCAATTTGGTGTGATGGGCTTTTTTCAAACTCC
AGTAGAAGGTGCCAGACTTCCATTTATTTGGCCTCTTACCTGAGGTAGAAGGAGTGTGAGGAAGATACTTTGG
GGATTGTAAAGAGGAAGAAGTGTGCCCCAAGCTATGGATGAATCTGTTGCAAGAAAAGTCTGGGATATCAGTGA
AGTGATGGTTGGCCTGCTAAAA**TAGGA**ACAAGGAGTAAAGAGCTGTTTATAAACTGCATATCAGTTATATCTG
TGATCAGGAATGGTGTGGATTGAGAACTTGTTACTTGAAGAAAAAGAAATTTTGATATTGGAATAGCCTGCTAAGA
GGTACATGTGGGTATTTTGGAGTTACTGAAAAATTATTTTGGGATAAGAGAATTTAGCAAGAGATGTTTTAAAT
ATATATAGTAAGTATAATGAATAATAAGTACAATGAAAAATACAATTATATTGTAATAATTATACTGGGCAAGCA
TGGATGACATATTAATATTTGTCAGAAATTAAGTGACTCAAAGTGCTATCGAGAGGTTTTTCAAGTATCTTTGAGT
TTCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTGTTGTGTGGAATATCTGCCTGGTGTGTGCA
CACAAGTCTTACTTGAATAAAATTTACTGGTAC

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FIGURE 182

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58747
<subunit 1 of 1, 336 aa, 1 stop
<MW: 36865, pI: 9.15, NX(S/T): 2
MAVATAAAVLAAALGGALWLAARRFVGPRVQRLRRGGDPGLMHGKTVLITGANSGLGRATAAELLRLGARVIMGCR
DRARAEEAAGQLRREL RQAAECGPEPGVSGVGELIVRELDLASLRSVRAFCQEMLQEEPRLDVLINNAGIFQCPY
MKTEDGFEMQFGVNH LGHFLLTNLL LGLLKSSAPSRIVVVSSKLYKYGDINFDDLNSEQSYNKSFCYSRSLANI
LFTRELARLEG TNVTNVNLHPGIVRTNLGRHIH IPLL VKPLFNLVSWAFFKTPVEGAQTSIYLASSPEVEGVSG
RYFGDCKEEELL PKAMDES VARKLWDISEVMVGLLK

Important features:**Signal peptide:**

amino acids 1-21

Short-chain alcohol dehydrogenase family protein

amino acids 134-144, 44-56 and 239-248

N-glycosylation site.

amino acids 212-215 and 239-242

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FIGURE 183

AACAGGATCTCCTCTTGCAGTCTGCAGCCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGCAGCCCGAAGATTC
ACT**ATGGT**GAAAATCGCCTTCAATACCCCTACCGCCGTGCAAAAGGAGGAGGCGCGGCAAGACGTGGAGGCCCTC
CTGAGCCGCACGGTCAGAACTCAGATACTGACCGGCAAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCC
TCTGGGAGATGTATGCTTACTCTCTTAGGCCTTTTCATTCATCTTGGCAGGACTTATTGTTGGTGGAGCCTGCATT
TACAAGTACTTCATGCCCAAGAGCACCATTTACCGTGGAGAGATGTGCTTTTTTATTCTGAGGATCCTGCAAAAT
TCCCTTCGTGGAGGAGAGCCTAACTTCCTGCCTGTGACTGAGGAGGCTGACATTCGTGAGGATGACAACATTGCA
ATCATTGATGTGCCTGTCCCCAGTTTCTCTGATAGTGACCCTGCAGCAATTATTCATGACTTTGAAAAGGGAATG
ACTGCTTACCTGGACTTGTTGCTGGGGAACTGCTATCTGATGCCCCCTCAATACTTCTATTGTTATGCCTCCAAAA
AATCTGGTAGAGCTCTTTGGCAAACCTGGCGAGTGGCAGATATCTGCCTCAAACCTTATGTGGTTCGAGAAGACCTA
GTTGCTGTGGAGGAAATTCGTGATGTTAGTAACCTTGGCATCTTTATTTACCAACTTTGCAATAACAGAAAGTCC
TTCCGCCTTCGTGCGCAGAGACCTCTTGCTGGGTTTCAACAAACGTGCCATTGATAAATGCTGGAAGATTAGACAC
TTCCCCAACGAATTTATTGTTGAGACCAAGATCTGTCAAGAG**TAA**GAGGCAACAGATAGAGTGTCTTGGTAAATA
AGAAGTCAGAGATTTACAATATGACTTTAACATTAAAGGTTTATGGGATACTCAAGATATTTACTCATGCATTTAC
TCTATTGCTTATGCTTTAAAAAAGGAAAAAATACTACTAACCCTGCAAGCTCTTGTCAAATTTTAGTT
TAATTGGCATTGCTTGTTTTTGAACCTGAAATTACATGAGTTTCATTTTTCTTTGCATTTATAGGGTTTAGAT
TTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATCCATCCGTTGTTTTTTGTTGTTTGT
TTTTCTTTTCCCTTTAAGTAAGCTCTTTATTCATCTTATGGTGGAGCAATTTTAAATTTGAAATATTTTAAATT
GTTTTTGAACCTTTTTGTGTAAATATATCAGATCTCAACATTGTTGGTTTCTTTGTTTTTCATTTGTACAAC
TTCTTGAAATTTAGAAATTACATCTTGCAGTTCTGTTAGGTGCTCTGTAATTAACCTGACTTATATGTGAACAAT
TTTCATGAGACAGTCATTTTAACTAATGCAGTGATTCTTCTCACTACTATCTGTATTGTGGAATGCACAAAAT
TGTGTAGGTGCTGAATGCTGTAAGGAGTTTAGGTTGTATGAATTCTACAACCCTATAATAAATTTACTCTATAC
AAAAAAAAAAAAAAAAAAAA

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FIGURE 184

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828
<subunit 1 of 1, 263 aa, 1 stop
<MW: 29741, pI: 5.74, NX(S/T): 1
MVKIAFNTPTAVQKEEARQDVEALLSRTVTRTQILTGKELRVATQKEGSSGRCMLTLLGLSFILAGLIVGGACIY
KYFMPKSTIYRGEMCFFDSEDPANSLRGGEPNFLPVTEEADIREDDNIAIIDVPVPSFSDSDPAATIHDFEKGMT
AYLDLLLGNCYLMLNLSIVMPPKNLVELFGKLASGRYLPQTYVVREDLVAVEEIRDVSNLGIFTYQLCNNRKSF
RLRRRDLLLGFNKRAIDKCWKIRHFPNEFIVETKICQE

Type II transmembrane domain:
amino acids 53-75

N-glycosylation site.
amino acids 166-170

Casein kinase II phosphorylation site.
amino acids 35-39, 132-136, 134-138

N-myristoylation site.
amino acids 66-72, 103-109

Prokaryotic membrane lipoprotein lipid attachment site.
amino acids 63-74

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FIGURE 185

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACGATGGCACTGAGCTCCCAGATCTGGGCCGCTTGCCT
CCTGCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTTCCACAACAGACGGGACAACTTGCAGAGCT
GCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTGGATGCCCATGTTCCAGAGGCGAAGGAGGCGAGACACCCA
CTTCCCCATCTGCATTTTCTGCTGCGGCTGCTGTCATCGATCAAAGTGTGGGATGTGCTGCAAGACGTAGAACCT
ACCTGCCCTGCCCCCGTCCCCTCCCTTCCTTATTTATTCCTGCTGCCCCAGAACATAGGTCTTGGAATAAAATGG
CTGGTTCTTTTGTTCCTTCCAA
AA

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FIGURE 186

MALSSQIWAACLLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTHFPICIFCCGCCHR
SKCGMCCKT

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FIGURE 187

CTGTCAGGAAGGACCATCTGAAGGCTGCAATTTGTTCTTAGGGAGGCAGGTGCTGGCCTGGCCTGGATCTTCCAC
CATGTTCTCTGTTGCTGCCTTTTGATAGCCTGATTGTCAACCTTCTGGGCATCTCCCTGACTGTCCTCTTCACCCCT
CCTTCTCGTTTTCATCATAGTGCCAGCCATTTTGGAGTCTCCTTTGGTATCCGCAAACCTCTACATGAAAAGTCT
GTTAAAAATCTTTGCGTGGGCTACCTTGAGAATGGAGCGAGGAGCCAAGGAGAAGAACCACCAGCTTTACAAGCC
CTACACCAACGGAATCATTGCAAGGATCCCACTTCACTAGAAGAAGAGATCAAAGAGATTCTGCGAAGTGGTAG
TAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGCCGAAAGGAATGGAGAC
CATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAACTGGAGTCTTGGAACTGCTGAGCAGAACCAA
TTATAACTTCCAGTACATCAGCCTTCGGCTCACGGTCTGTGGGGGTAGGAGTGTGATTCTGGTACTGCTTTCT
GCTGCCGCTCAGGATAGCACTGGCTTTCACAGGGATTAGCCTTCTGGTGGTGGGCACAACCTGTGGTGGGATACTT
GCCAAATGGGAGGTTTAAAGGAATTCATGAGTAAACATGTTCACTTAATGTGTTACCGGATCTGCGTGGCAGCGCT
GACAGCCATCATCACCTACCATGACAGGGAAAACAGACCAAGAAATGGTGGCATCTGTGTGGCCAATCATACCTC
ACCGATCGATGTGATCATCTTGGCCAGCGATGGCTATTATGCCATGGTGGGTCAAGTGCACGGGGGACTCATGGG
TGTGATTTCAGAGAGCCATGGTGAAGGCCTGCCACACGCTCTGGTTTGGAGCGCTCGGAAGTGAAGGATCGCCACCT
GGTGGCTAAGAGACTGACTGAACATGTGCAAGATAAAGCAAGCTGCCTATCCTCATCTTCCCAGAAGGAACCTG
CATCAATAATACATCGGTGATGATGTTCAAAAAGGGAAGTTTTGAAATTGGAGCCACAGTTTACCCTGTTGCTAT
CAAGTATGACCCTCAATTTGGCGATGCCTTCTGGAACAGCAGCAAATACGGGATGGTGACGTACCTGCTGCGAAT
GATGACCAGCTGGGCCATTGTCTGCAGCGTGTGGTACCTGCCTCCCATGACTAGAGAGGCAGATGAAGATGCTGT
CCAGTTTGCGAATAGGGTGAAATCTGCCATTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGGCT
GAAGAGGGAGAAGGTGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAACCA
CAAGGACAGGAGCCGCTCTGAGCCTGCCTCCAGCTGGCTGGGGCCACCGTGCGGGGTGCCAACGGGCTCAGAGC
TGGAGTTGCCGCCGCCGCCCTGCTGTGTCTTTCAGACTCCAGGGCTCCCCGGGCTGCTCTGGATCCCAG
GACTCCGGCTTTCGCCGAGCCGCGAGCGGATCCCTGTGCACCCGGCGCAGCCTACCCTTGGTGGTCTAAACGGAT
GCTGCTGGGTGTTGCGACCCAGGACGAGATGCCTTGTCTTTTACAATAAGTCGTTGGAGGAATGCCATTAAG
TGAACCTCCACCTTTGCACGCTGTGCGGGCTGAGTGGTTGGGGAGATGTGGCCATGGTCTTGTGCTAGAGATGG
CGGTACAAGAGTCTGTTATGCAAGCCGCTGTGCCAGGGATGTGCTGGGGCGGCCACCCGCTCTCCAGGAAAGGC
ACAGCTGAGGCACTGTGGCTGGCTTCGGCCTCAACATCGCCCCCAGCCTTGGAGCTCTGCAGACATGATAGGAAG
GAAACTGTCTCTGCAGGGGCTTTCAGCAAAATGAAGGGTTAGATTTTATGCTGCTGCTGATGGGGTTACTAAA
GGGAGGGGAAGAGGCCAGGTGGGCCGCTGACTGGGCCATGGGGAGAACGTGTGTTGCTACTCCAGGCTAACCCCTG
AACTCCCCATGTGATGCGCGCTTTGTTGAATGTGTCTCGGTTTCCCCATCTGTAATATGAGTCGGGGGGAATG
GTGGTGATTCTACCTCACAGGGCTGTTGTGGGGATTAAAGTGCTGCGGGTGAGTGAAGGACACATCACGTTTCA
TGTTTCAAGTACAGGCCACAAAACGGGGCACGGCAGGCCTGAGCTCAGAGCTGCTGCACTGGGCTTTGGATTTG
TTCTTGTGAGTAAATAAACTGGCTGGTGAATGA

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FIGURE 188

MFLLLPFDSLIVNLLGISLTVLFTLLLVFIIVPAIFGVSEFGIRKLYMKSLLKIFAWATLRMERGAKEKNHQLYKP
YTNGIIAKDPTSLEEEIKEIRRGSSKALDNTPEFELSDIFYFCRKGMETIMDDEVTKRFSAAELESWNLLSRTN
YNFQYISLRLTVLWGLGVLIRYCFLPLRLIALAFTGISLLVVGTTVVGYLPNGRFKEFMSKHVHLMCYRICVRAL
TAIITYHDRENRRPRNGGICVANHTSPIDVILLASDGYAMVGQVHGGLMGVIQRAMVKACPHVWFERSEVKDRHL
VAKRLTEHVQDKSKLPILIFPEGTCINNTSVMFKKGSFEIGATVYPVAIKYDQFGDAFWNSSKYGMVTYLLRM
MTSWAIVCSVWYLPMTREADEDAVQFANRVKSAIARQGGLVDLLWDGGLKREKVKDTFKEEQQKLYSKMIVGNH
KDRSRS

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FIGURE 189

GCCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCCGCCCTCACCCGGACCCCTGGCCCTCACGTCTCCTCCAGG
GATGGCGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCTCCACACCTGGCAGGCCCAGGCTGTTCCCAC
CATCCTGCCCCCTGGGCCTGGCTCCAGACACCTTTGACGATACCTATGTGGGTTGTGCAGAGGAGATGGAGGAGAA
GGCAGCCCCCTGCTAAAGGAGGAAATGGCCCACCATGCCCTGCTGCGGGAATCCTGGGAGGCAGCCAGGAGAC
CTGGGAGGACAAGCGTCCAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCCAGAATGGAATAGCCATTATGGTCTA
CACCAACTCATCGAACACCTTGTACTGGGAGTTGAATCAGGCCGTGCGGACGGGCGGAGGCTCCCGGGAGCTCTA
CATGAGGCACCTTCCCTTCAAGGCCCTGCATTTCTACCTGATCCGGGCCCTGCAGCTGCTGCGAGGCAGTGGGGG
CTGCAGCAGGGGACCTGGGGAGGTGGTGTTCGAGGTGTGGGCAGCCTTCGCTTTGAACCAAGAGGCTGGGGGA
CTCTGTCCGCTTGGGCCAGTTTGCCCTCCAGCTCCCTGGATAAGGCAGTGGCCACAGATTTGGGGAGAAGAGGCG
GGGCTGTGTCTGCGCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGGCCTCCTCTCTGCCCCCTGGAAGAC
TCTGCTCTTGGCCCCTGGAGAGTTCCAGCTCTCAGGGGTGGGGCCCTTGAAGTCCAACATCTGCCACTTAGGAGC
CCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAGCAGCCTTGAGAAGCAAGAACATGGTTCCGGAC
CCAGCCCTAGCAGCCTTCTCCCCAACCAGGATGTTGGCCTGGGGAGGCCACAGCAGGGCTGAGGGAACTCTGCTA
TGTGATGGGGACTTCCTGGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGCAATGTGGA
GACATGGAGTTTATTGAGGTAGCTACGTGATTAAATGGTATTGCAGTGTGA

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FIGURE 190

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGCAEEMEEKAAPLLKEEMAHHALLRESWEAAQET
WEDKRRGLTLPPGFKAQNGIAIMVYTNSNTLYWELNQAVRTGGGSRELYMRHFPPKALHFYLIRALQLLRGSGG
CSRGPGEVVFRGVGSLRFEPKRLGDSVRLGQFASSSLDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPWKT
LLLAPGEFQLSGVGP

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FIGURE 191

GTGGCTTCATTTCACTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCCCAACATGCCTCACCCCTCATCTATAT
CCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTGGTCGGTTCCGTTGGTGGGGCCCGTGAC
TTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCACCAT
ACAGCCAGAAGGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTA
CTCCCTGAAGCTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACTCCA
GCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCA
GAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTTATAC
CTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTCCCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAGA
AAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCTGTCAGCAGAACTTCTCAAGCCCCATCCTTGCCAGGAA
GCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCCTCCTGTGTCTCCTGTTGGTGCCCCCTCCTGCT
CAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAA
GAGAGTGGACATTTGTCGGGAACTCCTAACATATGCCCCATTCTGGAGAGAACACAGAGTACGACACAATCCC
TCACACTAATAGAACAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGAT
GGAAAATCCCCACTCACTGCTCAGCATGCCAGACACACCAAGGCTATTTGCCTATGAGAATGTTATCTAGACAGC
AGTGCACTCCCCTAAGTCTCTGCTCA

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FIGURE 192

MAGSPTCLTLIYLWQLTGSAAAGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVTIQPEGGTIIIVTON
RNRERVDFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHVYEHLSKPKVTMGLQSNKNGTCVTNLT
CCMEHGEEEDVIYTWKALGQAANESHNGSILPISWRWGESDMTFICVARNPVS RNFS SPILARKLCEGAADDPDSS
MVLCLLLVPLLLSLFVLGLFLWFLKRERQEEYIEKKRVDICRETPNICPHSGENT EYDTIPHTNRTILKEDPA
NTVYSTVEIPKKMENPHSLTMPDTPRLFAYENVI

FIGURE 193

[illegible]

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FIGURE 194

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852
><subunit 1 of 1, 283 aa, 1 stop
><MW: 29191, pI: 4.52, NX(S/T): 0
MVSAAAPSLILLILLLLLSVLPATDARSVPLKATFLEDVAGSGEAEAGSSASSPSLPPPWTLPALSPTSMPGPQPTTLG
GPSPTNFDGIVDFFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKASAYYPSSFPPKKYVDQSDRAGGPRAF
SEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSPTRAALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVP
VETPEAQEEPCSGVLEGAVVAGEGQGELEGSLLLAQEAQGPVGPPEPCACSSVHPSV
```

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 94-118

N-myristoylation site.amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199, 211-217, 238-244,
242-248

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FIGURE 195

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAAATGAAGATGCTGCTGCTGCTGTGTTTGGGA
CTGACCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGAACTTAATGTAGAAAAGATTAATGGG
GAATGGCATACTATTATCCTGGCCTCTGACAAAAGAGAAAAGATAGAAGAACATGGCAACTTTAGACTTTTTCTG
GAGCAAATCCATGTCTTGGAGAATTCCCTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTA
TCTATGGTTGCTGACAAAACAGAAAAGGCTGGTGAATATCTGTGACGTATGATGGATTCAATACATTTACTATA
CCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAACGAAAAGGATGGGGAAACCTTCCAGCTGATG
GGGCTCTATGGCCGAGAACCAGATTTGAGTTCAGACATCAAGGAAAGGTTTGCACAACTATGTGAGGAGCATGGA
ATCCTTAGAGAAAATATCATTGACCTATCCAATGCCAATCGCTGCCTCCAGGCCCGAGAAATGAAGAATGGCCTGA
GCCTCCAGTGTTGAGTGGACACTTCTCACCAGGACTCCACCATCATCCCTTCCTATCCATACAGCATCCCAGTA
TAAATTCTGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATTCCAGTCTATCAACATGTTACCTAGGAT
ACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTTGATACACCCTTGACAATTTTTTCATGAAATTATTCCT
CTTCCTGTTCAATAAATGATTACCCTTGCACTTAA

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FIGURE 196

MKMLLLLCLGLTLVCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEEHG NFR LFLEQIHVLENSLV LKVH
TVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLINEKDGETFQLMGLYGREPDLSSDIKE
RFAQLCEEHGILRENIIDLSNANRCLQARE

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FIGURE 197

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAATGGATTGAGCCTG
CTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTGTCAGCTTAGTTGAGGAAGACCAATTT
TCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTCCCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCA
ACAACAATGTCCTTGACAGCAAGAAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTC
AGTGTGATCACAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAGGTCCTCTCATG
TGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGACATTATCCAGAATCC
TTCAACTTGCAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTGGTTTCAATAAACCCACCAGTAACGACACC
ATGGCGAGTGGCTGGAGAGCATCTAGTTTCCACTTCGATTCTGAAGAAAACAAACATAGGCTTATCCACTTCTCA
GTATTTTATAGGTCTATTGCTTGTTGGAATTCTGGAGGTCCTGTTGGGCTCAGTCAGATAGTCATCGGTTTCCTT
GGCTGTCTGTGTGGAGTCTCTAAGCGAAGAAGTCAAATTGTGTAGTTTAATGGGAATAAAATGTAAGTATCAGTA
GTTTGAAAAAAAAA

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FIGURE 198

MTCCEGWTS CNGFSLLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMAIPATTMSLTARKR
ACNNRTGMFLSSFFSVITVIGALYCM LISIQALLKGPLMCNSPNSNANCEFSLKNISDIHPESFNLOWFFNDS
CAPPTGFNKPTSNDT MASGWRASSFHFDSEENKHRLIHFSVFLGLLLVGILEVLFGLSQIVIGFLGCLCGVSKRR
SQIV

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FIGURE 199

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGGTGAAGGAGCAGTG
AGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTGGAGCAGATCCGTGGGCTGCAGACCCC
CGCCCCAGTGCCCTCTCCCCCTGCAGCCCTGCCCCCTCGAACTGTGACATGGAGAGAGTGACCCCTGGCCCTTCTCCT
ACTGGCAGGCCTGACTGCCTTGGAAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAA
AAACCTGCAGCTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGGCAA
ATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCCACTCATCACTCCAGGCTC
TGCCACTACTTGCTGAGCACAGGACTGGCCTCCAGGGATGGCCTGAAGCCTAACACTGGCCCCCAGCACCTCCTC
CCCTGGGAGGCCTTATCCTCAAGGAAGGACTTCTCTCCAAGGGCAGGCTGTTAGGCCCTTTCTGATCAGGAGGC
TTCTTTATGAATTAAACTCGCCCCACCACCCCTCA

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FIGURE 200

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAAGIAAVLSGKCKYKSSQKQHSPVPE
KAIP LITPGSATTC

FIGURE 201

[illegible]

FIGURE 202

Cell attachment sequence.
amino acids 301-304

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FIGURE 203

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGGATGTCGCTGCTGAGCCTGCCCTGGCTGGGCCTCA
GACCGGTGGCAATGTCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTCCTGGCTACTCGCCCGCATCCTGGCTT
GGACCTATGCCTTCTATAACAAGTGGCGCCGGCTCCAGTGTTTCCCACAGCCCCAAAACGGAAGTGGTTTTGGG
GTCACCTGGGCCTGATCACTCCTACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTCGGCCACCTATTCCCAGG
GCTTTACGGTATGGCTGGGTCCCATCATCCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATCACCA
ATGCCTCAGCTGCCATTGCACCCAAGGATAATCTCTTCATCAGGTTCCCTGAAGCCCTGGCTGGGAGAAGGGATAC
TGCTGAGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGACGCCCGCCTTCCATTTCAACATCCTGAAGT
CCTATATAACGATCTTCAACAAGAGTGCAAACATCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCA
GTGCTCTGGACATGTTTGAGCACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTTGACA
GCCATTGTCAGGAGAGGCCCCAGTGAATATATTGCCACCATCTTGGAGCTCAGTGCCCTTGTAGAGAAAAGAAGCC
AGCATATCCTCCAGCACATGGACTTTCTGTATTACCTCTCCCATGACGGGCGGCGCTTCCACAGGGCCTGCCGCC
TGGTGCATGACTTCACAGACGCTGTATCCGGGAGCGGCGTCGCACCCTCCCCACTCAGGGTATTGATGATTTTT
TCAAAGACAAAGCCAAAGTCCAAGACTTTGGATTTTATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGG
CATTGTGAGATGAGGATATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACGGCCAGTGGCC
TCTCCTGGGTCCTGTACAACCTTGCGAGGCACCCAGAATACCAGGAGCGCTGCCGACAGGAGGTGCAAGAGCTTC
TGAAGGACCGCATCCTAAAGAGATTGAATGGGACGACCTGGCCCAGCTGCCCTTCCCTGACCATGTGCGTGAAGG
AGAGCCTGAGGTTACATCCCCAGCTCCCTTCATCTCCCGATGCTGCACCCAGGACATTGTTCTCCAGATGGCC
GAGTCATCCCCAAAGGCATTACCTGCCTCATCGATATTATAGGGGTCCATCACAACCCAACTGTGTGGCCGGATC
CTGAGGTCTACGACCCCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTCACCTCTGGCTTTTATTCTTTCT
CCGAGGGCCCAGGAACTGCATCGGGCAGGCGTTCCGCATGGCGGAGATGAAAGTGGTCTGGCGTTGATGCTGC
TGCACTTCCGGTTCCTGCCAGACCACTGAGCCCCGAGGAAGCTGGAATTGATCATGCGCGCCGAGGGCGGGC
TTTGGCTGCGGTTGGAGCCCCCTGAATGTAGGCTTGCAGTGACTTTTCTGACCCATCCACCTGTTTTTTTGCAGATT
GTCATGAATAAAACGGTGCTGTCAA

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FIGURE 204

MSLLSLPWLGLRPVAMSPWLLLLLVVGSWLLARILAWTYAFYNNCRRLQCFPPQPPKRNWFWGHLGLITPTEGLK
DSTQMSATYSQGFTVWLGPPIPFIVLCHPDTIRSITNASAAIAPKDNLFIRFLKPWLGEGILLSGGDKWSRHRM
LTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGSSRLDMFEHISLMTLDSLQKCIFSFDSHCQERPSEYIATI
LELSALVEKRSQHILQHMDFLYYLSHDGRRFHRACRLVHDFTDAVIRERRRTLPTQGIDDFKDKAKSKTLDFID
VLLLSKDEDGKALSDEDIRAEADTFMFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEWDDL
AQLPFLTMCVKESLRLHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVWPDPEVYDPFRFDPENS
KGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHTEPRRKLELIMRAEGGLWLRVEPLNVGLQ

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FIGURE 205

TCCCTTGACAGGTCTGGTGGCTGGTTCGGGGTCTACTGAAGGCTGTCTTGATCAGGAACTGAAGACTCTCTGCT
TTTGCCACAGCAGTTCCTGCAGCTTCCTTGAGGTGTGAACCCACATCCCTGCCCCAGGGCCACCTGCAGGACGC
CGACACCTACCCCTCAGCAGACGCCGGAGAGAAATGAGTAGCAACAAAGAGCAGCGGTGACAGTGTTCGTGATC
CTCTTTGCCCTCATCACCATCCTCATCCTCTACAGCTCCAACAGTGCCAATGAGGTCTTCCATTACGGCTCCCTG
CGGGCCCGTAGCCGCCGACCTGTCAACCTCAAGAAGTGGAGCATCACTGACGGCTATGTCCCCATTCTCGGCAAC
AAGACACTGCCCTCTCGGTGCCACCAGTGTGTGATTGTGACGAGCTCCAGCCACCTGCTGGGCACCAAGCTGGGC
CCTGAGATCGAGCGGGCTGAGTGTACAATCCGCATGAATGATGACCCACCACTGGCTACTCAGCTGATGTGGGC
AACAAGACCACCTACCGCGTCGTGGCCCATTCAGTGTGTTCCGCGTCTGAGGAGGCCCCAGGAGTTTGTCAAC
CGGACCCCTGAAACCGTGTTCATCTTCTGGGGGCCCCGAGCAAGATGCAGAAGCCCCAGGGCAGCCTCGTGCGT
GTGATCCAGCGAGCGGGCCTGGTGTTCCTCAACATGGAAGCATATGCCGTCTCTCCCGGCCGCATGCGGCAATTT
GACGACCTCTTCCGGGTGAGACGGGCAAGGACAGGGAGAACTCTCATTCTGTTGAGCACAGGCTGGTTTACC
ATGGTGATCGCGGTGGAGTTGTGTGACCAGTGCATGTCTATGGCATGGTCCCCCCTAACTACTGCAGCCAGCGG
CCCCGCTCCAGCGCATGCCCTACCACTACTACGAGCCCAAGGGGCCGACGAATGTGTACCTACATCCAGAAT
GAGCAGTTCGCAAGGGCAACCACCACCGCTTCATCACCAGAGAAAAGGCTCTTCTCATCGTGGGCCAGCTGTAT
GGCATCACCTTCTCCACCCCTCCTGGACCTAGGCCACCCAGCCTGTGGGACCTCAGGAGGGTCAGAGGAGAAGC
AGCCTCCGCCAGCCGCTAGGCCAGGGACCATCTTCTGGCCAATCAAGGCTTGCTGGAGTGTCTCCAGCCAATC
AGGGCCTTGAGGAGGATGTATCCTCCAGCCAATCAGGGCCTGGGGAATCTGTTGGCGAATCAGGGATTTGGGAGT
CTATGTGGTTAATCAGGGGTGTCTTTCTTGTGCAGTCAGGGTCTGCGCACAGTCAATCAGGGTAGAGGGGTATT
TCTGAGTCAATCTGAGGCTAAGGACATGTCTTTCCCATGAGGCCTTGGTTCAGAGCCCCAGGAATGGACCCCC
AATCACTCCCCACTCTGCTGGGATAATGGGGTCTGTCCCAAGGAGCTGGGAATTTGGTGTGGCCCCCTCAATTT
CCAGCACCAGAAAGAGAGATTGTGTGGGGGTAGAAGCTGTCTGGAGGCCCGGCCAGAGAATTTGTGGGGTTGTGG
AGGTTGTGGGGGCGGTGGGGAGGTCCAGAGGTGGGAGGCTGGCATCCAGGTCTTGGCTCTGCCCTGAGACCTTG
GACAAACCTTCCCCCTCTCTGGGCACCTTCTGCCCACACCACTTCCAGTGCGGAGTCTGAGACCTTTCCAC
CTCCCCACAAGTGCCCTCGGGTCTGTCTCCCCGTCTGGACCTCCAGCCACTATCCCTTGCTGGAAGGCTCA
GCTCTTTGGGGGTCTGGGGTGACCTCCCCACCTCCTGGAAAACCTTAGGGTATTTTTCGCGAACTCCTTCAGG
GTTGGGGGACTCTGAAGGAAACGGGACAAAACCTTAAGCTGTTTTCTTAGCCCCTCAGCCAGCTGCCATTAGCTT
GGCTCTTAAAGGGCCAGGCCTCCTTTTCTGCCCTCTAGCAGGGAGGTTTTCCAAGTGTGGAGGCGCCTTTGGGG
CTGCCCCCTTGTCTGGAGTCACTGGGGGCTTCCGAGGGTCTCCCTCGACCTCTGTCTGCTGCGGATGGCTGTCTG
GGAGCTGTATCACCTGGGTCTGTCCCCTGGCTCTGTATCAGGCATTTATTAAAGCTGGGCTCAGTGGGGGTGT
GTTTGTCTCCTGCTCTTCTGGAGCCTGGAAGGAAAGGGCTTCAAGAGGAGGCTGTGAGGCTGGAGGGACAGATG
GAGGAGGCCAGCAGCTAGCCATTGCACACTGGGTGATGGGTGGGGGCGGTGACTGCCCCAGACTTGGTTTTGTA
ATGATTTGTACAGGAATAAACACACCTACGCTCCGGAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 206

MSSNKEQRSAVEFVILFALITILILYSSNSANEVFHYGSLRGRSRPVLKKWSITDGYVPILGNKTLPSRCHQCV
IVSSSSHLLGTLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAHSSVFRVLRRPQEFVNRTPETVFIFWG
PPSKMQKPQGS�VRVIQRAGLVFPNMEAYAVSPGRMRQFDDLFRGETGKDREKSHSWLSTGWFTMVIAVELCDHV
HVGMPVPPNYCSQRRLQRMPIHYEYPKGPDECVTYIQNEHSRKGNNHHRFITEKRVFSSWAQLYGITFSHPST

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 9-31 (type II)

N-glycosylation site.

amino acids 64-68, 115-119

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 50-54

Casein kinase II phosphorylation site.

amino acids 3-7, 29-33, 53-57, 197-201

Tyrosine kinase phosphorylation site.

amino acids 253-262

N-myristoylation site.

amino acids 37-43, 114-120, 290-294

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FIGURE 207

GTAGCGCGTCTTGGGTCTCCCGGCTGCCGCTGCTGCCGCCGCCGCTCGGGTCGTGGAGCCAGGAGCGACGTCAC
CGCC**ATGG**CAGGCATCAAAGCTTGATTAGTTTGCTCTTTGGAGGAGCAATCGGACTGATGTTTTTGTGCTGG
ATGTGCCCTTCCAATATACAACAAATACTGGCCCCTCTTTGTTCTATTTTTTTACATCCTTTACCTATTCCTATA
CTGCATAGCAAGAAGATTAGTGGATGATACAGATGCTATGAGTAACGCTTGTAAGGAACCTGCCATCTTTCTTAC
AACGGGCATTGTCGTGTGAGCTTTGGACTCCCTATTGTATTTGCCAGAGCACATCTGATTGAGTGGGGAGCTTG
TGCACCTTGTTCTCACAGGAAACACAGTCATCTTTGCACTATACTAGGCTTTTTCTTGGTCTTTGGAAGCAATGA
CGACTTCAGCTGGCAGCAGTGG**TG**AAAAAGAAATTACTGAACTATTGTCAAATGGACTTCCTGTCATTTGTTGGCC
ATTCACGCACACAGGAGATGGGGCAGTTAATGCTGAATGGTATAGCAAGCCTCTTGGGGGTATTTTAGGTGCTCC
CTTCTCACTTTTATTGTAAGCATACTATTTTACAGAGACTTGCTGAAGGATTAAGGATTTTCTCTTTTGGA
AAGCTTGACTGATTTACACTTATCTATAGTATGCTTTTTGTGGTGTCTGCTGAATTTAAATATTTATGTGTTT
TTCCTGTTAGGTTGATTTTTTTTGGAAATCAATATGCAATGTAAACACTTTTTTAATGTAATCATTTGCATTGGT
TAGGAATTCAGAATTCGCCCGGCTCTATTACTGGTCAAGTACATCTTTTCTCTTAAATTAATTTAGCCTCCATTA
TTACAAAAAATTATAAAAAATAAGTTTTCAGTCAGTCAGGATGACATCACTCCCAATGTTATGCAGACATACAGAC
GGTTGGCATACTGTATAGACTGTATACTCAGTGCAAATATAGCTGCATTATACCTCAGAGGGGCCAAGTGTTAA
TGCCCATGCCCTCCGTTAAGGGTTGTTGGTTTTACTGGTAGACAGATGTTTTGTGGATTGAAAATTATTTTATGG
AATTGCTACAGAGGAGTGCTTTTCTTCTCAATTGTTAGAAGAATTTATGTTAAACTTTAAGGTAAGGGTGTA
ACATTTTTGAGATAAGGTTTTTATTTATGTTTATTATTGTTAGAGTGAGTTGCAATGTGGGAAGAAATGACATTG
AAATTCAGTTTTTTGAATCCTGTTTCTATTTATAAGTGAATTTGTGATCTCCTATCAACCTTTTCATGTTTTACC
CTGTTAAATGGACATACATGGAACCACTACTGATGAGGGACAGTTGTATGTTGCATCATATATGCCAGAAAC
CTTCCTCTGCTTCCTCCTTTTGACTTATTTGGTATGTTGTATATATTACATAAAAAATAACTTTTCAAATATAGTTT
AATAACACTTAGAAGTGTTTACTTACCTGGAATAAATTGCTATGCCGTACATTACAGAGTGCCCCCTCCCCTGCA
AGGCCTTGCCATGATTAACAAGTAACCTGTTAGTCTTACAGATAAATTCATGCATTAACAGTTTAAGATTTAGACC
ATGGTAATAGTAGTTCTTATTCTCTAAGGTTATATCATATGTAATTTAAAGTATTTTTAAGACAAGTTTCCTGT
ATACCTCTGAACTGTTTTGATTTTGAGTTCATCATGATAGATCTGCTGTTTCCTTATAAAAGGCATTTGTGTGT
GAGTTAATGCAAAGTAGCCAAGTCCAGCTATATAGCAGCTTCAGAAACATACCTGACCAAAAAATTCAGTAAC
CAGGCATGATCAATTTATAGTGGTCGTTTACATCTAATAATTATCAGGACTTTTTTTCAGGAGTGGGTTATAAAAA
CATTCAAGTTGGTCTGACAGTATTTTGTTAAGGATATTTGTTTGTATGTTTATTACGTATACTTACATAAAAAAT
ATTTGCCCATCAGCCAAAACCTCAGTAATCATGACAGCTGTCTGTTGTTTTATGAAGTTTATTTCTCAAGAAAATG
GGAATAAATTTGGGATTTGTTTCAGCTTTTTTACTAAAGATGCCATAAGCCACAGGTTTTATTGCCCTAACTTAAGC
CATGACTTTTAGATATGAGATGACGGGAAGCAGGACGAAATATCGGCCGTGTGGCTGGAGCCTTCCCACTGGAGGC
TGAAAGTGGCTTGTGGTATTATAATGTTTCAAGAGGAAGGTGCAGGTACACATGAGTTAGAGAGCTGGT
GAGACAGTTGGGAACCTTTTGTGCTTGTGATCTACTGGACTTTTTTTTTTGCAGGAAGTGCATTCCTCTGGTCCTTC
CCTATTTTCTGTTCTGGATGTCAGTGCAGTGCAGTCTACTGTTTTATCCACTTGGCCACAGACTTTTTCTAACA
GCTGCGTATTATTTCTATATACTAATTGCATTGGCAGCATTTGTGTCTTTGACCTTGATATACTAGCTTGACATAGT
GCTGTCTCTGATTTCTAGGCTAGTTACTTGAGATATGAATTTTCCATAGAATATGCACTGATACACATTACCAT
TCTTCTATGGAAGAAAACCTTTTGATGATGAACAATAAAGATTTTAAATATCTATTTTAAAAA

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FIGURE 208

MAGIKALISLSFGGAIGLMFLMLGICALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTDAMSNACKELAIFLT
T
GIVVSAFGLPIVFARAHLEWGACALVLTGNTVIFATILGFFLVFGSNDDFSWQQW

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FIGURE 209

CTTGCAAGAGAAAGAGTCTTTTGTGCAGCACCCCTTTAAAGGGTGACTCGTCCCACCTTGTGTTCTCTCTCCTGGTGC
AGAGTTGCAAGCAAGTTTATCAGAGTATCGCCATGAAGTTTCGTCCCCTGCCTCCTGCTGGTGACCTTGTCTGCTGCC
TGGGGACTTTGGGTCAGGCCCCGAGGCAAAAGCAAGGAAGCACTGGGGAGGAATTCATTTCCAGACTGGAGGGA
GAGATTCTGCACTATGCGTCCCAGCAGCTTGGGGCAAGGTGCTGGAGAAGTCTGGCTTCGCGTCGACTGCCGCA
ACACAGACCAGACCTACTGGTGTGAGTACAGGGGGCAGCCCAGCATGTGCCAGGCTTTTGCTGCTGACCCCAAAC
CTTACTGGAATCAAGCCCTGCAGGAGCTGAGGCGCCTTCACCATGCGTGCCAGGGGGCCCCGGTGCTTAGGCCAT
CCGTGTGCAGGGAGGCTGGACCCCAGGCCCATATGCAGCAGGTGACTTCCAGCCTCAAGGGCAGCCCAGAGCCCA
ACCAGCAGCCTGAGGCTGGGACGCCATCTCTGAGGCCCAAGGCCACAGTGAAACTCACAGAAGCAACACAGCTGG
GAAAGGACTCGATGGAAGAGCTGGGAAAAGCCAAACCCACCACCCGACCCACAGCCAAACCTACCCAGCCTGGAC
CCAGGCCCCGGAGGGAATGAGGAAGCAAAGAAGAAGGCCTGGGAACATTGTTGGAACCCCTTCCAGGCCCTGTGCG
CCTTTCTCATCAGCTTCTTCCGAGGGTTGACAGGTGAAAGACCCCTACAGATCTGACCTCTCCCTGACAGACAACC
ATCTCTTTTTATATTATGCCGCTTTCAATCCAACGTTCTCACACTGGAAGAAGAGAGTTTCTAATCAGATGCAAC
GGCCCAAATTCTTGATCTGCAGCTTCTCTGAAGTTTGGAAAAGAAACCTTCCTTTCTGGAGTTTGCAGAGTTCAG
CAATATGATAGGGAACAGGTGCTGATGGGCCCAAGAGTGACAAGCATACACAATACTATTATTCTGTAGAAGTT
TTGCTTTGTTGATCTGAGCCTTCTATGAAAGTTTAAATATGTAACGCATTTCATGAATTTCCAGTGTTTCAGTAAAT
AGCAGCTATGTGTGTGCAAAATAAAAGAATGATTTTCAGAAAAA

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FIGURE 210

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59602
<subunit 1 of 1, 223 aa, 1 stop
<MW: 24581, pI: 9.28, NX(S/T): 0
MKFVPCLLLVTLSCLTGLGQAPRQKQGSGTGEFFHFQTGGRDSCTMRPSSLGQGAGEVWLR
VDCRNTDQTYWCEYRGQPSMCQAFADPKPYWNQALQELRRLHHACQGAPVLRPSVCREA
GPQAHMQQVTSSLKGSPEPNQQPEAGTPSLRPKATVKLTEATQLGKDSMEELGKAKPTTR
PTAKPTQPGPRPGGNEEAKKKAWEHCWKPFQALCAFLISFFRG
```

Important features:**Signal peptide:**

Amino acids: 1-19

N-myristoylation sites:

Amino acids: 38-44;51-57;194-200

DNA photolyases class 1 proteins:

Amino acids: 58-69

Tyrosine kinase phosphorylation site:

Amino acids: 64-71

N-myristoylation sites:

Amino acids: 38-44;51-57;194-200

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids: 4-15

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FIGURE 211

GTGCAAGGAGCCGAGGCGAG**ATG**GGCGTCCTGGGCGGGTCCTGCTGTGGCTGCAGCTCTGCCCACTGACCCAGGCG
GTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTCGCAGCCAACTGGAGCCAGAACCGGACCCCGTGCGCC
GGCGGCGCCGTTGAGTTCCTCGCGGACAAGATGGTGTCACTCCTGGTGCAAGAAGGTCACGCCGTCTCAGACATG
CTCCTGCCGCTGGATGGGGAACCTCGTCCTGGCTTCAGGAGCCGGATTGCGCGTCTCAGACGTGGGCTCGCACCTG
GACTGTGGCGCGGGCGAACCTGCCGTCTTCCGCGACTCTGACCGCTTCTCCTGGCATGACCGCACCTGTGGCGCT
CTGGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCGTGCCCTGCCGCCACGACGACGTCTTCTTTC
CGCCTAGTGCCCTCCTTCCGCGTGCGGGCTCGGCCCTGGCGCTAGCCCCGTGCGTGTCCGCAGCATCTCGGCTCTGG
GCCGGACGTTACGCGCGACGAGGACCTGGCTGTTTTCTGCGGTCCCGCGCGGGCCGCCTACGCTTCCACGGGC
CGGGCGCGCT**TGAG**CGTGCGCCCCGAGGACTGCGCGGACCCGTGCGGCTGCGTCTGCGGCAACGCGGAGGCGCAGC
CGTGGATCTGCGCGGCCCTGCTCCAGCCCCT

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FIGURE 212

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59603
<subunit 1 of 1, 197 aa, 1 stop
<MW: 20832, pI: 8.74, NX(S/T): 2
MGVLGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLV
QEGHAVSDMLLPLDGELVLASGAGFGVSDVGSHLDCGAGEPAVFRSDRFSWHDRTCCGAL
GTRHLASSSWTPSACPAATTSSFRVLVPPSAWGSALALAPCVSAASRLWAGRSRATRTWL
FSWRPARAAYASTGRAR
```

Important features:**Signal peptide:**

Amino acids 1-19

N-glycosylation site:

Amino acids 35-39

Glycosaminoglycan attachment site:

Amino acids 81-85

N-myristoylation sites:

Amino acids 82-88;118-124;153-159

C-type lectin domain proteins:

Amino acids 108-118

FIGURE 213

[illegible]

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FIGURE 214

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGLALIFCILQSLALTWYSLSFIPFARDAVKKCFVCLA

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FIGURE 215

GGATTTTTGTGATCCGCGATTGCTCCACGGGCGGGACCTTTGTAAGTGGGGAGGCCCAGGACAGGCCCACCC
TGCGGGGCGGGAGGCAGCCGGGGTGAGGGAGGTGAAGAAACCAAGACGCAGAGAGGCCAAGCCCCTTGCCTTGGG
TCACACAGCCAAAGGAGGCAGAGCCAGAATCACAACCAGATCCAGAGGCAACAGGGACATGGCCACCTGGGACG
AAAAGGCAGTCACCCGCAGGGCCAAGGTGGCTCCCGCTGAGAGGATGAGCAAGTTCTTAAGGCACTTCACGGTCG
TGGGAGACGACTACCATGCCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGGAGC
AGCCACCACCCACACCAGTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCCCTGACGTTGCCCCCTGCCCTGGCCCCG
CAGCCAGGGCCCCCCTTGACTTCAGGGGCATGTTGAGGAACTGTTGAGCTCCACAGGTTTCAGGTCATCATCA
TCTGCTTGGTGGTTCTGGATGCCCTCCTGGTGCTTGCTGAGCTCATCCTGGACCTGAAGATCATCCAGCCCGACA
AGAATAACTATGCTGCCATGGTATTCCACTACATGAGCATCACCATCTTGGTCTTTTTTATGATGGAGATCATCT
TTAAATTATTTGTCTTCCGCCTGAGTTCTTTTACCACAAGTTTGAGATCCTGGATGCCCCGTCGTGGTGGTGGTCT
CATTTCATCCTGGACATTGTCCTCCTGTTCCAGGAGCACCAGTTTGAGGCTCTGGGCCTGCTGATTCTGCTCCGGC
TGTGGCGGGTGGCCCGGATCATCAATGGGATTATCATCTCAGTTAAGACACGTTTCAAGACGGCAACTCTTAAGGT
TAAACAGATGAATGTACAATTGGCCGCCAAGATTCAACACCTTGAGTTCAGCTGCTCTGAGAAGCCCCCTGGACT
GATGAGTTTTGCTGTATCAACCTGTAAGGAGAAGCTCTCTCCGGATGGCTATGGGAATGAAAGAATCCGACTTCTA
CTCTCACACAGCCACCGTGAAAGTCCTGGAGTAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAGCAGGCTGGC
ATGTTCACTGGGCTGGTGTACGACAGAGAACCTGACAGTCACTGGCCAGTTATCACTTCAGATTACAAATCACA
CAGAGCATCTGCCTGTTTTCAATCACAAGAGAACAAACCAAAATCTATAAAGATATTCTGAAATATGACAGAA
TTTGACAAATAAAAGCATAAACGTGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 216

MATWDEKAVTRRAKVAPAERM SKFLRHFTTVVGDDYHAWNINYKKWENEEEEEEEQPPPTPVS GEEGRAAAPDVA
PAPGPAPRAPLDFRGMLRKL FSSHREQV IICLVVLDALLVLAELIDLKIIQPDKN NYAAMVFHYMSITILVFF
MMEIIFKLFV FRLSSFTTSLRSWMPVVVVVSFILDIVLLFQEHQFEALGLLILLRLWRVARIINGIIISVKTRSE
RQLRLKQMN VQLAAKIQHLEFSCSEKPLD

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FIGURE 217

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCATGGCTTCCCTGGGG
CAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTTCTGGCTGGAGCAATTGCACTCATCATTGGCTTTGGT
ATTTCCAGGGAGACACTCCATCACAGTCACTACTGTGCGCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGC
TGCACTTTTGAACCTGACATCAAACCTTTCTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTC
CATGAGTTCAAAGAAGGCAAAGATGAGCTGTGCGAGCAGGATGAAATGTTGAGAGGCCGGACAGCAGTGTGCT
GATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGCTGGCACCTACAAATGT
TATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATAAACTGGAGCCTTCAGCATGCCGGAAGTG
AATGTGGACTATAATGCCAGCTCAGAGACCTTGCGGTGTGAGGCTCCCCGATGGTTCCCCCAGCCCACAGTGGTC
TGGGCATCCCAAGTTGACCAGGGAGCCAACCTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACCTCTGAGAAT
GTGACCATGAAGGTTGTGTCTGTGCTCTACAATGTTACGATCAACAACACATACTCCTGTATGATTGAAAAATGAC
ATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAGGCGGAGTCACCTACAGCTGCTAAAC
TCAAAGGCTTCTCTGTGTGTCTCTTCTTTTGGCCATCAGCTGGGCACCTTCTGCCTCTCAGCCCTTACCTGATG
CTAAAATAATGTGCCTTGGCCACAAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTACAGAACTATTTAC
CACCAGATATGACCTAGTTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAAACAAG
AGCAAGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAAAGACATATTA
GAAGTTGGGAAAATAATTGATGTGAAGTACAGCAAGTGTGTTAAGAGTGATAAGTAAATGCACGTGGAGACAAGT
GCATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTCACCTGGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTG
TCTCTGAATTTTTAGTTATATGTGCTGTAATGTTGCTCTGAGGAAGCCCCTGGAAAGTCTATCCCAACATATCCA
CATCTTATATTCACAAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAG
GGGCGGCTGCATTTTAGTAATGGGTCAAATGATTCACCTTTTTATGATGCTTCCAAAGGTGCCTTGGCTTCTCTTC
CCAACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAAACAGAGCAGTCGGGGACACCGATTT
TATAAATAAAGTGAAGACCTTCTTTTTTAAACAAA
AAAAAAA

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FIGURE 218

MASLGQILFWSIIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDIKLSDIVIQWLKEG
VLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRKKNVQLTDAGTYKCYIITSKGKGNANLEYKTGAF
SMPEVNVVDYNASSETLRCEAPRWFPQPTVVWASQVDQGANFSEVSNTSEFELNSENVTMKVSVLYNVTINNTYSC
MIENDIAKATGDIKVTESEIKRRSHLQLLNSKASLCVSSFFAISWALLPLSPYLMLK

FIGURE 219

[illegible]

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FIGURE 220

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLQEMKTLFLNTEYLMPFLLNQCGSILYYLTL
ASTDLTLAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGSRHTCVSSFPEPISPEWVRTRPFPILP
FPLQLFCFLVAIRVPFPWTVVRKTEAGVWD

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FIGURE 221

CTTCTGTAGGACAGTCACCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTGGAAGATGACAGCA
ATTATAGCAGGACCCTGCCAGGCTGTGCGAAAAGATTCCGCAATAAAACTTTGCCAGTGGGAAGTACCTAGTGAAA
CGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCTTGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTC
CAGCACCATGAAGGGCATCCTCGTTGCTGGTATCACTGCAGTGCTTGTGTCAGCTGTAGAATCTCTGAGCTGCGT
GCAGTGTAATTCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAGCTG
TATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGTTCTGCTCAGCGGAGAA
CTGCAGTGAGGAGACACACATTACAGCCTTCACTGTCCACGTGTCTGCTGAAGAACACTTTCATTTTGTAAAGCCA
GTGCTGCCAAGGAAAGGAATGCAGCAACACCAGCGATGCCCTGGACCCTCCCCTGAAGAACGTGTCCAGCAACGC
AGAGTGCCCTGCTTGTTATGAATCTAATGGAATTCTGTGCTGGGAAGCCCTGGAAATGCTATGAAGAAGAACA
GTGTGCTTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTTCCAACGT
CAGTAACGCCACCTGTCAGTTCCTGTCTGGTGAACAAGACTCTTGGAGGAGTCATCTTTCGAAAGTTTGAGTG
TGCAAATGTAAACAGCTTAACCCCCACGTCTGCACCAACCACTTCCACAACGTGGGCTCCAAAGCTTCCCTCTA
CCTCTTGGCCCTTGCCAGCCTCCTTCTTCGGGGACTGCTGCCCTGAGGTCTCTGGGGCTGCACTTTGCCCAGCACC
CCATTTCTGCTTCTCTGAGGTCCAGAGCACCCCTGCGGTGCTGACACCCTCTTCCCTGCTCTGCCCCGTTTAA
CTGCCCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTTGTTCTTCATTATTAAAGCACTGG
TTCATTCAC TGCCAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 222

MKGILVAGITAVLVAAVESLSCVQCNSWEKSCVNSIASECPSHANTSCISSSASSSSLETPVRLYQNMFCSAENCS
EETHITAFTVHVSAAEHFHFVSQCCQGKECSNTSDALDPPLKNVSSNAECPACYESNGTSCRGKPKWCYEEEQCV
FLVAELKNDIESKSLVLKGCSNVSNATCQFLSGENKTLGGVIFRKFEKANVNSLTPTSAPTTSNHNVGSKASLYLL
ALASLLLRGLLP

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FIGURE 223

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCAGGGCTTGCCTCAC
TGGCCACCCTCCCAACCCCAAGAGCCCAGCCCCATGGTCCCCGCCGCGCGCTGCTGTGGGTCCCTGCTGCTG
AATCTGGGTCCCCGGGCGGCGGGGGCCCAAGGCCTGACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGC
TTTGGGGGCCCCATGACCCGAGCTACCGGAGCACCGCCCGACTGGTCTTCCCCGGAAGACAAGGATAATCCTA
GAGGACGAGAATGATGCCATGGCCGACGCCGACCGCCTGGCTGGACCAGCGGCTGCCGAGCTCTTGGCCGCCACG
GTGTCCACCGGCTTTAGCCGGTCGTCCGCCATTAACGAGGAGGATGGGTCTTCAGAAGAGGGGGTTGTGATTAAT
GCCGGAAGGATAGCACCAGCAGAGAGCTTCCAGTGCGACTCCAATACAGCGGGGAGTTCCAGCACGAGGTTT
ATAGCCAATAGTCAGGAGCCTGAAATCAGGCTGACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGAC
CTGCCAGGCTCGCAGGCCACCCTGAGCCAGTGGTCCACACCTGGGTCTACCCGAGCCGGTGGCCGTCACCCCTCA
CCCACAGCCATGCCATCTCCTGAGGATCTGCGGCTGGTGCTGATGCCCTGGGGCCCGTGGCACTGCCACTGCAAG
TCGGGCACCATGAGCCGAGCCGGTCTGGGAAGCTGCACGGCCTTTCGGGGCGCCTTCGAGTTGGGGCGCTGAGC
CAGCTCCGCACGGAGCACAAAGCCTTGACCTATCAACAATGTCCCTGCAACCGACTTCGGGAAGAGTGCCCCCTG
GACACAAGTCTCTGTACTGACACCAACTGTGCCTCTCAGAGCACCACAGTACCAGGACCACCACTACCCCCCTC
CCCACCATCCACCTCAGAAGCAGTCCCAGCCTGCCACCCGCCAGCCCCCTGCCAGCCCTGGCTTTTGGAAACGG
GTCAGGATTGGCCTGGAGGATATTTGGAATAGCCTCTCTTCAGTGTTACAGAGATGCAACCAATAGACAGAAAC
CAGAGGTAATGGCCACTTCATCCACATGAGGAGATGTCAGTATCTCAACCTCTCTTGCCCTTTCATCCTAGCAC
CCACTAGATATTTTTAGTACAGAAAAACAAAACCTGAAAAACACAA

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FIGURE 224

MVPAAGALLWVLLNLGPRAAGAQGLTQTPTEMQRVSLRFGGPMTRSYRSTARTGLPRKTRIILEDENDAMADAD
RLAGPAAAEELLAATVSTGFSSAINEEDGSSEEGVVINAGKDSTSRELPSATPNTAGSSSTRFIANSQEPEIRL
TSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWPSPTAMPSPEDLRLVLMFWGPWHCHCKSGTMSRSRSGK
LHGLSGRLRVGALSQLRTEHKPCTYQQCPCNRLREECPLDTSLCDTNCASQSTTSTRTTTTPFPTIHLRSSPSL
PPASPCPALAFWKRVIRIGLEDIWNLSLVFTEMQFIDRNQR

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FIGURE 225

CCCGGGTCGACCCACGCGTCCGGGGAGAAAGGATGGCCGGCCTGGCGGGCGGGTTGGTCCTGCTAGCTGGGGCAG
CGGCGCTGGCGAGCGGCTCCCAGGGCGACCGTGAGCCGGTGTAACGCGACTGCGTACTGCAGTGCGAAGAGCAGA
ACTGCTCTGGGGGCGCTCTGAATCACTCCGCTCCGCGCAGCCAATCTACATGAGTCTAGCAGGCTGGACCTGTC
GGGACGACTGTAAGTATGAGTGTATGTGGGTCAACGTTGGGCTCTACCTCCAGGAAGGTCACAAAGTGCCTCAGT
TCCATGGCAAGTGGCCCTTCTCCCGGTTCTGTTCTTTCAAGAGCCGGCATCGGCCGTGGCCTCGTTTCTCAATG
GCCTGGCCAGCCTGGTGATGCTCTGCCGCTACCGCACCTTCGTGCCAGCCTCCTCCCCATGTACCACACCTGTG
TGGCCTTCGCCTGGGTGTCCCTCAATGCATGGTTCTGGTCCACAGTCTTCCACACCAGGGACACTGACCTCACAG
AGAAAATGGACTACTTCTGTGCCTCCACTGTCACTCACTCAATCTACCTGTGCTGCGTCAGGACCGTGGGGC
TGCAGCACCCAGCTGTGGTCAGTGCTTCCGGGCTCTCCTGCTGCTCATGCTGACCGTGCACGTCTCCTACCTGA
GCCTCATCCGCTTCGACTATGGCTACAACCTGGTGGCCAACGTGGCTATTGGCCTGGTCAACGTGGTGTGGTGGC
TGGCCTGGTGCCTGTGGAACAGCGGGCGGCTGCCTCACGTGCGCAAGTGGTGGTGGTCTTGTGCTGCAGG
GGCTGTCCCTGCTCGAGCTGCTTGACTTCCCACCGCTCTTCTGGGTCTGGATGCCCATGCCATCTGGCACATCA
GCACCATCCCTGTCCACGTCTCTTTTCAGCTTTCTGGAAGATGACAGCCTGTACCTGCTGAAGGAATCAGAGG
ACAAGTTCAAGCTGGACTGAAGACCTTGGAGCGAGTCTGCCCCAGTGGGGATCCTGCCCCCGCCCTGCTGGCCCTC
CCTTCTCCCCTCAACCTTGAGATGATTTTCTCTTTTCAACTTCTTGAACCTGGACATGAAGGATGTGGGCCAG
AATCATGTGGCCAGCCACCCCTGTTGGCCCTCACCAGCCTTGGAGTCTGTTCTAGGGAAGGCTCCACAGCATC
TGGGACTCGAGAGTGGGCAGCCCTCTACCTCCTGGAGCTGAACTGGGGTGGAACTGAGTGTGTTCTTAGCTCTA
CCGGGAGGACAGCTGCCTGTTTCTCCCCACCAGCCTCCTCCCCACATCCCCAGCTGCCTGGCTGGGTCTGAAG
CCCTCTGTCTACCTGGGAGACCAGGGACCACAGGCCTTAGGGATACAGGGGGTCCCCTTCTGTTACCACCCCCCA
CCCTCCTCCAGGACACCACTAGGTGGTGTGGATGCTTGTCTTTGGCCAGCCAAGGTTACGGCGATTCTCCCC
ATGGGATCTTGAGGGACCAAGCTGCTGGGATTGGGAAGGAGTTTACCCTGACCGTTGCCCTAGCCAGGTTCCCA
GGAGGCCTCACCATACTCCCTTTCAGGGCCAGGGCTCCAGCAAGCCCAGGGCAAGGATCCTGTGCTGCTGTCTGG
TTGAGAGCCTGCCACCGTGTGTGCGGAGTGTGGGCCAGGCTGAGTGCATAGGTGACAGGGCCGTGAGCATGGGCC
TGGGTGTGTGTGAGCTCAGGCCTAGGTGCGCAGTGTGGAGACGGGTGTGTGCGGGGAAGAGGTGTGGCTTCAAAG
TGTGTGTGTGCAGGGGGTGGGTGTGTTAGCGTGGGTAGGGGAACGTGTGTGCGCGTGTGGTGGGCATGTGAGA
TGAGTGACTGCCGGTGAATGTGTCCACAGTTGAGAGGTTGGAGCAGGATGAGGGAATCCTGTCAACATCAATAAT
CACTTGTGGAGCGCCAGCTCTGCCAAGACGCCACCTGGGCGGACAGCCAGGAGCTCTCCATGGCCAGGCTGCCT
GTGTGCATGTTCCCTGTCTGGTGCCCTTTGCCCGCCTCTGCAAACCTCACAGGGTCCCCACACAACAGTGCCC
TCCAGAAGCAGCCCCCTCGGAGGCAGAGGAAGGAAATGGGGATGGCTGGGGCTCTCTCCATCCTCCTTTTCTCCT
TGCCTTCGCATGGCTGGCCTTCCCCTCCAAAACCTCCATTCCCCTGCTGCCAGCCCCCTTGGCCATAGCCTGATTT
TGGGGAGGAGGAAGGGGCGATTTGAGGGAGAAGGGGAGAAAGCTTATGGCTGGGTCTGGTTTCTTCCCTTCCCAG
AGGGTCTTACTGTTCCAGGGTGGCCCCAGGGCAGGCAGGGGCCACACTATGCCTGTGCCCTGGTAAAGGTGACCC
CTGCCATTTACCAGCAGCCCTGGCATGTTCTGCCCCACAGGAATAGAATGGAGGGAGCTCCAGAACTTTCCAT
CCCAAAGGCAGTCTCCGTGGTTGAAGCAGACTGGATTTTTGCTCTGCCCTGACCCCTTGTCCCTCTTTGAGGGA
GGGGAGCTATGCTAGGACTCCAACCTCAGGGACTCGGGTGGCCTGCGCTAGCTTCTTTTGATACTGAAAACCTTTT
AAGGTGGGAGGGTGGCAAGGGATGTGCTTAATAAATCAATTCCAAGCCTCAAAAAAAAAAAAAAAAAA

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FIGURE 226

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGWTCRDDCKYECMWV
TVGLYLQEGHKVPQFHGKWPFSRFLFFQEPASAVASFNLGLASLVMLCRYRTFVPASSPMYHTCVAFAWVSLNAW
FWSTVFHTRDLDLTKMDYFCASTVILHSIYLCCVRTVGLQHAPVVSAFRALLLMLTVHVSYSLSLIRFDYGYNL
VANVAIGLVNVVWVWLAWCLWNQRRLPVVRKCVVVVLLQLGLSLELLDFFPLFWVLDAAHAIWHISTIPVHVLFSS
FLEDDSLYLLKESEDKFKLD

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

FIGURE 227

TTCCGGCTTCCGTAGAGGAAGTGGCGCGGACCTTCAATTGGGGGTTTCGGTTCCCCCCTTCCCCTTCCCCGGGGTTC
TGGGGGTGACATTGCACCGCGCCCCCTCGTGGGGTGCAGTTGCCACCCACGCGGACTCCCAGCTGGCGCGCCCC
TCCCATTGCTGTCTTGGTCAGGCCCCACCCCCCTTCCACCTGACCAGCCATGGGGGCTGCGGTGTTTTTTCG
GCTGCACTTTTCTGCGCTTCGGCCCGGCTTTCGCGCTTTTCTTGATCATCTGGCTGGGGACCCCGCTTCGCGTTA
TCATCCTGGTTCGACGGGGCATTTTTCTGGCTGGTCTCCCTGCTCTGGCTCTGTGGTCTGTGTTCACTTGGTCC
ATGTGACCCAGCGTCAGATGCCGGCTCCAGTACGCGCTCCTGATTTTTGGTGCTGCTGTCTGTCTCTTCTAC
AGGAGTGTTCCGCTTTGGCTACTACAAGCTGCTTAAGAAGGCAGATGAAGGGTTAGCATCGCTGAGTGAGGACG
GAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTGGTCTCTCCTTCCGTATCATCAGTGGTGTCTTCT
CTGTTATCAATATTTTGGCTGATGCATTGGGCCAGGTGTGGTGGGATCCATGGAGACTCACCTATTACTTCC
TGACTTCAGCCTTTCTGACAGCAGCCATTATCCTGCTCCATACCTTTTGGGAGTTGTGTTCTTGATGCTGTG
AGAGGAGACGGTACTGGGCTTTGGGCTGTGGTGGGAGTCACTACTGACATCGGAGACTGACATCTCTGAACC
CCTGGTATGAGGCCAGCCTGCTGCCATCTATGTCAGTCACTGTTTCCATGGGGCTCTGGGCTTCATCACAGCTG
CAGGGTCCCTCCGAAGTATTAGCGCAGCCTCTTGTTGAAGGACTGACTACCTGGACTGATCGCTGACAGATCC
CACCTGCCCTGTCCACTGCCCATGACTGAGCCCAGCCCCAGCCGGTCCATTGCCACATTCTCTGTCTCCTTCT
CGTCGGTCTACCCCACTACCTCCAGGGTTTTGCTTTGTCTTTTGTGACCGTTAGTCTCTAAGCTTTACCCAGGAG
CAGCTTGGGTTCCAGCCAGTCAGTGACTGGTGGGTTTGAATCTGCATTTATCCCCACCACCTGGGGACCTCCTGT
TGTGTCAGGACTCCCCCTGTGTGTCAGTGCTCTGCTCACCTGCCAAGACTCACCTCCCTTCCCCTCTGCAGG
CCGACGGCAGGAGGACAGTCGGGTGATGGTGTATTCTGCCCTGCGCATCCCACCCGAGGACTGAGGGAACCTAGG
GGGGACCCCTGGGCTGGGGTGCCTCCTGATGTCTCGCCCTGTATTTCTCCATCTCCAGTTCTGGACAGTGCA
GGTTGCCAAGAAAAGGGACCTAGTTTAGCCATTGCCCTGGAGATGAATTAATGGAGGCTCAAGGATAGATGAGC
TCTGAGTTTCTCAGTACTCCCTCAAGACTGGACATCTTGCTTTTCTCAGGCTGAGGGGAACCATTTTGG
TGTGATAAATACCTTAACCTGCCTTTTTTCTTTTGGAGTGGGGGAGGGAGGATATATTGGAACCTCTCT
AACCTCCTTGGGCTATATTTTCTCTCCTCGAGTTGCTCCTCATGGCTGGGCTCATTTCCGGTCCCTTTCTCCTTGG
TCCCAGACCTTGGGGGAAAGGAAGGAAGTGCATGTTTGGGAACTGGCATTACTGGAATAATGGTTTTAACCCTCC
TTAACCACCAGCATCCCTCCTCTCCCAAGGTGAAGTGGAGGGTGTGTGGTGAGCTGGCCACTCCAGAGCTGCA
GTGCCACTGGAGGAGTCAGACTACCATGACATCGTAGGGAAGGAGGGGAGATTTTTTGTAGTTTTTAATTTGGG
TGTGGGAGGGGCGGGGAGGTTTTCTATAAACTGTATCATTTTCTGTGAGGGTGGAGTGTCCCATCCTTTTAAATC
AAGGTGATTTGTGATTTTACTAATAAAAAAGAAATTTGTAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA
AAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA

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FIGURE 228

MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIIILVAGAFFWLVSILLASVVWFILVHVTDRSDARLQYGLLIFG
AAVSVLLQEVFRFAYYKLLKKADEGLASLSEGRSPISIRQMAYVSGLSFGIISGVFSVINILADALGPGVVGIH
GDSPYYFLTSAFLTAAIILLHTFWGVVFFDACERRRYWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMG
LWAFITAGGSLRSIQRSLLCKD

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FIGURE 229

CGGGAGGCTGGGTGCTCATGATCCGGACCCATTGTGCGGCTCTGCCCATCGCCTGCTCCTCCCAGGCTCCCGCG
GCCGACCCCCGCGCAAC**ATG**CAGCCACGGGCCGCGAGGGTTCCCGCGCGCTCAGCCGGCGGTATCTGCGGCGTC
TGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCAGCCCGTAACCCGCGCGGAGACCACGCCGGCGCCCCAGAG
CCCTCTCCACGCTGGGCTCCCCAGCCTCTTACCACGCCGGGTGTCCCAGCGCCCTCACTACCCAGGCCTCA
CTACGCCAGGCACCCCCAAAACCCTGGACCTTCGGGGTCGCGCGCAGGCCCTGATGCGGAGTTTCCCACTCGTGG
ACGGCCACAATGACCTGCCCCAGGTCCTGAGACAGCGTTACAAGAATGTGCTTCAGGATGTTAACCTGCGAAATT
TCAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGTGGGTGCCAGTTCTGGTCAGCCTCCGTCT
CATGCCAGTCCCAGGACCAGACTGCCGTGCGCCTCGCCCTGGAGCAGATTGACCTCATTACCCGCATGTGTGCCT
CCTACTCTGAACTCGAGCTTGTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAAGCTGGCCTGCCTCATTGGCG
TGNAGGGTGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGGTGCGCTACCTGA
CACTTACCTTCACCTGCAGTACACCATGGGCAGAGAGTTCCACCAAGTTCAGACACCACATGTACACCAACGTCA
GCGGATTGACAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAACCGCCTGGGCATGATGATAGATTTGTCTTATG
CATCGGACACCTTGATAAGAAGGGTCCTGGAAGTGTCTCAGGCTCCTGTGATCTTCTCCCACTCAGCTGCCAGAG
CTGTGTGTGACAATTTGTTGAATGTTCCCGATGATATCCTGCAGCTTCTGAAGAACGGTGGCATCGTGATGGTGA
CACTGTCCATGGGGGTGCTGCAGTGCAACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTGACCACATCA
GGGCAGTCATTGGATCTGAGTTCATCGGCATTGGTGGAATTATGACGGGACTGGCCGGTTCCCTCAGGGGCTGG
AGGATGTGTCCACATACCCAGTCCTGATAGAGGAGTTGCTGAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTG
TCCTTCGTGGAACCTGCTGCGGGTCTTCAGACAAGTGGAAGAGGTGAGAGAGGAGAGCAGGGCGCAGAGCCCCG
TGGAGGCTGAGTTTCCATATGGGCAACTGAGCACATCCTGCCACTCCACCTCGTGCCTCAGAATGGACACCAGG
CTACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCCTGGAGGTCTCAAATGCCTCCCCATACCTTG
TTCCAGGCCTTGTGGCTGCTGCCACCATCCCAACCTTCACCCAGTGGCTCTGCT**TGA**CACAGTCGGTCCCCGCAGA
GGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCTCCTAGTTCATTACAAAGCATATGCTGAGAATAAACATGTTA
CACATGGAAAA

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FIGURE 230

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817
><subunit 1 of 1, 487 aa, 1 stop, 2 unknown
><MW: 53569.32, pI: 7.68, NX(S/T): 5
MQPTGREGSRALSRRYLRRLLLLLLLLLLLLLRQPVTRAETTPGAPRALSTLGSPSLFTTPGVPSALTTPGLTTPGTP
KTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSGQTSLDRLRDGLVGAQFWSASVSCQSQD
QTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSSQKLACLIGVXGGHSLDSSLSVLRSFYVLGVRYLTLTFTC
STPWAESSTKFRHHMYTNVSGLTSGFEKVVEELNRLGMMIDLSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNL
LNVPPDILQLLKNGGIVMVTLSMGVLQCNNLANVSTVADHFDHIRAVIGSEFIGIGGNYDGTGRFPQGLEDVSTY
PVLIEELLSRXWSEELQGVLRGNLLRVFRQVEKVREESRAQSPVEAEFPYQQLSTSCHSHLVPQNGHQATHLEV
TKQPTNRVPWRSSNASPYLVPGLVAAATIPTFTQWLC
```

Important features of the protein:**Signal peptide:**

amino acids 1-36

Transmembrane domain:

amino acids 313-331

N-glycosylation sites.

amino acids 119-122, 184-187, 243-246 and 333-336

N-myristoylation sites.

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 136-146

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FIGURE 231

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGATTGGCAAGCGCTGG
CCACCTCCCCACACCCCTTGCGAACGCTCCCCTAGTGGAGAAAAGGAGTAGCTATTAGCCAATTTCGGCAGGGCCC
GCTTTTTAGAAAGCTTGATTTCCTTTGAAGATGAAAGACTAGCGGAAGCTCTGCCTCTTTCCCCAGTGGGCGAGGG
AACTCGGGGCGATTGGCTGGGAACTGTATCCACCCAAATGTCACCGATTCTTCCTATGCAGGAAATGAGCAGAC
CCATCAATAAGAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACCTGGAGGCAAAGAGG
GTTGCTCAACGCCCCGCTCATTGGAAAACCAAATCAGATCTGGGACCTATATAGCGTGGCGGAGGCGGGGCGAT
GATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTTCTTTCCCCGCCCCCTGAGACCCTGCAGACCA
TCTGTCAATGGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGCTCCCG
GCCGCCCGCGTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCTGTGGCGGAAAGCGGCCC
CCAGAACCGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAAACCTGTATGAGAAGAACCCAGACTCC
CATGGTTATGACAAGGACCCCGTTTGGACGTCTGGAACATGCGACTTGTCTTCTTCTTTGGCGTCTCCATCATC
CTGGTCCTTGGCAGCACCTTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCGAAGCTGAG
AGGCTTGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAACCTGCTTCGACCCACGCAAGATCCAG
CTGCCAGAGGATGAGTGAACAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCTGCCTGCCATTCT
TGACCTCTTCTCAGAGCACCTAATTAAAGGGGCTGAAAGTCTGAA

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FIGURE 232

MAAGLFGLSARLLAAAATRGLPAARVRWESSFSRTVVAPSAVAGKRPPEFTTPWQEDPEPEDENLYEKNPDSHG
YKDPVLDVWNMLVFFFGVSIILVLGSTFVAYLPDYRMKEWSRREAERLVKYREANGLPIMESNCFDPSKIQLPEDE

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FIGURE 233

GCGGGGGCTATGCCGCTTGCTCTGCTCGTCCTGTTGCTCCTGGGGCCCGCGGGCTGGTGCCTTGACAGAACCCCCA
CGCGACAGCCTGCGGGAGGAACTTGTATCACCCTCGCTGCCTTCCGGGGACGTAGCCGCCACATTCAGTTCCGC
ACGCGCTGGGATTTCGGAGCTTCAGCGGGAAGGAGTGTCCCATTCAGGCTCTTTCCCAAAGCCCTGGGGCAGCTG
ATCTCCAAGTATTCTCTACGGGAGCTGCACCTGTCTTACACAAAGGCTTTGGAGGACCCGATACTGGGGGCCA
CCCTTCTGTCAGGCCCCATCAGGTGCAGAGCTGTGGGTCTGGTTCCAAGACACTGTCACTGATGTGGATAAATCT
TGAAGGAGCTCAGTAATGTCTCTCAGGGATCTTCTGCGCCTCTCTCAACTTCATCGACTCCACCAACACAGTC
ACTCCCACTGCCTCCTTCAAACCCCTGGGTCTGGCCAATGACACTGACCACTACTTTCTGCGCTATGCTGTGCTG
CCGCGGGAGGTGGTCTGCACCGAAAACCTCACCCCTGGAAGAAGCTCTTGCCCTGTAGTTCCAAGGCAGGCCTC
TCTGTGCTGCTGAAGGCAGATCGCTTGTCCACACCAGCTACCCTCCAGGCAGTGCATATCCGCCCTGTTTGC
AGAAATGCACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCCTGTCAGTTGTATTTGATGCCTTCATCAG
GGGCAGGGAAGAAAGACTGGTCCCTCTCCGGATGTTCTCCGAACCTCACGGAGCCCTGCCCCCTGGCTTCA
GAGAGCCGAGTCTATGTGGACATCACCACTACAACCAGGACAACGAGACATTAGAGGTGCACCCACCCCGACC
ACTACATATCAGGACGTCTCCTAGGCACTCGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCCATGATC
AACAACCTCTCGAAACCTCAACATCCAGCTCAAGTGGAAGAGACCCCCAGAGAATGAGGCCCCCCCAGTGCCCTTC
CTGCATGCCCAGCGGTACGTGAGTGGCTATGGGCTGCAGAAGGGGGAGCTGAGCACACTGCTGTACAACACCCAC
CCATACCGGGCCTTCCCGGTGCTGCTGCTGGACACCGTACCCTGGTATCTGCGGCTGTATGTGCACACCCCTCACC
ATCACCTCCAAGGGCAAGGAGAACAACCAAGTTACATCCACTACCAGCCTGCCAGGACCGGCTGCAACCCAC
CTCCTGGAGATGCTGATTAGCTGCCGCCAACTCAGTCACCAAGGTTTCCATCCAGTTTGAGCGGGCGTGCTG
AAGTGGACCGAGTACACGCCAGATCCTAACCATGGCTTCTATGTGAGCCCATCTGTCTCAGCGCCCTTGTGCCC
AGCATGGTAGCAGCCAAGCCAGTGGACTGGGAAGAGAGTCCCCTCTCAACAGCCTGTTCCAGTCTCTGATGGC
TCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCCGACACCGGACTTCAGCATGCCCTAC
AACGTGATCTGCCTCACGTGCACTGTGGTGGCCGTGTGCTACGGCTCCTTCTACAATCTCCTCACCCGAACCTTC
CACATCGAGGAGCCCCGCACAGGTGGCCTGGCCAAGCGGCTGGCCAACCTTATCCGGCGCGCCGAGGTGTCCCC
CCACTCTGATTCTTGGCCCTTTCAGCAGCTGCAGCTGCCGTTTCTCTGCGGGAGGGGAGCCCAAGGGCTGTTTC
TGCCACTTGCTCTCCTCAGAGTTGGCTTTTGAACCAAAGTGCCCTGGACCAGGTGAGGGCTACAGCTGTGTTGT
CCAGTACAGGAGCCACGAGCCAAATGTGGCATTGTGAATTTGAATTAACCTAGAAATTCATTTCTCACCTGTAGT
GGCCACCTCTATATTGAGGTGCTCAATAAGCAAAAGTGGTGGTGGCTGTATTGGACAGCACAGAAAAAGAT
TTCCATCACCACAGAAAGGTGCGCTGGCAGCACTGGCCAAGGTGATGGGGTGTGCTACACAGTGTATGTCACTGT
GTAGTGGATGGAGTTTACTGTTGTGGAATAAAAACGGCTGTTTCCGTGGAAAAA

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FIGURE 234

MPLALLVLLLLGPGGWCLAEPPRDSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHYRLFPPKALGQLISK
YSLRELHLSFTQGFWRTRYWGPPFLQAPSGAELWVWFQDTVTDVDSWKELSNVLSGIFCASLNFIDSTNTVTPT
ASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWKLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCRNA
RCTSISWELRQTL SVVFDAFITGQKKDWSLFRMFSRTLTEPCPLASESRVYVDITTYNQDNETLEVHPPPTTTY
QDVILGTRKTYAIYDLLDTAMINNSRNLNIQLKWKRPENEAPPVPFLHAQRYVSGYGLQKGE LSTLLYNTHPYR
AFPVLLLDTPWYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANSVTKVSIQFERALLKWT
EYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLFPVSDGSNYFVRLYTEPLL VNLPTPDFSMPYNVI
CLTCTVVAVCYGSFYNLLTRTFHIEEPRTGGLAKRLANLIRRARGVPPL

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FIGURE 235

TGACGTCAGAATCACCATGGCCAGCTATCCTTACCGGCAGGGCTGCCAGGAGCTGCAGGACAAGCACCAGGAGC
CCCTCCGGGTAGCTACTACCCTGGACCCCCAATAGTGGAGGGCAGTATGGTAGTGGGCTACCCCTGGTGGTGG
TTATGGGGGTCTGCCCCGAGGGCCTTATGGACCACCAGCTGGTGGAGGGCCCTATGGACACCCCAATCCTGG
GATGTTCCCTCTGGAACTCCAGGAGGACCATATGGCGGTGCAGCTCCCGGGGGCCCCCTATGGTCAGCCACCTCC
AAGTTCCTACGGTGCCCAGCAGCCTGGGCTTTATGGACAGGGTGGCGCCCCCTCCCAATGTGGATCCTGAGGCCTA
CTCCTGGTTCCAGTCGGTGGACTCAGATCACAGTGGCTATATCTCCATGAAGGAGCTAAAGCAGGCCCTGGTCAA
CTGCAATTGGTCTTCATTCAATGATGAGACCTGCCTCATGATGATAAACATGTTTGACAAGACCAAGTCAGGCCG
CATCGATGTCTACGGCTTCTCAGCCCTGTGGAAATTCATCCAGCAGTGGGAAGAACCTCTCCAGCAGTATGACCG
GGACCGCTCGGGCTCCATTAGCTACACAGAGCTGCAGCAAGCTCTGTCCCAATGGGCTACAACCTGAGCCCCA
GTTACCCAGCTTCTGGTCTCCCGCTACTGCCACGCTCTGCCAATCCTGCCATGCAGCTTGACCGCTTCATCCA
GGTGTGCACCCAGCTGCAGGTGCTGACAGAGGCCCTCCGGGAGAAGGACACAGCTGTACAAGGCAACATCCGGCT
CAGCTTCGAGGACTTCGTCACCATGACAGCTTCTCGGATGCTATGACCCCAACCATCTGTGGAGAGTGGAGTGCAC
CAGGGACCTTTCTGGCTTCTTAGAGTGAGAGAAGTATGTGGACATCTCTTCTTTCTGTCCCTCTAGAAGAAC
ATTCTCCCTTGCTTGATGCAACACTGTTCCAAAAGAGGGTGGAGAGTCCTGCATCATAGCCACCAATAGTGAGG
ACCGGGGCTGAGGCCACACAGATAGGGGCTGATGGAGGAGAGGATAGAAGTTGAATGTCCTGATGGCCATGAGC
AGTTGAGTGGCACAGCCTGGCACAGGAGCAGGTCCTTGTAAATGGAGTTAGTGTCCAGTCAGCTGAGCTCCACCC
TGATGCCAGTGGTGAGTGTTTCATCGGCCTGTTACCGTTAGTACCTGTGTTCCCTCACCAGGCCATCCTGTCAAAC
GAGCCCATTTTCTCCAAAGTGGAACTCTGACCAAGCATGAGAGAGATCTGTCTATGGGACCAGTGGCTTGGATTCT
GCCACACCCATAAATCCTTGTGTGTTAACTTCTAGCTGCCTGGGGCTGGCCCTGCTCAGACAAATCTGCTCCCTG
GGCATCTTTGGCCAGGCTTCTGCCCCCTGCAGCTGGGACCCCTCACTTGCTGCCATGCTCTGCTCGGCTTCAGT
CTCCAGGAGACAGTGGTCACCTCTCCCTGCCAATACTTTTTTAAATTTGCATTTTTTTTCATTTGGGGCCAAAAG
TCCAGTGAAATTGTAAGCTTCAATAAAAGGATGAAACTCTGA

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FIGURE 236

MASYPYRQGCPGAAGQAPGAPPGSYYPGPPNSGGQYGSGLPPGGGYGGPAPGGPYGPPAGGGPYGHPNPGMFPSG
TPGGPYGGAAPGGPYGQPPSSYGAQQPGLYGQGGAPPNVDPEAYSWFQSVDSHSGYISMKELKQALVNCNWSS
FNDETCLMMINMFDKTKSGRIDVYGFSA LWKFIQWKNLFQQYDRDRSGSISYTELQQALSQMGYNLSPQFTQLL
VSRYCPRSANPAMQLDRFIQVCTQLQVLTEAFREKDTAVQGNIRLSFEDFVTMTASRML

Important features of the protein:**Signal peptide:**

amino acids 1-19

N-glycosylation site.

amino acids 147-150

Casein kinase II phosphorylation sites.

amino acids 135-138, 150-153, 202-205, 271-274

N-myristoylation sites.

amino acids 9-14, 15-20, 19-24, 33-38, 34-39, 39-44, 43-48, 61-66, 70-75, 78-83, 83-88, 87-92, 110-115

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FIGURE 238

MQGRVAGSCAPLGLLLVCLHLPGLFARSIGVVEEKVSQNFGTNLPQLGQPSTGSPNSEHPQPALDPRSNDLARV
PLKLSVPPSDGFPFAGGSAVQRWPPSWGLPAMDSWPPEDPWQMMAAAAEEDRLGEALPEELSYLSSAAALAPGSGP
LPGESSPDATGLSPEASLLHQDSESRRLPRSNSLGAGGKILSQRPWSLIHRVLPDHPWGTLPNPSVSWGGGGPGT
GWGTRPMPHPEGIWGINNQPPGTSGWGNINRYPGGSWGNNINRYPGGSWGNNINRYPGGSWGNIHLYPGINNPFPFPGV
LRPPGSSWNIPAGFPNPPSPRLQWG

Important features of the protein:**Signal peptide:**

amino acids 1-26

Casein kinase II phosphorylation sites.

amino acids 56-59, 155-158

N-myristoylation sites.

amino acids 48-53, 220-225, 221-226, 224-229, 247-252, 258-263, 259-264, 269-274, 270-275, 280-285, 281-286, 305-310

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FIGURE 239

GGGCGTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCGCTGTGCCTGCTGTGCCGCGCTGTGCGCG
CTGCTACCGCGTCTGCTGGACGCGGGAGACGCCAGCGAGCTGGTGATTGGAGCCCTGCCGAGAGCTCAAGCGCCC
AGCTCTGCCCCAGGAGCCCAGGCTGCCCCGTGAGTCCCATAGTTGCTGCAGGAGTGGAGCCATGAGCTGCGTCTCT
GGGTGGTGTATCCCCCTTGGGGCTGCTGTTCTTGGTCTGCGGATCCCAAGGCTACCTCCTGCCCAACGTCACTCT
CTTAGAGGAGCTGCTCAGCAAATACCAGCACAAACGAGTCTCACTCCCGGGTCCGAGAGCCATCCCCAGGGAGGA
CAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCTCCAACATGGAGTACAT
GGTGAGCGCCGGCTCCGGCCGAGAGGCTGGCACCGGGGTGGGGCCTGGGCCACCAGCCTGCTCTGTTCCCCAG
CCAGCTCTGTTCCCCAGCCAGTGCCTGTGATGGCTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCCGGCTCTG
TTCTGTTTTGTTTGTGTTGTTTTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGCACAATCGTCA
TGCCCTGAAACCTTAGACTCCCGGGGTAAAGCGATCCTGCTTCAGCCTCCCAAGTAGCTGGAACACAGGCATGC
ACCATGGTGCCAGCTAGATTTTAAATATTTTGTGGAGATGGGGGTCTTGCTACGTTGCCAGGCTGGTCTTGAA
CTCCTAGGCTCAAGCAATCCTCCTGCCTCAGCCTCTCAAAGTGCTAGGATTATAGGCATGAGTCAACCTGTCTGG
CTCTGGCTCTGTTCTTAACATTCTGCCAAAACAACACAGTGGGTTCCTGTGCAGAGCCTGCCTCGTTGCCTTC
ATGTCACTCTTGGTAGCTCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGGAGGGGGCC
AGGGCTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCACCCTGACTTCTCCTTAGCCCC
TGTGAGCCTCACTTTCCACTTGGAGAGTCCTTCCTCGGTGGTTGCCATGACTGTGAGATAAGTCGAGGCTGTGA
AGGGCCCGGCACAGACTGACCTGCCTCCCCAACCCCTAGGCTTTGCTAACCGGGAAGGAGCTAACGGTGACAGA
AGACAGCCAAGGTCAACCCTCCCGGGTGATTGTGATGGGTGTTCCAGGTGTGGTTGGGCGATGCTGCTACTTGAC
CCCAAGCTCCAGTGTGGAACTTCCTTCCTGGCTGGTTTTCCAGAACTACAGAGGAATGGACCACAGTCTTCCAG
GGTCCCTCCTCGTCCACCAACCGGGAGCCTCCACCTTGGCCATCCGTCAGCTATGAATGGCTTTTTTAAACAAACC
CACGTCCCAGCCTGGGTAACATGGTAAAGCCCCGTCTCTACAAAAAATCCAAGTTAGCCGGGCATGGTGGTGCG
CACCTGTAGTCCCAGCTGCAGTGGGACTGAGGTGGAGGTGGAGGTGGGGGTGGGAGCTGAGGAAGGAGGATCGC
TTGAGCCTGGGAAGTCGAGGCTGCAGTGAGCTGAGATTGCACCACTGCACTCCAGCCTGGGTGACAGAGCAAGAC
CCTGTCTCAAAAA

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FIGURE 240

MSCVLGGVIPLGLLFLVCGSQGYLLPNVTLLLEELLSKYQHNEHSRVRRAIPREDKEEILMLHNKLRGQVQPQAS
NMEYMVSAAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGWLRVSSGRGGSRLCSVLFVCFETGSHSATDAGVQ
WHNRHALKP

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

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FIGURE 241

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACTATGGGGTCTGGGCTGCCC
CTTGTCCTCCTCTTGACCCCTCCTTGGCAGCTCACATGGAACAGGGCCGGGTATGACTTTGCAACTGAAGCTGAAG
GAGTCTTTTCTGACAAATTCCTCCTATGAGTCCAGCTTCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCAT
CTCCCTTCAGGGACCAGCGTCACCCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACATTGACAGCCA
TTGAAGCCTGTGTCCTTCTTGGCCCGGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTTCAG
CAGGCCCCCACCTCCTGAGTGGCAATAAATAAAATTCGGTATGCTG

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FIGURE 242

MSGGLPLVLLLTLLGSSHGTGPGMTLQLKLKESFLTNSSESSFLELLEKLCLLLHLPSGTSVTLHHARSQHHVCNT

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FIGURE 243

GGCAAGTGGAACCACTGGCTTGGTGGATTTTGCTAGATTTTCTGATTTTAACTCCTGAAAAATATCCCAGAT
AACTGTCATGAAGCTGGTAACTATCTTCCTGCTGGTGACCATCAGCCTTTGTAGTTACTCTGCTACTGCCTTCCT
CATCAACAAAGTGCCCTTCCTGTTGACAAGTTGGCACCTTTACCTCTGGACAACATTCTTCCCTTATGGATCC
ATTAAAGCTTCTTCTGAAAACCTCTGGGCATTTCTGTTGAGCACCTTGTGGAGGGGCTAAGGAAGTGTGTAATGA
GCTGGGACCAGAGGCTTCTGAAGCTGTGAAGAACTGCTGGAGGCGCTATCACACTTGGTGTGACATCAAGATAA
AGAGCGGAGGTGGATGGGGATGGAAGATGATGCTCCTATCCTCCCTGCCTGAAACCTGTTCTACCAATTATAGAT
CAAATGCCCTAAAATGTAGTGACCCGTGAAAAGGACAAATAAAGCAATGAATACATTA

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FIGURE 244

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59855  
<subunit 1 of 1, 93 aa, 1 stop  
<MW: 10161, pI: 7.39, NX(S/T): 0  
MKLVTFLLVTISLCSYSATAFLINKVPLPVDKLAPLPDNLFPMDPLKLLKTLGISV  
EHLVEGLRKCVNELGPEASEAVKKLLEALSHLV
```

Important features:**Signal peptide:**

Amino acids 1-18

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FIGURE 245

TGCTAGGCTCTGTCCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGATCCCTCTATGACT
GCAATGTGAGGTGTCCGGCTTTGCTGGCCAGCAAGCCTGATAAGCATGAAGCTCTTATCTTTGGTGGCTGTGGT
CGGGTGTGTGCTGGTGGCCAGCTGAAGCCAACAAGAGTTCTGAAGATATCCGGTGCAAATGCATCTGTCCACC
TTATAGAAACATCAGTGGGCACATTTACAACCAGAATGTATCCAGAAAGGACTGCAACTGCCTGCACGTGGTGGA
GCCCATGCCAGTGCCTGGCCATGACGTGGAGGCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAGCAC
CACCACCATCAAGGTCATCATTGTCATCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCTACATGGCCTTCCTGAT
GCTGGTGGACCCTCTGATCCGAAAGCCGGATGCATACACTGAGCAACTGCACAATGAGGAGGAGAATGAGGATGC
TCGCTCTATGGCAGCAGCTGCTGCATCCCTCGGGGGACCCCGAGCAAACACAGTCCTGGAGCGTGTGGAAGGTGC
CCAGCAGCGGTGGAAGCTGCAGGTGCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGCTAGAT
GGGCTGGTGTGGTTGGGTCAAGGCCCCAACACCATGGCTGCCAGCTTCCAGGCTGGACAAAGCAGGGGGCTACTT
CTCCCTTCCCTCGGTTCCAGTCTTCCCTTTAAAAGCCTGTGGCATTTTTCCTCCTTCTCCCTAACTTTAGAAATG
TTGTACTTGGCTATTTTGTATTAGGGAAGAGGGATGTGGTCTCTGATCTCTGTTGTCTTCTTGGGTCTTTGGGGTT
GAAGGGAGGGGGAAGGCAGGCCAGAAGGGAATGGAGACATTGAGGCGGCCTCAGGAGTGGATGCGATCTGTCTC
TCCTGGCTCCACTCTTGCCGCCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCCCTTGAAGATAAAGCTGGGTC
TTCAGGAACCTCAGTGTCTGGGAGGAAAGCATGGCCCAGCATTGAGCATGTGTTCCCTTCTGCAGTGGTTCCTATC
ACCACCTCCCTCCAGCCCCGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTGAGGACAGCTCTGATGGGAGAGC
TGGGCCCCCTGAGCCCACTGGGTCTTCAGGGTGCACTGGAAGCTGGTGTTCGCTGTCCCCTGTGCACTTCTCGCA
CTGGGGCATGGAGTGCCCATGCATACTCTGCTGCCGGTCCCCTCACCTGCACTTGAGGGGTCTGGGCAGTCCCTC
CTCTCCCCAGTGTCCACAGTCACTGAGCCAGACGGTCGGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGA
ACACCACAGCCCCTGTACTTGGGTTCCTCTTGTCCCTGAACCTTCGTTGTACCACTGCATGGAGAGAAAATTTTG
TCCTCTTGTCTTAGAGTTGTGTGTAAATCAAGGAAGCCATCATTAATTTGTTTTATTTCTCTCA

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FIGURE 246

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278
<subunit 1 of 1, 183 aa, 1 stop
<MW: 20574, pI: 6.60, NX(S/T): 3
MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEPMPVPGHDVEAYCLI
CECRYEERSTTTIKVIIIVYLSVVGALLLYMAFLMLVDPLIRKPDAYTEQLHNEEENEDARSMAAAAASLGGPRA
NTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS
```

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 90-112

N-glycosylation sites.

amino acids 21-24, 38-41 and 47-50

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FIGURE 247

AATTGTATCTGTGTAATGTTAAAACAAACGAAATAAAATAGAAGGAAAACTTTCTGAGTTTCAAAAACAACAGA
CTAGTACTCTAAAGAACTCTTTAAAACAATTAAGTGTAGGATTGCAGTTATGATTGGATATTATTTAATTCTGT
TTCTGATGTGGGGTTCCCTCCACTGTGTTCTGTGTGCTATTAATATTTACCATTGCAGAAGCTTCATTCAGTGTG
AAAATGAATGCTTAGTGGATCTGTGCCTCTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAG
TTCCCTCCCTCCGATTGTTCTAAATTAATTGAAAGATGTCTGCTGTGGAAAAAGGCATGTATTTAAATCTGTAT
GATTCTCAACCATCTTTAGTTGGGAAAGGTCCTTGAAAGCCAATGGAAATACTTTTTTTTTTTCTTGGCACTAAT
CAAGTGAGTGTTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTAGTAAAATAGAAACCTGTGTTTATTCTCAG
GTATTTTAGAAACAACAGCCATCATTTTATTTTATGTGTGTGTTCTTGGCTGTATTCAATAATTATATATTTGG
GCTATCAAATATTACTTCATTCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTTCTAGTTGCA
TTTTCTCAGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTACAGTACTGTCTCTCTACTATCTTCA
GATTACTTGATTCAAATAAACCAATTATGTTTGTAATTGATATTAATAAAACCAGAATAAAAGTTCATATCTACCC

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FIGURE 248

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVENECLVDLCLLRICYKLSGVPNQCRVPLPSDCSK

Important features:

Signal peptide:

amino acids 1-29

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FIGURE 249

AGCGGGTCTCGCTTGGGTTCGGCTAATTTCTGTCTGAGGCGTGAGACTGAGTTCATAGGGTCCTGGGTCCCCGA
ACCAGGAAGGGTTGAGGGAACACAATCTGCAAGCCCCCGCAGCCCAAGTGAGGGGGCCCCGTGTTGGGGTCCTCCC
TCCCTTTGCATTCCCACCCCTCCGGGCTTTGCGTCTTCTGAGGACCCCTCGCCGGGAGATCGCCGCGTTGATG
CGGAGCAAGGATTCGTCTGCTGCTGCTCCTACTGGCCGCGGTGCTGATGGTGGAGAGCTCACAGATCGGCAGT
TCGCGGGCCAACTCAACTCCATCAAGTCTCTCTGGGCGGGGAGACGCTGGTCAGGCCGCCAATCGATCTGCG
GGCATGTACCAAGGACTGGCATTGCGGCGGCAGTAAGAAGGGCAAAAACCTGGGGCAGGCCTACCCTTGTAGCAGT
GATAAGGAGTGTGAAGTTGGGAGGTATTGCCACAGTCCCCACCAAGGATCATCGGCCTGCATGGTGTGTCGGAGA
AAAAAGAAGCGCTGCCACCGAGATGGCATGTGCTGCCCCAGTACCCGCTGCAATAATGGCATCTGTATCCCAGTT
ACTGAAAGCATCTTAACCCCTCACATCCCGGCTCTGGATGGTACTCGGCACAGAGATCGAAACCACGGTCATTAC
TCAAACCATGACTTGGGATGGCAGAATCTAGGAAGACCACACACTAAGATGTCACATATAAAGGGCATGAAGGA
GACCCCTGCCTACGATCATCAGACTGCATTGAAGGGTTTTGCTGTGCTCGTCATTTCTGGACCAAAATCTGCAAA
CCAGTGCTCCATCAGGGGGAAGTCTGTACCAAAACAACGCAAGAAGGGTTCTCATGGGCTGGAAATTTTCCAGCGT
TGCGACTGTGCGAAGGGCCTGTCTTGCAAAGTATGGAAAGATGCCACCTACTCCTCAAAGCCAGACTCCATGTG
TGTCAGAAAATTTGATCACCATTGAGGAACATCATCAATTGCAGACTGTGAAGTTGTATTTAATGCATTATAG
CATGGTGGAAAATAAGGTTCCAGATGCAGAAGAATGGCTAAAATAAGAAACGTGATAAGAATATAGATGATCACA
AAAGGGAGAAAGAAAACATGAAGTGAATAGATTAGAATGGGTGACAAATGCAGTGCAGCCAGTGTTCATTATG
CAACTTGTCTATGTAAATAATGTACACATTTGTGGAAAATGCTATTATTAAGAGAACAAGCACACAGTGGAAAT
ACTGATGAGTAGCATGTGACTTTCCAAGAGTTTAGGTTGTGCTGGAGGAGAGGTTTCCTTCAGATTGCTGATTGC
TTATACAAATAACCTACATGCCAGATTTCTATTCAACGTTAGAGTTTAACAAAATACTCCTAGAATAACTTGTTA
TACAATAGGTTCTAAAAATAAAATTGCTAAACAAGAAATGAAAACATGGAGCATTTGTTAATTTACAACAGAAAAT
TACCTTTTGTATTTGTAACACTACTTCTGCTGTTCAATCAAGAGTCTTGCTAGATAAGAAAAAATCAGTCAATAT
TTCCAAATAAATGCAAAATAATGGCCAGTTGTTTAGGAAGGCCCTTAGGAAGACAAATAAATAACAACAAACAG
CCACAAATACTTTTTTTTCAAATTTTAGTTTTACCTGTAAATTAATAAGAACTGATACAAGACAAAACAGTTCC
TTCAGATTTCTACGGAATGACAGTATATCTCTTTATCCTATGTGATTCTGCTCTGAATGCATTATATTTTCCA
AACTATACCCATAAATTTGTGACTAGTAAAATACTTACACAGAGCAGAATTTTTCAGATGGCAAAAAAATTTAAA
GATGTCCAATATATGTGGGAAAAGAGCTAACAGAGAGATCATTATTTCTTAAAGATTGGCCATAACCTATATTTT
GATAGAATTAGATTGGTAAATACATGTATTACATACATACTCTGTGGTAATAGAGACTTAAGCTGGATCTGTACTG
CACTGGAGTAAGCAAGAAAATTTGGGAAAACTTTTCTGTTTGTTCAGGTTTTGGCAACACATAGATCATATGCTG
AGGCACAAGTTGGCTGTTTCATCTTTGAAACCAGGGGATGCAGTCTAAATGAATATCTGCATGGGATTTGCTAT
CATAATATTTACTATGCAGATGAATTCAGTGTGAGGTCTGTGTCCGTACTATCCTCAAATTATTTATTTTATAG
TGCTGAGATCCTCAAATAATCTCAATTTCAGGAGGTTTTACAAAATGTACTCCTGAAGTAGACAGAGTAGTGAGG
TTTCATTGCCCTCTATAAGCTTCTGACTAGCCAATGGCATCATCCAATTTTCTTCCCAAACCTCTGCAGCATCTG
CTTTATTGCCAAAGGGCTAGTTTCGGTTTTCTGCAGCCATTGCGGTTAAAAAATATAAGTAGGATAACTTGTAAA
ACCTGCATATTGCTAATCTATAGACACCACAGTTTCTAAATTTCTTGAACCACTTTACTACTTTTTTTTAACTT
AACTCAGTTCTAAATACTTTGTCTGGAGCACAAAACAATAAAAGGTTATCTTATAGTCGTGACTTTAACTTTTG
TAGACCACAATTCATTTTTAGTTTTCTTTTACTTAAATCCCATCTGCAGTCTCAAATTTAAGTTCTCCAGTAG
AGATTGAGTTTGAGCCTGTATATCTATTAATAAATTTCAACTTCCACATATATTTACTAAGATGATTAAGACTTA
CATTTTCTGCACAGGTCTGCAAAAACAAAATTATAAACTAGTCCATCCAAGAACCAAGTTTGTATAAACAGGT
TGCTATAAGCTTGTGAAATGAAAATGGAACATTTCAATCAAACATTTCTATATAACAATTATTATTTTACAAT
TTGGTTTCTGCAATATTTTTCTTATGTCCACCCTTTTAAAAATTATTATTTGAAGTAATTTATTTACAGGAAATG
TTAATGAGATGTATTTTCTTATAGAGATATTTCTTACAGAAAGCTTTGTAGCAGAATATATTTGCAGCTATTGAC
TTTGTAATTTAGGAAAAATGTATAATAAGATAAAATCTATTAAATTTTTCTCCTCTAAAAACTGAAAAA

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FIGURE 250

MAALMRSKDSSCCLLLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLAFGGSKKGKNLGQA
YPCSSDKECEVGRYCHSPHQSSACMVCRRKKKRCHRDGMCCPSTRCNGICIPVTESILTPHIPALDGTTRHRDR
NHGHYSNHDLGWQNLGRPHTKMSHIKGHEGDPCLRSSDCIEGFCCARHFWTKICKPVLHQGEVCTKQRKKGSHGL
EIFQRCDCAKGLSCKVWKDATYSSKARLHVCQKI

Signal peptide:
amino acids 1-25

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FIGURE 251

TCTCAATCTGCTGACCTCGTGATCCGCGCTGACCTTGTAATCCACCTACCTTGGCCTCCCAAAGTGTTGGGATTAC
AGGCGTGAGCCACCGCGCCCGGCCAACATCACGTTTTTAAAAATTGATTTCTTCAAATTCATGGCAAATATTTCC
CTTCCCTTTAACTTCTTATGTCAGAATGAGGAAGGATAGCTGCATTTATTTAGTCAGTTTTTCATTGCATAGTAAT
ATTTTCATGTAGTATTTTCTAAGTTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTAACATACTTGTG
AAAATACTTGATGTTTTTAAAGCCTTGGGCAGAAATTCGTATTGTTGAGGATTTGTTCTTTTATCCCCCTTTT
AAAGTCATCCGTCCTTGGCTCAGGATTTGGAGAGCTTGCAACCAAAAAATGGCAAACATCACCAGCTCCAGAT
TTTGGACCAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACCCCAAGTACACAGCAGAATAGTACAAGTCA
CCCTACAACCTACTACTTCTTGGGACCTCAAGCCCCCAACATCCCAGTCCTCAGTCCTCAGTCATCTTGACTTCAA
ATCTCAACCTGAGCCATCCCCAGTTCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCACGTGT
TCCTCCTCCTGGTTTGGAGTCCTTTCCCTTCCCAGGCAAACTTCGAGAATCAACACCTGGAGACAGTCCCTCCAC
TGTGAACAAGCTTTTGCAGCTTCCCAGCACGACCATTTGAAAAATATCTCTGTGTCTGTCCACCAGCCACAGCCCAA
ACACATCAAACCTTGCTAAGCGGCGGATACCCCCAGCTTCTAAGATCCCAGCTTCTGCAGTGGAAATGCCTGGTTC
AGCAGATGTCACAGGATTAAATGTGCAGTTTGGGGCTCTGGAATTTGGGTCAGAACCTTCTCTCTCTGAATTTGG
ATCAGCTCCAAGCAGTGAAAATAGTAATCAGATTCCCATCAGCTTGTATTGGAAGTCTTTAAGTGAGCCTTTGAA
TACATCTTTATCAATGACCAGTGCAGTACAGAATCCACATATACAACCTCCGTCATTACCTCCTGCAGTCTGAC
AAGCTCATCACTGAATCTGCTAGTCCAGTAGCAATGTCTTCTCTTATGACCAGAGTTCTGTGCATAACAGGAT
CCCATACCAAAGCCCTGTGAGTTCATCAGAGTCAGCTCCAGGAACCATCATGAATGGACATGGTGGTGGTCTGAAG
TCAGCAGACACTAGACAGTAAGTATAGCAGCAAGCTACTCTTGTCTATGGCTGGTGCCAACCAAACAGAGGAAGAG
GATAGCTCACGTGATGTGGAAAACACCAGTTGGTCAATGGCTCATTCGTTAAAAGCAGCCCTTTTGCTTTTGTG
TTTTTGGACCAGGTGTTGGCTGTGGTGTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGTGGTGGTCTCATA
TTCTTCTGCCCTAATCAGACTGCACCACAAGTGCAGCATACAGTATGCATTTTAAAGATGCTTGGGCCAGGCGGG
GTGGCTGATGCCATAATCCCAGTGCTTTGGGGGGCCAAGGCAGGCAGATTGCCAAGCTCAGGAGTTTGAGACC
ACCTGGGCAACATGGTGAAACTCTGTCTCTACTAAAAATACGAAAACTAGCCGGGTGTGGTGGCGGCGCGTGCC
TGTAATCCCAGCTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCCGT
CTGAAAAGA

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FIGURE 252

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTTPSTQQNSTSHPTT
TTSWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAQVTVPPPGLESFPSQAKLRESTPGDSPSTVVK
LLQLPSTTIENISVSVHQPQPKHIKLAQRRIPPASKIPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAP
SSNSNQIPISLYSKSLSEPLNTSLSMSTSAVQNSTYTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIYQ
SPVSSSESAPGTIMNGHGGGRSQQTLDISKYSSKLLLSWLVPVKQKRIAHVMWKTPVGQWLIR

Signal peptide:
amino acids 1-24

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FIGURE 254

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPPDKSSGSKKQKQYQRIRKEKPQQH
NFTHRLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQREHRSMRANVELDHATLVRFSPDCRA
FIVWLANGDTLRVFKMTKREDGGYTFTATPEDFPKKHKAPVIDIGIANTGKFIMTASSDTTVLIWSLKGQVLSTI
NTNQMNNTHAAVSPCGRFVASCFTPDVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKD
GTWKLWDTDVEYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVHGEC
IANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGHKLRASNESTRQRLQQQLTQAQETLKSLGALKK

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

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FIGURE 255

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCCGGGCCAGGTGCCCC
GTCGCAGGTGCCCCCTGGCCGGAGATGCGGTAGGAGGGGCGAGCGGAGAAGCCCCCTTCCTCGGCGCTGCCAACCC
GCCACCCAGCCC**ATG**GCGAACCCCGGGCTGGGGCTGCTTCTGGCGCTGGGCCTGCCGTTCTTGCTGGCCCGCTGG
GGCCGAGCCTGGGGGCAAATACAGACCACTTCTGCAAATGAGAATAGCACTGTTTGCCTTCATCCACCAGCTCC
AGCTCCGATGGCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTGCTC
CTGGCTGTGGGGCTGGCACTGTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGGCACCTACCGGCCCACT
AGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGGACTCCAAGGAGACGGTGCAGGGCTGCCTG
CCCATC**TAG**GTCCCCTCTCCTGCATCTGTCTCCCTTCATTGCTGTGTGACCTTGGGGAAAGGCAGTGCCCTCTCT
GGGCAGTCAGATCCACCCAGTGCTTAATAGCAGGGAAGAAGTACTTCAAAGACTCTGCCCCTGAGGTCAAGAGA
GGATGGGGCTATTCACTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAAAAA

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FIGURE 256

MANPGLGLLLALGLPFLARWGRAWGQIQTTSANENSTVLPSTSSSSDGNLRPEAITAIIVVFSLLAALLAVG
LALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

FIGURE 257

[illegible]

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FIGURE 258

MGLFRGFVFLVLCLLHQSNTSFIKLNNGFEDIVIVIDPSVPEDEKIIIEQIEDMVTASTYLFEATEKRFFFKN
VSILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTECGEKGEYIHFTPDLLLGKKQNEYGPPG
KLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATRCASISGRNRVYKCQGGSCLSRACRIDSTTKLYGKDCQF
FPDKVQTEKASIMFMSIDSVVEFCNEKTHNQEAPSLQNIKCNRSTWEVISNSEDFKNTIPMVTPPPPPVFSL
KISQRIVCLVLDKSGSMGGKDRNLNRMNQAAKHFLQTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLMAGL
PTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLTGDGENTASSCIDEVKQSGAIVHFIALGRAADEAVIEMS
KITGGSHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLTLNSNAWMNDTVIIDSTVGKDTFFLITWNS
LPPSISLWDPSGTIMENFTVDATSKMAYLSIPGTAKVGTWAYNLQAKANPETLTITVTSTRAANSSVPPITVNAKM
NKDVNSFSPMIVYAEILQGYVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNMGVYSRYFTAYTENGRYS
LKVRAHGGANTARLKLRPPLNRAAYIPGWVNGEIEANPPRPEIDEDTQTLEDFSRASGGAFFVSQVPSLPLP
DQYPPSQITDLDATVHEDKIILTWTAPGDNFVDGKVQRYIIRISASILDLRDSFDDALQVNTTDLSPKEANSKES
FAFKPENISEENATHIFIAIKSIDKSNLTSKVSNIQVTLFIPQANPDDIDPTPTPTPTPTPKSHNSGVNISTL
VLSVIGSVVIVNFILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592, 628-632,
811-815, 832-836, 837-841, 852-856, 896-900

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FIGURE 259

CGCCGGAGGCAGCGGGCGGCGTGGCGCAGCGGCGACATGGCCGTTGTCTCAGAGGACGACTTTCAGCACAGTTCAA
ACTCCACCTACGGAACCACAAGCAGCAGTCTCCGAGCTGACCAGGAGGCACTGCTTGAGAAGCTGCTGGACCGCC
CGCCCCCTGGCCTGCAGAGGCCCCGAGGACCGCTTCTGTGGCACATACATCATCTTCTTCAGCCTGGGCATTGGCA
GTCTACTGCCATGGAACTTCTTTATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCGCAACTCCTCCAGCCCAG
CCACCGGGGAGGACCCCTGAGGGCTCAGACATCCTGAACACTTTTGAGAGCTACCTTGCCGTTGCCTCCACCGTGC
CCTCCATGCTGTGCCTGGTGCCAACTTCTGCTTGTCAACAGGGTTGCAGTCCACATCCGTGTCTGGCCCTCAC
TGACGGTCATCCTGGCCATCTTCATGGTGATAACTGCACTGGTGAAGGTGGACACTTCTCCTGGACCGCTGGTT
TTTTTGGCGGTACCATTTGTCTGCATGGTGATCCTCAGCGGTGCCTCCACTGTCTTCAGCAGCAGCATCTACGGCA
TGACCGGCTCCTTTCTATGAGGAACTCCCAAGCACTGATATCAGGAGGAGCCATGGGCGGGACGGTCAGCGCCG
TGGCCTCATTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCTGACGGCCACCA
TCTTCCTCGTGCTCTGCATGGGACTCTACCTGCTGCTGTCCAGGCTGGAGTATGCCAGGTACTACATGAGGCCGTG
TTCTTGCGGCCCCATGTGTTTTCTGGTGAAGAGGAGCTTCCCCAGGACTCCCTCAGTGCCCTTCGGTGGCCCTCCA
GATTCAATTGATTCCCACACACCCCCCTCTCCGCCCCATCCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGTACCT
ACGTCTTCTTCATCACCAGCCTCATCTACCCCGCCGTCTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCT
CACTGTGGACCACCAAGTTTTTCATCCCCCTCACTACCTTCTCCTGTACAACTTTGCTGACCTATGTGGCCGGC
AGCTCACCGCCTGGATCCAGGTGCCAGGGCCCCAACAGCAAGGCGCTCCAGGGTTCGTGCTCCTCCGACCTGCC
TCATCCCCCTCTTCGTGCTCTGTAACCTACCAGCCCCGCGTCCACCTGAAGACTGTGGTCTTCCAGTCCGATGTGT
ACCCGCACTCCTCAGCTCCCTGCTGGGGCTCAGCAACGGCTACCTCAGCACCCCTGGCCCTCCTCTACGGGCCCTA
AGATTGTGCCCAGGGAGCTGGCTGAGGCCACGGGAGTGGTGATGTCTTTTATGTGTGCTTGGGCTTAACACTGG
GCTCAGCCTGCTCTACCTCCTGGTGACCTCATCTAGAAAGGGAGGACACAAGGACATTGGTGCTTCAGAGCCTT
TGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGGCCATGGAGGAAAGGCCTAAAGTTTCACTTGGGGACAGAGAG
CAGAGCACACTCGGGCCTCATCCCTCCCAAGATGCCAGTGAGCCACGTCCATGCCCATTCCGTGCAAGGCAGATA
TTCCAGTCATATTAACAGAACAACCTCCTGAGACAGTTGAAGAAGAAAATAGCACAAATCAGGGGTACTCCCTTCACA
GCTGATGGTTAACATTCCACCTTCTTTCTAGCCCTTCAAAGATGCTGCCAGTGTTCGCCCTAGAGTTATTACAAA
GCCAGTGCCAAAACCCAGCCATGGGCTCTTTGCAACCTCCCAGCTGCGCTCATTCAGCTGACAGCGAGATGCAA
GCAAATGCTCAGCTCTCCTTACCCTGAAGGGGTCTCCCTGGAATGGAAGTCCCCTGGCATGGTCAGTCTCAGGC
CCAAGACTCAAGTGTGCACAGACCCCTGTGTTCTGCGGGTGAACAACCTGCCCCTAACCAGACTGGAAAACCCAG
AAAGATGGGCTTCCATGAATGCTTCATTCCAGAGGGACCAGAGGGCCTCCCTGTGCAAGGGATCAAGCATGTCT
GGCCTGGGTTTTTCAAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCCTGGGTCAAGATGAGGGTCTTTCA
GTGTTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAATACTTGCGTATTCAAAA

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FIGURE 260

MAVVS EDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPPGQLQRPEDRFCGTYYIIFSLGIGSLLPWNFFITAK
EYWMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFLLVNRVAVHIRVLASLTVILAI FMVIT
ALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSIYGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSD
VRNSALAFFLTATIFLVLCMGLYLLLSRLEYARYYMRPVLAHVFSGEEELPQDSL SAPSVASRFIDSHTPPLRP
ILKKTASLGFCVTYVFFITS LIYPAVCTNIESLNKSGSGLWTTKFFIPLTTFLLYNFADLCGRQLTAWIQVPGPN
SKALPGFVLLRTCLIPLFVLCNYQPRVHLKTVVFQSDVYPALLSSLLGLSNGYLSTLALLYGPKIVPRELAEATG
VVMSFYVCLGLTLGSACSTLLVHLI

Transmembrane domain:

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252, 305-330,
448-472

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FIGURE 261

CGGACGCGTGGGCTGCTGGTGGGAAGGCCTAAAGAACTGGAAAGCCCCTCTCTTGGAAACCACACCTGTTTTA
AAGAACCTAAGCACCATTAAAGCCACTGGAAATTTGTTGTCTAGTGGTTGTGGGTGAATAAAGGAGGGCAGAAAT
GGATGATTTTCATCTCCATTAGCCTGCTGTCTCTGGCTATGTTGGTGGGATGTTACGTGGCCGGAATCATTCCCTT
GGCTGTTAATTTCTCAGAGGAACGACTGAAGCTGGTACTGTTTTGGGTGCTGGCCTTCTCTGTGGAACCTGCTCT
GGCAGTCATCGTGCCCTGAAGGAGTACATGCCCTTTATGAAGATATTCTTGAGGGAAAAACACCACCAAGCAAGTGA
AACACATAATGTGATTGCATCAGACAAAGCAGCAGAAAAATCAGTTGTCCATGAACATGAGCACAGCCACGACCA
CACACAGCTGCATGCCCTATATTGGTGTTCCTCGTTCTGGGCTTCGTTTTTCATGTTGCTGGTGGACCAGATTGG
TAACTCCCATGTGCATTCTACTGACGATCCAGAAGCAGCAAGGTCTAGCAATTCCAAAATCACCACCACGCTGGG
TCTGGTTGTCCATGCTGCAGCTGATGGTGTTCCTTGGGAGCAGCAGCATCTACTTCACAGACCAGTGTCCAGTT
AATTGTGTTTGTGGCAATCATGCTACATAAGGCACCAGCTGCTTTTGGACTGGTTTCCTTCTTGATGCATGCTGG
CTTAGAGCGGAATCGAATCAGAAAGCACTTGCTGGTCTTTGCATTGGCAGCACCAGTTATGTCCATGGTGACATA
CTTAGGACTGAGTAAGAGCAGTAAAGAAGCCCTTTAGAGGTGAACGCCACGGGAGTGGCCATGCTTTTCTCTGC
CGGGACATTTCTTTATGTTGCCACAGTACATGTCTCCCTGAGGTGGGCGGAATAGGGCAGACCAAGCCCGA
TGCCACGGGAGGGAGAGGCTCAGCCGCTGGAAGTGGCAGCCCTGGTTCTGGGTTGCCTCATCCCTCTCATCCT
GTCAGTAGGACACCAGCATTAATGTTCAAGGTCCAGCCTTGGTCCAGGGCCGTTGCCATCCAGTGAGAACAGC
CGGCACGTGACAGCTACTCACTTCCTCAGTCTCTTGTCTCACCTTGCGCATCTCTACATGTATTCTAGAGTCCA
GAGGGGAGGTGAGGTTAAACCTGAGTAATGGAAAAGCTTTAGAGTAGAAACACATTTACGTTGCAGTTAGCTA
TAGACATCCCATTTGTGTTATCTTTTAAAGGCCCTTGACATTTTGCCTTTTAAATATTTCTCTTAACCTATTCTC
AGGGAAGATGGAAATTTAGTTTTAAGGAAAAGAGGAGAACTTCATACTACAATGAAATAGTGATTATGAAAATAC
AGTGTCTGTAAATTAAGCTATGTCTCTTTCTTCTAGTTTAGAGGCTCTGCTACTTTATCCATTGATTTTTTAACA
TGGTTCCACCATGTAAGACTGGTGCTTTAGCATCTATGCCACATGCGTTGATGGAAGGTATAGCACCACCTCA
CTTAGATGCTAAAGGTGATTCTAGTTAATCTGGGATTAGGGTCAGGAAAATGATAGCAAGACACATTGAAAGCTC
TCTTTATACTCAAAAGAGATATCCATTGAAAAGGGATGTCTAGAGGGATTTAAACAGCTCCTTTGGCAGTGCCCT
CTCTGAATCCAGCCTGCCATTCCATCAAATGGAGCAGGAGAGGTGGGAGGAGCTTCTAAAGAGGTGACTGGTATT
TTGTAGCATTCCTTGTCAAGTTCTCCTTTGCAGAATACCTGTCTCCACATTCCTAGAGAGGAGCCAAGTTCTAGT
AGTTTCAGTTCTAGGCTTTCCTTCAAGAACAGTCAGATCACAAAGTGTCTTTGGAAATTAAGGGATATTAAATTT
TAAGTGATTTTTGGATGGTTATTGATATCTTTGTAGTAGCTTTTTTTTAAAGACTACCAAAATGTATGGTTGTCC
TTTTTTTTTGTTTTTTTTTTTTTTTAATTATTTCTCTTAGCAGATCAGCAATCCCTCTAGGGACCTAAATACTAGG
TCAGCTTTGGCGACACTGTGTCTTCTCACATAACCACCTGTAGCAAGATGGATCATAAATGAGAAGTGTTCCT
ATTGATTTAAAGCTTATTGGAATCATGTCTCTTGTCTCTTCGTCCTTTCTTTGCTTTTCTTCTAATTTTCCCTC
TAGCCTCTCCTCGCCACAATTTGCTGCTTACTGCTGGTGTAAATATTTGTGTGGGATGAATTCCTATCAGGACAA
CCACTTCTCGAACTGTAATAATGAAGATAATAATATCTTTATCTTTATCCCCCTTCAAAGAAATTACCTTTGTG
TCAAATGCCGCTTTGTTGAGCCCTTAAATACCACCTCCTCATGTGTAAATTGACACAATCACTAATCTGGTAAT
TTAAACAATTGAGATAGCAAAAGTGTAAACAGACTAGGATAATTTTTTTTCATATTTGCCAAAATTTTTGTAA
ACCCTGTCTTGTCAAATAAGTGTATAATATTGTATTATTAATTTATTTTACTTTCTATACCATTTCAAAACACA
TTACACTAAGGGGGAACCAAGACTAGTTTCTTCAGGGCAGTGGACGTAGTAGTTTGTA AAAACGTTTTCTATGAC
GCATAAGCTAGCATGCCATGATTTATTTCTTCTCATGAATTTGTCACTGGATCAGCAGCTGTGGAATAAAGCTT
GTGAGCCCTCTGCTGGCCACAGTGAGGAAAGTAGCACAAATAGGATACAGTTGTATGTAGTCATTGGCAACAATT
GCATACAATTTTACTACCAAGAGAAGGTATAGTATGGAAAGTCCAATGACTTCCTTGATTGGATGTTAACAGCT
GACTGGTGTGAGACTTGAGGTTTCATCTAGTCTTCAAACTATATGGTTGCCTAGATTCTCTCTGGAACTGAC
TTTGTCAAATAAATAGCAGATTGTAGTGTCAAAAAAA

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FIGURE 262

MDDFISISLLSLAMLVGCYVAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHALYEDILEGKHHQAS
ETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMLLVDQIGNSHVHSTDDPEAARSSNSKITTTL
GLVVHAAADGVALGAAASTSQTSLIVFVAIMLHKAPAAFGLVSFLMHAGLERNRIRKHLVFAAAPVMSMVT
YLGLSKSSKEALSEVNATGVAMLFSAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPLI
LSVGHQH

Signal peptide:
amino acids 1-18

Transmembrane domain:
amino acids 37-56, 106-122, 211-230, 240-260, 288-304

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FIGURE 263

CTCCTTAGGTGGAAACCCCTGGGAGTAGAGTACTGACAGCAAGACCGGGAAAGACCATACGTCCCCGG
GCAGGGGTGACAAACAGGTGTCATCTTTTTGATCTCGTGTGTGGCTGCCTTCTATTTCAAGGAAAGAC
GCCAAGGTAATTTTGACCCAGAGGAGCAATGATGTAGCCACCTCCTAACCTTCCCTTCTTGAACCCCC
AGTTATGCCAGGATTTACTAGAGAGTGTCAACTCAACCAGCAAGCGGCTCCTTCGGCTTAACCTTGTGG
TTGGAGGAGAGAACCTTTGTGGGGCTGCGTTCTCTTAGCAGTGCTCAGAAGTGACTTGCCTGAGGGTG
GACCAGAAGAAAGGAAAGGTCCCCTCTTGCTGTGGCTGCACATCAGGAAGGCTGTGATGGGAATGAA
GGTGAACAACTTGGAGATTTCACTTCAGTCATTGCTTCTGCCTGCAAGATCATCCTTTAAAGTAGAGA
AGCTGCTCTGTGTGGTGGTTAACTCCAAGAGGCAGAACTCGTTCTAGAAGGAAATGGATGCAAGCAGC
TCCGGGGGGCCCCAAACGCATGCTTCCTGTGGTCTAGCCCAGGGAAGCCCTTCCGTGGGGGGCCCCGGCT
TTGAGGGATGCCACCGGTTCTGGACGCATGGGAGTGATTCCTGAATGATGATGGTTCGCCGGGGGGCTGCT
TGGCTGGATTTCCCGGGTGGTGGTTTTGCTGGTGTCTCCTCTGCTGTGCTATCTCTGTCTGTACATGT
TGGCCTGCACCCCAAAGGTGACGAGGAGCAGCTGGCACTGCCCAGGGCCAACAGCCCCACGGGGGAAG
GAGGGGTACCAGGCCGTCTTCAGGAGTGGGAGGAGCAGCACCAGCAACTACGTGAGCAGCCTGAAGCG
GCAGATCGACAGCTCAAGGAGGAGCTGCAGGAGGAGTGAATGCTGGCGTCAAGCTGGCCACAGAGTATGCAGC
CCAGCGATGCTGCTGGCCTGGGTCTGGACAGGAGCCCCCAGAGAAAACCCAGGGCCGACCTCCTGGCC
TTCCTGCACTCGCAGGTGGACAAGGCAGAGGTGAATGCTGGCGTCAAGCTGGCCACAGAGTATGCAGC
AGTGCCTTTGATAGCTTTACTCTACAGAAGGTGTACCAGCTGGAGACTGGCCTTACCCGCCACCCCCG
AGAGAAGCCTTGTAGGAAGGACAAGCGGGATGAGTTGGTGGAAAGCCATTGAATCAGCGAGTTGAGACC
CTGAACAATCCTGCAGAGAACAGCCCCAATCACCGTCTTACACGGCCTCTGATTTTCATAGAAGGGAT
CTACCGAACAGAAAGGGACAAAGGGACATTGTATGAGCTCACCTTCAAAGGGGACCACAAACACGAAT
TCAAACGGCTCATCTTATTTGACCAATTACGCCCCATCATGAAAGTGAAAAATGAAAAGCTCAACATG
GCCAACACGCTTATCAATGTTATCGTGCTCTAGCAAAAAGGGTGGACAAGTTCGGCGAGTTTCATGCA
GAATTTAGGGAGATGTGCATTGAGCAGGATGGGAGAGTCCATCTCACTGTTGTTTACTTTGGGAAAG
AAGAAATAAATGAAGTCAAAGGAATACTTGAAAACACTTCCAAAGCTGCCAACTTCAGGAACCTTTACC
TTCATCCAGCTGAATGGAGAATTTTCTCGGGGAAAGGGACTTGATGTTGGAGCCCGCTTCTGGAAGGG
AAGCAACGCTCTTCTCTTTTCTGTGATGTGGAGCTACTTACATCTGAATTCCTCAATACGTGTA
GGCTGAATACACAGCCAGGGAAGAAGGTATTTTATCCAGTTCTTTTCAGTCAGTACAATCCTGGCATA
ATATACGGCCACCATGATGCAGTCCCTCCCTTGGAAACAGCAGCTGGTCATAAAGAAGGAAACTGGATT
TTGGAGAGACTTTGGATTTGGGATGACGTGTGATGCTCGGTGAGCTTCATCAATATAGGTGGGTTTG
ATCTGGACATCAAAGGCTGGGGCGGAGAGGATGTGCACCTTTATCGCAAGTATCTCCACAGCAACCTC
ATAGTGGTACGGACGCCTGTGCGAGGACTCTTCCACCTCTGGCATGAGAAGCGCTGCATGGACGAGCT
GACCCCCGACAGTACAAGATGTGCATGCAGTCCAAGGCCATGAACGAGGCATCCCACGGCCAGCTGG
GCATGCTGGTGTTCAGGCACGAGATAGAGGCTCACCTTCGCAACAGAAACAGAACAGTGAAGCAAA
AAAACATGAACCTCCAGAGAAGGATTGTGGGAGACACTTTTTCTTTCTTTGCAATTACTGAAAGTG
GCTGCAACAGAGAAAAGACTTCCATAAAGGACGACAAAAGAATTGGACTGATGGGTGAGAGATGAGAA
AGCCTCCGATTTCTCTCTGTGGGCTTTTTTACAACAGAAATCAAATCTCCGCTTTGCTGCAAAAGT
AACCAGTTGCACCCCTGTGAAGTGTCTGACAAAGGCAGAATGCTTGTGAGATTATAAGCCTAATGGTG
TGGAGGTTTTGATGGTGTTTACAATACACTGAGACCTGTTGTTTTGTGTGCTCATTGAAATATTCATG
ATTTAAGAGCAGTTTTGTAAAAAATTCATTAGCATGAAAGGCAAGCATATTTCTCCTCATATGAATGA
GCCTATCAGCAGGGCTCTAGTTTCTAGGAATGCTAAAATATCAGAAGGCAGGAGAGGAGATAGGCTTA
TTATGATACTAGTGAGTACATTAAGTAAATAAAATGGACCAGAAAAGAAAACCATAAATATCG
TGTCATATTTTCCCCAAGATTAACCAAAAATAATCTGCTTATCTTTTTGGTTGCTTTTTAACTGTCT
CCGTTTTTTTTCTTTTATTTAAAAATGCACTTTTTTTCCCTTGTGAGTTATAGTCTGCTTATTTAATTA
CCACTTTGCAAGCCTTACAAGAGAGCACAAGTTGGCCTACATTTTTTATATTTTTTAAAGAGATACTTT
GAGATGCATTATGAGAACTTTAGTTCAAAGCATCAAATTTGATGCCATATCCAAGGACATGCCAAATG
CTGATTCGTGCAGGCACTGAATGTCAGGCATTGAGACATAGGGAAGGAATGGTTTGTACTAATACAGA
CGTACAGATACTTTCTCTGAAGAGTATTTTCGAAGAGGAGCAACTGAACACTGGAGGAAAAGAAAATG
ACACTTTCTGCTTTACAGAAAAGGAAACTCATTCAGACTGGTGATATCGTGATGTACCTAAAAGTCAG
AAACCACATTTTCTCCTCAGAAGTAGGGACCGCTTCTTACCTGTTTAAATAAACCAAAGTATACCGT
GTGAACCAACAATCTCTTTCAAACAGGGTGCTCCTCCTGGCTTCTGGCTTCCATAAGAAGAAATG
GAGAAAATATATATATATATATATATATATTGTGAAAGATCAATCCATCTGCCAGAATCTAGTGGGATG
GAAGTTTTTGTCTACATGTTATCCACCCAGGCCAGGTGGAAGTAACTGAATTATTTTTTAAATTAAGC
AGTCTCACTAATCACCAAGATGCTTCTGAAGAAATGCAATTTTATTACCATTTCAACTTTTTTAA
AATAAATACAGTTAACATAGAGTGGTTTTCTTCATTCATGTGAAAATTATTAGCCAGCACCAGATGCAT
GAGCTAATTATCTCTTTGAGTCTTGTCTTGTGTTGCTCACAGTAAACTCATTGTTTAAAGCTTCAA
GAACATTCAAGCTGTTGGTGTGTTAAAAATGCATTGTATTGATTTGTACTGGTAGTTTATGAAATTT
AATTAACACAGGCCATGAATGGAAGGTGGTATTGCACAGCTAATAAAATATGATTTGTGGATATGAA

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FIGURE 264

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQALALPRANSP TGKEGYQAVLQEWEEQHRNYVSSL
KRQIAQLKEELQERSEQLRNGQYQASDAAGLGDRSPPEKTQADLLAFLHSQVDKAEVNAGVKLATEYAAVPFDS
FTLQKVYQLETGLTRHPEEKPV RKDKRDELVEAIESALET LNNPAENSPNHRPYTASDFIEGIYRTERDKGTLYE
LTFKGDHKHEFKRLILFRPFSPIMKVKNEKLN MANTLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVY
FGKEEINEVKGILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTCRLNT
QPGKKVFYPVLF SQYNPGIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFINIGGFDDLKGGWGGED
VHLYRKYLHSNLIVVRTPV RGLFHLWHEKRCMDELTPEQYKCMQSKAMNEASHGQLGMLVFRHEIEAHLRKQKQ
KTSSKKT

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FIGURE 265

GGATGCAGAAAGCCTCAGTGTGCTCTTCCTGGCCTGGGTCTGCTTCCTCTTCTACGCTGGCATTGCCCTCTTCA
CCAGTGGCTTCCTGCTCACCCGTTTGGAGCTCACCAACCATAGCAGCTGCCAAGAGCCCCAGGCCCTGGGTCCC
TGCCATGGGGGAGCCAAGGGAAACCTGGGGCCTGCTGGATGGCTTCCGATTTTCGCGGGTGTGTGGTGTCTGA
TAGATGCTCTGCGATTTGACTTCGCCCAGCCCCAGCATTCACACGTGCCTAGAGAGCCTCCTGTCTCCCTACCCCT
TCCTGGGCAACTAAGCTCCTTGACAGAGGATCCTGGAGATTAGCCCCACCATGCCGGCTCTACCGATCTCAGG
TTGACCCTCCTACCACCACCATGCAGCGCTCAAGGCCCTCACCCTGGCTCACTGCCCTACCTTTATTGATGCTG
GTAGTAACCTTCCGAGCCACGCCATAGTGAAGACAATCTCATTAAGCAGCTCACCAGTGCAGGAAGGCGTGTAG
TCTTCATGGGAGATGATACCTGGAAAGACCTTTTCCCTGGTGTCTTCTCCAAAGCTTTCTTCTTCCCATCCTTCA
ATGTCAGAGACCTAGACACAGTGGACAATGGCATCCTGGAACACCTCTACCCACCATGGACAGTGGTGAATGGG
ACGTGCTGATTGCTCACTTCCTGGGTGTGGACCACTGTGGCCACAAGCATGGCCCTCACCACCCTGAAATGGCCA
AGAACTTAGCCAGATGGACCAGGTGATCCAGGGCTTGTGGAGCGTCTGGAGAATGACACACTGCTGGTAGTGG
CTGGGGACCATGGGATGACCACAAATGGAGACCATGGAGGGGACAGTGAGCTGGAGGTCTCAGCTGCTCTCTTTC
TGTATAGCCCCACAGCAGTCTTCCCAGCACCCCCACCAGAGGAGCCAGAGGTGATTCTCAAGTTAGCCTTGTGC
CCACGCTGGCCCTGCTGCTGGGCCTGCCCATCCCATTGGGAATATCGGGGAAGTGATGGCTGAGCTATTCTCAG
GGGTGAGGACTCCCAGCCCCACTCCTCTGCTTTAGCCCCAGCCTCAGCTCTCCATCTCAATGCTCAGCAGGTGT
CCCGATTTCTCATACCTACTCAGCTGCTACTCAGGACCTTCAAGCTAAGGAGCTTCATCAGCTGCAGAACCTCT
TCTCCAAGGCCCTCTGCTGACTACCAGTGGCTTCTCCAGAGCCCCAAGGGGGCTGAGGCGACACTGCCGACTGTGA
TTGCTGAGCTGCAGCAGTTCCTGCGGGGAGCTCGGGCCATGTGCATCGAGTCTTGGGCTCGTTTCTCTCTGGTCC
GCATGGCGGGGGGTACTGCTCTCTGGCTGCTTCCTGCTTTATCTGCCTGCTGGCATCTCAGTGGGCAATATCCC
CAGGCTTTCCATCTGCCCTCTACTCCTGACACCTGTGGCCTGGGGCCTGGTTGGGGCCATAGCGTATGCTGGAC
TCCTGGGAACATTAGAGCTGAAGCTAGATCTAGTGCTTCTAGGGGCTGTGGCTGCAGTGAGCTCATTCTCCCTT
TTCTGTGGAAGCCTGGGCTGGCTGGGGSTCCAAGAGGCCCTGGCAACCCTGTTTCCATCCCTGGGCCCCGTCC
TGTTACTCCTGCTGTTTTGCTGGCTGTGTTCTTCTCTGATAGTTTTGTTGTAGCTGAGGCCAGGGCCACCCCT
TCCTTTTGGGCTCATTATCCTGCTCCTGGTTGTCCAGCTTCACTGGGAGGGCCAGCTGCTTCCACCTAAGCTAC
TCACAATGCCCCGCTTGGCACTTCAGCCACAACAACCCCCACGGCACAATGGTGCATATGCCCTGAGGCTTG
GAATTGGGTTGCTTTTATGTACAAGGCTAGCTGGGCTTTTTCATCGTTGCCCTGAAGAGACACCTGTTGCCACT
CCTCTCCCTGGCTGAGTCTCTGGCATCCATGGTGGGTGGTTCGAGCCAAGAATTTATGGTATGGAGCTTGTGTGG
CGGCGCTGGTGGCCCTGTTAGCTGCCGTGCGCTTGTGGCTTCGCGCTATGGTAATCTCAAGAGCCCCGAGCCAC
CCATGCTCTTTGTGCGCTGGGACTGCCCTAATGGCATTTGGGTACTGCTGCCTACTGGGCAATGGCGCTCGGGG
CAGATGAGGCTCCCCCGCTCTCCGGGTCTGGTCTCTGGGGCATCCATGGTGTGCTCGGGCTGTAGCAGGGC
TGGCTGCTTCAGGGCTCGCGCTGCTGCTCTGGAAGCCTGTGACAGTGTGGTGAAGGCTGGGGCAGGCGCTCCAA
GGACCAGGACTGTCTCACTCCCTTCTCAGGCCCCCCACTTCTCAAGCTGACTTGGATTATGTGGTCCCTCAAA
TCTACCGACACATGCAGGAGGAGTTCCGGGGCCGGTTAGAGAGGACCAAATCTCAGGGTCCCCTGACTGTGGCTG
CTTATCAGTTGGGGAGTGTCTACTCAGCTGCTATGGTCACAGCCCTCACCCTGTTGGCCTTCCACTTCTGCTGT
TGCATGCGGAGCGCATCAGCCTTGTGTTCTGCTTCTGTTTCTGCAGAGCTTCTTCTCCTACATCTGCTTGGCTG
CTGGGATACCCGTCACCACCCCTGGTCTTTTACTGTGCCATGGCAGGCAGTCTCGGCTTGGGCCCTCATGGCCA
CACAGACCTTCTACTCCACAGGCCACCAGCCTGTCTTCCAGCCATCCATTGGCATGCAGCCTTCTGTTGGATTCC
CAGAGGGTCAATGGCTCCTGTACTTGGCTGCCTGCTTGTCTAGTGGGAGCCAACACCTTGTCTCCCACCTCCTCT
TTGCAGTAGGTTGCCCACTGCTCCTGCTCTGGCCTTCTCTGTGTGAGAGTCAAGGGCTGCGGAAGAGACAGCAGC
CCCCAGGGAATGAAGCTGATGCCAGAGTCAGACCCGAGGAGGAAGAGGAGCCACTGATGGAGATGCGGCTCCGGG
ATGCGCCTCAGCACTTCTATGCAGCACTGCTGCAGCTGGGCCCTCAAGTACCTCTTTATCCTTGGTATTCAGATTC
TGGCCTGTGCTTGGCAGCCTCCATCCTTCGACAGGCATCTCATGGTCTGGAAAGTGTGTTGCCCTAAGTTCATAT
TTGAGGCTGTGGGCTTCATTGTGAGCAGCGTGGGACTTCTCCTGGGCATAGCTTTGGTGATGAGAGTGGATGGTG
CTGTGAGCTCCTGGTTCAGGCAGCTATTTCTGGCCAGCAGAGGTAGCCTAGTCTGTGATTACTGGCACTTGGCT
ACAGAGAGTGTGGAGAACAGTGTAGCCTGGCCTGTACAGGTACTGGATGATCTGCAAGACAGGCTCAGCCATAC
TCTTACTATCATGCAGCCAGGGGCCGCTGACATCTAGGACTTCATTATTCTATAATTAGGACCACAGTGGAGTA
GATCCCTAACTCCTGATTGATGATCTGAGGACAAGGGGGCGGTCTCCGAAGTGGAAATAAATAGGCCGG
GCGTGCTGACTTGCACCTATAATCCAGCACTTTGGGAGGCAGAGGTGGGAGGATTGCTTGGTCCCAGGAGTTCA
AGACCAGCCTGTGGAACATAACAAGACCCCGTCTACTATTTAAAAAAGTGAATAAATGATAATAT

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FIGURE 266

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809

<subunit 1 of 1, 1089 aa, 1 stop

<MW: 118699, pI: 8.49, NX(S/T): 2

MQKASVLLFLAWVCFLEYAGIALFTSGFLLTRLELTNHSSCQEPFPGSLPWGSQGKPGACWMASRFSRVVLVLI
DALRFDFAPQHQSHVPREPPVSLPFLGKLSSLQRILEIQPHHARLYRSQVDPPTTTMQRLKALTGSLPTFIDAG
SNFASHAIVEDNLIKQLTSAGRRVVFMGDDTWKDLFPGAFSKAFFPFSFNVRDLDTVDNGILEHLYPTMDSGEWD
VLIAHFLGVHDHCGHKHGHHPHPEMAKKLSQMDQVIQGLVERLENDTLLVVAGDHGTTNGDHGGDSELEVSAALFL
YSPTAVFPSTPPEEPEVIPQVSLVPTLALLLGLPIPFNGIGEVMAELEFSGGEDSQPHSSALAQASALHLNAQQVS
RFLHTYSAATQDLQAKELHQLQNLFSKASADYQWLLQSPKGAETLPTVIAELQQFLRGARAMCIESWARFSLVR
MAGGTALLAASCFCICLLASQWAI SPGFPPCPLLLTPVAWGLVGAIAYAGLLGTIELKLDLVLLGAVAAVSSFLPF
LWKAWAGWGSKRPLATLFPIPGPVLLLLLFLRLAVFFSDSFVVAEARATPFLLGSFILLLVVQLHWEGQLLPKLL
TMPRLGTSATTNPPRHNGAYALRLGIGLLLCTRLAGLFHRCPEETPVCHSSPWLSPLASMVGGRAKNLWYGACVA
ALVALLAAVRLWRLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPPRLRVLVSGASMVLPRAVAGL
AASGLALLLWKPVTVLVKAGAGAPRTTRTVLTPFSGPPTSQADLDYVVPQIYRHMQEEFRGRLETKSQGPLTVAA
YQLGSVYSAMVTALTLLAFPLLLHAERISLVFLLFLQSFLLHLLAAGIPVTTGPFTVPWQAVSAWALMAT
QTFYSTGHQPVFPPIHWHAAFVGFPEGHGSCTWLPALLVGANTFASHLLFAVGCPLLLLPFLCESQGLRKRQQP
PGNEADARVRPEEEEEPIMEMRLRDAPQHFYAALLQLGLKYLFI LGIQILACALAASILRRHLMVWKVFAPKFIF
EAVGFIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domains:amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850, 1016-1034,
1052-1070**Leucine zipper pattern.**

amino acids 843-864

N-glycosylation sites.

amino acids 37-40, 268-271

FIGURE 267

[illegible]

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FIGURE 268

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWFPASYPECGNNAQSPIDIQTDSVTFDPLPALQPHGYDQPGTE
PLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQINSEATFAELHIVHYDSDSYDSLSEA
AERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRHKDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSV
LWTVFYRRSQISMEQLEKLGQTLFSTEEEPSKLLVQNYRALQPLNQRMVVFASFIQAGSSYTTGEMLSLGVGILVG
CLCLLLAVYFIARKIRKKRLENRKS VVFTSAQATTEA
```

Important features of the protein:**Signal peptide:**

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

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FIGURE 269

GTGGCGCTGGCGGTTGCTGTGCTGATTCCCGGGGTTGGTGGCAGCGGCGGTAGCAGCAATGGACTTTCTCCTG
GGGAACCCGTTGAGCTCTCCAGTGGGACAGCGCATCGAGAAAGCCACAGATGGCTCCCTGCAGAGCGAGGACTGG
GCCCTCAACATGGAGATCTGCGACATCATCAACGAGACGGAGGAAGGTCCCAAAGATGCCCTCCGAGCAGTAAAG
AAGAGAATCGTGGGGAATAAGAACTTCCACGAGGTGATGCTGGCTCTCACAGTCTTAGAAACCTGTGTCAAGAAC
TGCGGGCACCCTTCCACGTGCTGGTGGCCAGCCAGGACTTCGTGGAGAGTGTGCTGGTGGAGGACCATCCTGCCC
AAGAACAACCCACCCACCATCGTGCATGACAAAGTGCTCAACCTCATCCAGTCCTGGGCTGACGCGTTCGCGAGC
TCGCCCCGATCTGACAGGTGTGGTCACCATCTATGAGGACCTGCGGAGGAAAGGCCTGGAGTTCCCATGACTGAC
CTGGACATGCTGTCAACCATCCACACACCCAGAGGACCGTGTCAACTCAGAGACACAATCAGGACAGGATTCTG
TGGGCACTGACTCCAGCCAGCAAGAGGACTCTGGCCAGCATGCTGCCCTCTGCCCGCCCCGCCATACTCTCCG
GTGACACGCCCCATAGCACCACCCCGAACAGATTGGGAAGCTGCGCAGTGAGCTGGAGATGGTGAGTGGGAACG
TGAGGGTGATGTGCGGAGATGCTGACGGAGCTGGTGCCACCCAGGCCGAGCCCGCAGACCTGGAGCTGCTGCAGG
AGCTCAACCGCACGTGCCGAGCCATGCAGCAGCGGGTCTGAGTGATAACCCTGCTCCGGGCCCATGCCCCAAGGA
GCCCTTCAGAGCCCACACTGCCAGTCGAGGCCTGGCTGGAGGCTGGCCACAGTGGAATTCGCGGAGCCTATTG
TCCCTACCCTGCTCTGCTGCATGGGGCCCCATGGCTTTGGCTGGCCACTGAGGGTAGGGTGTGGAGGTGTGGAGG
CCCCCTGAGGAGCTGCGGCGGGCCAGGTACGAAGCTGCAACTCTGCGCGCAGTGGGCGAGATCTCATCAGCCCCA
GGCTGCAGGTGAGGCTTCAGGGGATGCTGGGGCCCCACTGCCCTCCGCTGCCTTGCCCTCCATCCTTCCTCTGT
TCCTTCTGGCCGGGCACCACAGCACTGGGGCTCACCTCTTGTTGATCCTCTTGTAAGTGGGAGAGGTGCCTTTTG
TATCCCCAATTAAAGGTAGAAAACC

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FIGURE 270

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62813
><subunit 1 of 1, 209 aa, 1 stop
><MW: 23465, pI: 7.57, NX(S/T): 1
MDFLLGNPFSSPVGQRIEKATDGSLQSEDWALNMEICDIINETEEGPKDALRAVKKRIVGNKNFHEVMLALTVLE
TCVKNCGHRFHVIVASQDFVESVLVRTILPKNNPPTIVHDKVLNLIQSWADAFRSSPDLTGVVTIYEDLRRKGLE
FPMTDLDMLSPIHTPRGPCSTQRHNQDRILWALTPASKRTLASMLPLCPPRPYSPVTRP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-15

N-glycosylation site:

Amino acids 41-45

N-myristoylation sites:

Amino acids 6-12;23-29

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FIGURE 271

CGGACGCGTGGSCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCGTCTGCCATGGGGC
TCGGGTTGAGGGGCTGGGGACGTCTCTGCTGACTGTGGCCACCGCCCTGATGCTGCCCCGTGAAGCCCCCGCAG
GCTCCTGGGGGGCCAGATCATCGGGGGCCACGAGGTGACCCCCCACTCCAGGCCCTACATGGCATCCGTGCGCT
TCGGGGGCCAACATCACTGCGGAGGCTTCCTGCTGCGAGCCCGCTGGGTGGTCTCGGCCGCCCACTGCTTCAGCC
ACAGAGACCTCCGCACTGGCCTGGTGGTGTGTTGGGCGCCACGTCTGAGTACTGCGGAGCCCAACCAGCAGGTGT
TTGGCATCGATGCTCTCACCACGCACCCCGACTACCACCCCATGACCCACGCCAACGACATCTGCCTGCTGCGGC
TGAACGGCTCTGCTGTCTGGGCCCTGCAGTGGGGCTGCTGAGGCTGCCAGGGAGAAGGGCCAGGCCCCCACAG
CGGGGACACGGTGCCGGGTGGCTGGCTGGGGCTTCGTGTCTGACTTTGAGGAGCTGCCGCCTGGACTGATGGAGG
CCAAGGTCCGAGTGCTGGACCCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCA
CCCGCAGTGGGGACAGCCACAGACGGGGCTTCCTGCTCGGCCGACTCCGGAGGGCCCTGGTGTGCAGGAACCGGG
CTCACGGCTCGTTTCCTTCTCGGGCCTCTGGTGCGGCGACCCCAAGACCCCGACGTGTACACGCAGGTGTCCG
CCTTTGTGGCCTGGATCTGGGACGTGGTTCGGCGGAGCAGTCCCCAGCCCGGCCCTGCCTGGGACCACCAGGC
CCCCAGGAGAAGCCGCCTGAGCCACAACCTTGCGGCATGCAAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCG
TGGCTGGGCCCCACGGGAAGCCTGATGTTTCAGGGTTGGGGTGGGACGGGCAGCGGTGGGGCACACCCATTCCACA
TGCAAAGGGCAGAAGCAAACCCAGTAAAATGTAACTGACAAAAAAAAAAAAAAAAAAAAAGAAA

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FIGURE 272

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845
><subunit 1 of 1, 283 aa, 1 stop
><MW: 30350, pI: 9.66, NX(S/T): 2
MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAIIGGHEVTPHSRPYMASVRFGGQHHCGGFLLRARWVVSAAHC
FSHRDLRTGLVVLGAHVLSTAEP TQQVFGIDALTTHPDYHPMTHANDICLLRLNGSAVLGPAVGLLRPLPGRRARP
PTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPDVCNSSWKGHLLTMLCTRSGDSHRRGFCSADSGGPLVCR
NRAHGLVSFSGLWCGDPKTPDVYTQVSAFVAWIWDVVRSSPQPGPLPGTTRPPGEAA
```

Signal peptide:
amino acids 1-30

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FIGURE 273

GAAGTTCGCGAGCGCTGGCT**ATG**GGTCCTGGGGCGCGGCTGGCGGGCGCTGCTGGCGGTGCTGGCGCTCGGGACAG
GAGACCCAGAAAGGGCTGCGGCTCGGGGCGACACGTTCTCGGCGCTGACCAGCGTGGCGCGCGCCCTGGCGCCCC
AGCGCCGGCTGCTGGGGCTGCTGAGGCGGTACCTGCGCGGGGAGGAGGCGCGGCTGCGGGACCTGACTAGATTCT
ACGACAAGGTACTTTCTTTGCATGAGGATTCAACAACCCCTGTGGCTAACCCCTCTGCTTGCATTTACTCTCATCA
AACGCCTGCAGTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGGATG
GCTATGAGAAGGTGGAGCAAGACCTTCCAGCCTTTGAGGACCTTGAGGGAGCAGCAAGGGCCCTGATGCGGCTGC
AGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCCGAGGTGTCTTTAGAGAGTCACTGGCTCTGCCATCACTG
ACCTGTACAGCCCCAAACGGCTCTTTCTCTCACAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCTATGACA
TGGGGGATTATTACCATGCCATTCCATGGCTGGAGGAGGCTGTCAGTCTCTTCCGAGGATCTTACGGAGAGTGGA
AGACAGAGGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCCTTTGCTTATTTCCGGGCAGGAAATGTTT
CGTGTGCCCTCAGCCTCTCTCGGGAGTTTCTTCTCTACAGCCCAGATAATAAGAGGATGGCCAGGAATGTCTTGA
AATATGAAAGGCTCTTGGCAGAGAGCCCCAACCACGTGGTAGCTGAGGCTGTATCCAGAGGCCCAATATACCCC
ACCTGCAGACCAGAGACACCTACGAGGGGCTATGTGAGACCCTGGGTCCCAGCCCACCTCTCTACCAGATCCCTA
GCCTCTACTGTTCCCTATGAGACCAATFCCAACGCCTACCTGCTGCTCCAGCCCATCCGGAAGGAGGTCACTCCACC
TGGAGCCCTACATTGCTCTCTACCATGACTTCGTGAGTCACTGAGAGGCTCAGAAAATTAGAGAACTTGCAGAAC
CATGGCTACAGAGGTCAGTGGTGGCATCAGGGGAGAAGCAGTTACAAGTGGAGTACCGCATCAGCAAAAGTGCCT
GGCTGAAGGACACTGTTGACCCAAAAGTGGTGACCCTCAACCACCGCATTGCTGCCCTCACAGGCCTTGATGTCC
GGCCTCCCTATGCAGAGTATCTGCAGGTGGTGAAGTATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATG
CTACGTACCAAGCAGCCCCCTCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTTATGATCTATCTGAGCT
CGGTGGAAGCTGGAGGAGCCACAGCCTTCATCTATGCCAACCTCAGCGTGCCTGTGGTTAGGAATGCAGCACTGT
TTTGGTGAACCTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCATGCTGGCTGTCTGTCTGCTGGTGGGAG
ATAAGTGGGTGGCCAACAAGTGGATAACATGAGTATGGACAGGAATTCCGCAGACCCTGCAGCTCCAGCCCTGAAG
ACT**GGA**ACTGTTGGCAGAGAGAAGCTGGTGGAGTCTGTGGCTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGGTA
GGAGAGGAGAAAGCAGAGCAGCCTCCTGGAAGAAGGCCTTGTGAGCTTTGTCTGTGCCTCGCAAATCAGAGGCAA
GGGAGAGGTTGTTACCAGGGGACACTGAGAATGTACATTTGATCTGCCCCAGCCACGGAAGTCAGAGTAGGATGC
ACAGTACAAAGGAGGGGGGAGTGGAGGCCTGAGAGGGAAGTTTCTGGAGTTCAGATACTCTCTGTTGGGAACAGG
ACATCTCAACAGTCTCAGGTTGATCAGTGGGTCTTTTGGCACTTTGAACCTTGACCACAGGGACCAAGAAGTGG
CAATGAGGACACCTGCAGGAGGGGCTAGCCTGACTCCCAGAACTTTAAGACTTTCTCCCCACTGCCTTCTGCTGC
AGCCCCAAGCAGGGAGTGTCCCCCTCCCAGAAGCATATCCCAGATGAGTGGTACATTATATAAGGATTTTTTTTAA
GTTGAAAACAACCTTTCTTTTCTTTTGTATGATGGTTTTTTAACACAGTCATTAAAAATGTTTATAAATCAAAA

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FIGURE 274

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64849
><subunit 1 of 1, 544 aa, 1 stop
><MW: 61126, pI: 6.40, NX(S/T): 2
MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSVARALAPERRLGLLRRYLRGEEA
RLRDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLEASENIRALKDGY
EKVEQDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRVITGSAITDLYSPKRLFSIT
GDDCFQVGKVAIDMGDYYHAIPWLEEAVSLFRGSYGEWKTEDEASLEDALDHLAFAYFRA
GNVSCALSLSREFLLYSPDNKRMAENVLYKYLAEVSPNHVVAEAVIQRPNIPLQTRDT
YEGLCQTLGSOPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEA
QKIRELAEPWLQRSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRP
PYAEYLQVVNYGIGGHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSSEAGGATAFIY
ANLSVPVVRNAALFWWNLHRSGEGSDTLHAGCPVLVGDKWVANKWIEHYGQEFRPCSS
SPED
```

Important features of the protein:**Signal peptide:**

Amino acids 1-19

Leucine zipper pattern:

Amino acids 34-56;41-63

Ribonucleotide reductase small subunit signature:

Amino acids 340-356

N-glycosylation sites:

Amino acids 242-246;482-486

Cell attachment sequence:

Amino acids 27-30

Tyrosine kinase phosphorylation site:

Amino acids 189-198

N-myristoylation sites:Amino acids 4-10;135-141;153-159;164-170;241-247;303-309;309-315;
457-463;473-479

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FIGURE 275

GGCAACATGGCTCAGCAGGCTTGCCCCAGAGCCATGGCAAAGAATGGACTTGTAATTTGCATCCTGGTGATCACC
TTACTCCTGGACCAGACCAGCCACACATCCAGATTAAGGCCAGGAAGCACAGCAAACGTCGAGTGAGAGAC
AAGGATGGAGATCTGAAGACTCAAATTTGAAAAGCTCTGGACAGAAGTCAATGCCTTGAAGGAAATTCAGCCCTG
CAGACAGTCTGTCTCCGAGGCACTAAAGTTCACAAGAAATGCTACCTTGCTTCAGAAGGTTTGAAGCATTTCAT
GAGGCCAATGAAGACTGCATTTCAAAGGAGGAATCCTGGTTATCCCCAGGAACCTCCGACGAAATCAACGCCCTC
CAAGACTATGGTAAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGACATGGTCACGGAAGGC
AAGTTTGTGACGTCAACGGAATCGCTATCTCCTTCCTCAACTGGGACCGTGCACAGCCTAACGGTGGCAAGCGA
GAAACTGTGTCTCTCTCCCAATCAGCTCAGGGCAAGTGGAGTGATGAGGCCTGTGCGAGCAGCAAGAGATAC
ATATGCGAGTTCACCATCCCTAAATAGGTCTTTCTCCAATGTGTCTCCCAAGCAAGATTATCATAACTTATAGG
TTCATGATCTCTAAGATCAAGTAAAAATCATAATTTTACTTTATTAATAAATTTGCAACACAAGATCAATGTCCAT
AGCAATATGATAGCATCAGCCAATTTTGCTAACACATTTCTTTGGGATTTTGCCCTTCTGCGGGTATAGGGGATC
AGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCTGCTAAACAGACTAAAATCTTTCTCTCTAGTCTTTC
TCACTTGTAACAACCCAGTTTGTTCAAAAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTT
AGGCTACCTGAAAGATTTTCCCTTGGAAGTTTAGCGTATGTTTGACTAACAAAAATTCCTACATCAGAGACTCT
AGGTGCTATATAATCCAAAACTTTTCAGCCTGTTGCTCATTCTGTCCCATGCTGGCAATAATACCTTGTGAGCC
CATTACCCTTATTTTGAATTGCTCCATCTCCTGGTGGGACTTGATCTTGCTGCTGCCATATCAGAACACAAACCCC
TGAAGAGGTTCTGATTTGATTTTTTTTTTTCTTCATGCCTACCCTTTTTTTGGAAGTTTCCAGCCGCAATTTGA
AATGAAATGACAAGGTGTATATTTGATCAATTTTCATTCCACCATTGCATTACAACCTCTAACTTAAATGGGTA
ACCCTAAGGCATATCAAAGAAGCAGATTGCATGATAACGGAAATAGAAAAAAGAACCTACATTTATTTTGCTT
TAGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGACTTACATTTCTTTTACATTTTCGTATATTTAT
TTTTTTTAGCCATCATTATATGTTTAAGTCTATTATGGGCAACCAATCTTTGGAAGCTGAAAAGTGAATTTAAAG
AATGCTATCTTGGAATAATTCATACGTCTGTGCAATTTTTTATTCTGCCTAGTGCTATTCTGCTTGTTTAACTAG
ATTGTACAAAATAACTTCATTGCTTAATATCAAATTACAAAGTTTAGACTTGGAGGGAAATGGGCTTTTTAGAAG
CAAACAATTTTAAATATATTTTGTCTTCAAATAAATAGTGTAAACATTGAATGTGTTTTGTGAACAATATCC
CACTTTGCAAACTTTAACTACACATGCTTGGAATTAAGTTTTAGCTGTTTTCATTGCTCAATAATAAAGCCTGAA
TTCTGATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 276

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHRSKRRVRDKDGLKTQIEKLWTEVNALKEIQALQT
VCLRGTKVHKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQDYGKRSLPGVNDFWLGINDMVTEGKF
VDVNGIAISFLNWDRAQPNGGKRENCVLSQSAQGKWSDEACRSSKRYICEFTIPK

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FIGURE 277

GAGATAGGGAGTCTGGGTTTAAGTTCCTGCTCCATCTCAGGAGCCCCTGCTCCCACCCCTAGGAAGCCACCAGAC
TCCACGGTGTGGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCCACGAGCGCTGGCTGAGGGACCGAGCC
GGAGAGCCCCGGAGCCCCCGTAACCCGCGCGGGGAGCGCCAGGATGCGCGCGGGGACTCGGAGCAGGTGCGCT
ACTGCGCGCGCTTCTCCTACCTCTGGCTCAAGTTTTCACTTATCATCTATTCCACCGTGTCTGGCTGATTGGGG
CCCTGGTCTGTCTGTGGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCCCTTGAAAGTGCCTTCCTGG
CTCCAGCCATCATCCTCATCCTCCTGGGCGTCGTCATGTTTCATGGTCTCCTTCATTGGTGTGCTGGCGTCCCTCC
GTGACAACCTGTACCTTCTCCAAGCATTTCATGTACATCCTTGGGATCTGCCTCATCATGGAGCTCATTGGTGGCG
TGGTGGCCTTGACCTTCCGGAACCAGACCATTGACTTCCTGAACGACAACATTGGAAGAGGAATTGAGAACTACT
ATGATGATCTGGACTTCAAAAACATCATGGACTTTGTTCAAAAAAGTTCAAGTGCTGTGGCGGGGAGGACTACC
GAGATTGGAGCAAGAATCAGTACCACGACTGCAGTGCCCTGGACCCCTGGCCTGTGGGGTGCCCTACACCTGCT
GCATCAGGAACACGACAGAAGTTGTCAACACCATGTGTGGCTACAAAATATCGACAAGGAGCGTTTCAGTGTGC
AGGATGTCTCTACGTGCGGGGCTGCACCAACGCCGTGATCATCTGGTTCATGGACAACCTACACCATCATGGCGT
GCATCCTCCTGGGCATCCTGCTTCCCCAGTTCTTGGGGGTGCTGCTGACGCTGCTGTACATCACCAGGGTGGAGG
ACATCATCATGGAGCACTCTGTCACTGATGGGCTCCTGGGGCCCCGGTGCCAAGCCCAGCGTGGAGGCGGCAGGCA
CGGGATGCTGCTTGTGCTACCCCAATTAGGGCCCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTCTGGGATAGC
ACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGCCCCCTCTGCCCACACTCAGTACTGACCAAAGCCAGG
GCTGTGTGTGCCTGTGTGTAGTCCCACGGCCTCTGCCTCCCCAGGGAGCAGAGCCTGGGCCTCCCCTAAGAGGC
TTTCCCCGAGGCAGCTCTGGAATCTGTGCCCACCTGGGGCCTGGGGAAACAAGGCCCTCCTTTCTCCAGGCCTGGG
CTACAGGGGAGGGAGAGCCTGAGGCTCTGCTCAGGGCCCATTTTCATCTCTGGCAGTGCCTTGGCGGTGGTATTCA
AGGCAGTTTTGTAGCACCTGTAATTGGGGAGAGGGAGTGTGCCCCTCGGGGCAGGAGGGAAGGGCATCTGGGGAA
GGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCCATGGCCAGGTTGGCCTCTTCTCAGCCTCCCAGGTGCCTT
GAGCCCTCTTGCAAGGGCGGCTGCTTCTTGGCCCTAGTTTTTTTTTACGTGATTTTTGTAACATTCATTTTTTT
GTACAGATAACAGGAGTTTTCTGACTAATCAAAGCTGGTATTTCCCGCATGTCTTATTCTTGCCCTTCCCCAAC
CAGTTTGTTAATCAAACAATAAAAACATGTTTTGTTTTGTTTTAAAAA

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FIGURE 278

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863
><subunit 1 of 1, 294 aa, 1 stop
><MW: 33211, pI: 5.35, NX(S/T): 3
MPRGDSEQVRYCARFSYLWLKFSLLIIYSTVFWLIGALVLSVGIYAEVERQKYKTLES AFLAPAILILLGVVMFM
VSFIGVLASLRDONLYLLQAFMYILGICLIMELIGGVVALTFRNQTIDFLNDNIRRG IENYYDDLDFKNIMDFVQK
KFKCCGGEDYRDWSKNQYHDCSAPGPLACGVPYTCCIRNTTEVVNTMCGYKTIDKERFSVQDVIYVRGCTNAVII
WFMDNYTIMACILLGILLPQFLGVLLTLLYITRVEDIIMEHSVTDGLLGPGAKPSVEAAGTGCCLCYPN
```

Signal peptide:
amino acids 1-44

Transmembrane domains:
amino acids 22-42, 57-85, 93-116, 230-257

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FIGURE 279

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGACACCTGGGAAGAT
GGCCGGCCCGTGGACCTTCACCCCTTCTCTGTGGTTTGCTGGCAGCCACCTTGATCCAAGCCACCCCTCAGTCCCAC
TGCAGTTCTCATCCTCGGCCCAAAGTCATCAAAGAAAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAG
CATCCTGCAGCAGCTGCCGCTGCTCAGTGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCT
GGTGAACACCGTCCTGAAGCACATCATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAAGCC
CTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCAACACGCCCCCTGGTCAA
GACCATCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATCCGCATGGACACCAGTGCAAGTGGCCCCAC
CCGCTGGTCCCTCAGTGACTGTGCCACCAGCCATGGGAGCCTGCGCATCCAACCTGCTGTATAAGCTCTCCTTCCT
GGTGAACGCCCTTAGCTAAGCAGGTTCATGAACCTCCTAGTGCCATCCCTGCCCAATCTAGTAAAAACCAGCTGTG
TCCCGTGATCGAGGCTTCCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCATTTCCCTCAG
CATTGACCGTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCATTAGCTCTACCTGGGGGCCAA
GTTGTTGGACTCACAGGGAAAGGTGACCAAGTGGTTCAATAACTCTGCAGCTTCCCTGACAATGCCACCCTGGA
CAACATCCCGTTGAGCCTCATCGTGAGTCAGGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGA
ATTCATGGTCCCTGTTGGACTCTGTGCTTCCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGA
AAAGGCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCGAGTTTTTATAGA
CCAAGGCCATGCCAAGGTGGCCCAACTGATCCGTGCTGGAAGTGTTCCCTCCAGTGAAGCCCTCCGCCCTTTGTT
CACCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTTACACCAAAGGTGACCAACTTATACTCAACTGAATAA
CATCAGCTCTGATCGGATCCAGCTGATGAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCAT
CACTGAGATCATCCACTCCATCCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTATTGGT
GAAGGCCCTTGGGATTGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTTGTGCTTACTCCAGCCTCCTTGTG
GAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAGGGAAGGCTGGGTCCCAGCTGGGAGT
ATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAATCAATAAACACTTGCCCTGTGAAAAA

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FIGURE 280

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
><subunit 1 of 1, 484 aa, 1 stop
><MW: 52468, pI: 7.14, NX(S/T): 3
MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDNATSILOQLPLLSAMREKPAGGIPVLGS
LVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPLVKTIQEFHMTTEAQATIRMDTSASGP
TRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMNLLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISL
SIDRLEFDLLYPAIKGDITQLYLGAKLKLDLSDQGVTKWFNNSAASLTMPDLNIPFSLIVSQDVVKAAVAVALSPE
EFMVLLDSVLPESAHLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEALRPL
FTLGIEASSEAQFYTKGDQLILNLNINSSDRIQLMNSGIGWFQPDVLKNIITEIIHSILLPNQNGKLRSGVPVSL
VKALGFEEAAESSLTKDALVLTPLSLWKPSSPVSQ
```

Important features of the protein:**Signal peptide:**

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

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FIGURE 281

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCTTTCCCCGCGTTCT
CTTTCCACCTTTCTCTTCTTCCACCTTAGACCTCCCTTCCTGCCCTCCTTTCTTGCCACCGCTGCTTCCTGGC
CCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGGGGTCTGTGGGTGATCTGTGGCCCTGTGCCTCCGTGTC
CTTTTCGTCTCCCTTCCTCCCGACTCCGCTCCCGGACCAGCGGCCTGACCCTGGGGAAAGGATGGTTCCCGAGGT
GAGGGTCTCTCCTCCTTGCTGGGACTCGCGCTGCTCTGGTTCCCCCTGGACTCCACGCTCGAGCCCGCCGAGA
CATGTTCTGCCTTTTCCATGGGAAGAGATACTCCCCCGGCGAGAGCTGGCACCCCTACTTGGAGCCACAAGGCCT
GATGTACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGTTGTTACCGCCTCCACTGTCCGCCTGTCCA
CTGCCCCCAGCCTGTGACGGAGCCACAGCAATGCTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCG
GGCCCCACCAAAGTCTGCCAGCACAACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTT
CCCCCTCCCGCTGCCCAACCAAGTGTGTCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCACAACTG
CCCCGAACCAGGCTGCCCAGCACCCCTCCCACTGCCAGACTCCTGCTGCCAAGCCTGCAAAGATGAGGCAAGTGA
GCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTGAGACATCCTCAGGATCCATGTTCCAGTGATGC
TGGGAGAAAGAGAGGGCCCGGCGACCCAGCCCCACTGGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTT
CAGACCCAAGGGAGCAGGCAGCACAACCTGTCAAGATCGTCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGG
CGGGAAGACGTACTCCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCCCTTGCCTGCGATCCTATG
CACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCACCGAGTACCCCTGCCGTCACCCCGAGAA
AGTGGCTGGGAAGTGCTGCAAGATTGCCCAGAGGACAAAGCAGACCCTGGCCACAGTGAGATCAGTTCTACCAG
GTGTCCCAAGGCACCGGGCCGGGTCTCGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCTGCTTTGC
CCTGGAACACGAGGCCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAAACTGAGGCTCA
GAGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGAAAGTCAGGAAGC
AAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCACGAAGGTCACTGGAACGTCTTCTTAG
CCCAGACCCTGGAGCTGAAGGTCACGGCCAGTCCAGACAAAGTGACCAAGACATAACAAAGACCTAAACAGTTGCA
GATATGAGCTGTATAATTGTTGTTATTATATATTAATAAATAAGAAGTTGCATTACCCCTCAAAAAAAAAAAAAA
AAAAAA

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FIGURE 282

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902
><subunit 1 of 1, 451 aa, 1 stop
><MW: 49675, pI: 7.15, NX(S/T): 1
MVPEVRVLSSLLGLALLWFPLDSHARARPD MFCLFHGKRYSPGESWHPYLEPQGLMYCLRCTCSEGAHVSCYRLH
CPPVHCPQPVTEPQQCCPKC VEPHTPSGLRAPPKSCQHNGTMYQHGEIFSAHELFPSRLPNQCVLCSCTEGQIYC
GLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEEDSVQSLHGVRHPQDPCSSDAGRKRGP GTPAPTGLSAPLSF
IPRHFRPKGAGSTTVKIVLKEKHKKACVHGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPT EYPC
RHPEKVAGKCKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIY LWKLVKDE
ETEAQRGEVPGPRPHSQNLPLDSDQESQEARLPERG TALPTARWP PRRSLERLPSPDPGAEGHGQSRQSDQDITKT
```

Signal peptide:
amino acids 1-25

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FIGURE 283

GCGATGGTGC GCCCGGTGGCGGTGGCGGCGGCGGTTGCGGAGGCTTCCTTGGTGGGATTGCAACGAGGAGAAGAT
GACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGCGCCATGAGGAGCCTGCCGAGCCTGGGCG
GCCTCGCCCTGTTGTGCTGCGCCGCCGCCGCCGCCGCCGCTCGCCTCAGCCGCCCTCGGCGGGGAATGTCACCGGTG
GCGGCGGGGCGCGGGGCGAGGTGGACGCGTCGCCGGGCCCCGGGTTGCGGGGCGAGCCAGCCACCCCTTCCCTA
GGGCGAGGCTCCACGGCCAGGCCCCGAGGACCGGGCCCCGCGCGCCACCGTCCACCGACCCCTGGCTGCGA
CTTCTCCAGCCAGTCCCCGGAGACCACCCCTCTTTGGGCGACTGCTGGACCCTCTTCCACCACCTTTAGGGCGC
CGCTCGGCCCTCGCCGACCACCCCTCGGCGGGCGGAACGCACTTCGACCACCTCTCAGGCGCCGACCAGACCCG
CGCCGACCACCCCTTCGACGACCACTGGCCCGGCGCCGACCACCCCTGTAGCGACCACCGTACCGGCGCCACGA
CTCCCCGACCCCGACCCCGATCTCCCCAGCAGCAGCAACAGCAGCGTCCTCCCCACCCACCTGCCACCGAGG
CCCCCTCTTCGCTCCTCCAGAGTATGTATGTAAGTCTGTGGTTGGAAGCCTGAATGTGAATCGCTGCAACC
AGACCACAGGGCAGTGTGAGTGTGCGCCAGGTTATCAGGGGCTTCACTGTGAAACCTGCAAGAGGGCTTTTACC
TAAATTACACTTCTGGGCTCTGTGAGCATGTGACTGTAGTCCACATGGAGCTCTCAGCATACCGTGCAACAGGT
AAGCAACAGAGGGTGGAACTGAAGTTTATTTATTTTAGCAAGGGGAAAAAAAAAAGGCTGCTACTCTCAAGGACCA
TACTGGTTTAAACAAAGGAGGATGAGGGTCATAGATTTACAAAATATTTTATATACTTTTATTCTCTACTTTAT
ATGTTATATTTAATGTCAGGATTTAAAAACATCTAATTTACTGATTTAGTTCTTCAAAGCACTAGAGTCGCCAA
TTTTTCTCTGGGATAATTTCTGTAAATTTTCATGGGAAAAAATTATTGAAGAATAAATCTGCTTCTGGAAGGGCT
TTCAGGCATGAAACCTGCTAGGAGGTTTAGAAATGTTCTTATGTTTATTAATATACCATTGGAGTTTGAGGAAAT
TTGTTGTTTGGTTTATTTTCTCTCTAATCAAAATCTACATTTGTTTCTTTGGACATCTAAAGCTTAACCTGGG
GGTACCCTAATTTATTTAACTAGTGGTAAGTAGACTGGTTTACTCTATTTACCAGTACATTTTGGAGACCAAAA
GTAGATTAAGCAGGAATTATCTTTAACTATTATGTTATTTGGAGGTAATTTAATCTAGTGAATAATGTACTGT
TATCTAAGCATTTGCCTTGACTGCACTGAAAGTAATTATTCTTTGACCTTATGTGAGGCACCTGGCTTTTTGTG
GACCCCAAGTCAAAAACTGAAGAGACAGTATTAAATAATGAAAAAATAATGACAGGTTATACTCAGTGTAAAC
TGGGTATAACCCAAGATCTGCTGCCACTTACGAGCTGTGTTCCCTTGGGCAAGTAATTTCTTTCACTGAGCTTGT
TTCTTCTCAAGGTTGTTGTGAAGATTAAATGAGTTGATATATATAAAATGCCTAGCACATGTCACTCAATAAATT
CTGTTTTGTTTTAATTTCAAAGGAATATTATGGAAGTGAATGAGAGAACATGTTTTAAGAACTTTTAGCTCCTTG
ACAAAGAAGTGCTTTTATACTTTAGCACTAAATATTTTAAATGCTTTATAAATGATATTATACTGTTATGGAATAT
TGTATCATATTGTAGTTTATTTAAAAATGTAGAAGAGGCTGGGCGCGGTGGCTCACGCCTGTAATCCTAGCACTTT
GGGAGGCCAAGGCGGTGGATCACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAAACCCCGTCT
CTACTAAAAATACAAACAAATTAGCTGGGCGTGGTGGCACACACCTGTAGTCCCAGCTACTCGGGAGGCTGAGGC
AGGAGAATCGGTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCTGAGATCGCGCCACTGCACTCCAGCCTGGTGAG
AGAGGGGAGACTCTGTCTTAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 284

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRS LPS LGG LALLCCAAAAA VASAASAGNVTGGGGAAGQVDASPGPGLRGEPSHFFPRATAPTAQAPRTGPPRA
TVHRPLAATSPAQSPETTP L WATAGPSSTTFQAPLGPSPTTPPAERTSTTSQAPTRPAPTTLSTTTGPAPTTPV
ATTVPAPTTPTPTPDLPSSSNSSVLPTPPATEAPSSPPPEYVCNCSVVGSLNVNRCNQTTGQCECRPGYQGLHC
ETCKEGFYLN YTSGLCQPCDCSPHGALSIPCNR
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.

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FIGURE 285

AACACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCACAGACATGCTGCTGCTGCTGCTGCCCTGCTCTGGGGG
AGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTTCGGTGACGGTGCAGGAAGGCTGTGT
GTCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCATGGCTGGATTTACCTTGGCCAGTAGTTTCATGGCTACTGG
TTCCGGGAAGGGGCCAATACAGACCAGGATGCTCCAGTGGCCACAAACACCCAGCTCGGGCAGTGTGGAGGAG
ACTCGGAGCCGATTCCACCTCCTTGGGGACCCACATACCAAGAAATTGCACCTGAGCATCAGAGATGCCAGAAGA
AGTGATGCGGGGAGATCACTTCTTTCTGATGGAGAAAGGAAGTATAAAATGGAATTATAAACATCACCGGCTCTCT
GTGAATGTGACAGCCTTGACCCACAGGCCAACATCCTCATCCAGGCACCCTGGAGTCCGGCTGCCCCAGAAT
CTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAGGGGACACCCCTATGATCTCCTGGATAGGGACCTCCGTGTCC
CCCCTGGACCCCTCCACCACCCGCTCCTCGGTGCTCACCTCTCATCCCACAGCCCCAGGACCATGGCACAGCCCT
ACCTGTCAGGTGACCTTCCCTGGGGCCAGCGTGACCAGAACAGACCGTCCATCTCAACGTGTCCTACCGGCTC
CAGAACTTGACCATGACTGTCTTCCAAGGAGCAGGCACAGTATCCACAGTCTTGGGAAATGGCTCATCTCTGTCA
CTCCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAGTTGATGCAGTTGACAGCAATCCCCCTGCCAGGCTGAGC
CTGAGCTGGAGAGGCCTGACCCTGTGCCCTCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCTTGGGTGCAC
CTGAGGGATGCAGCTGAATTCACCTGCAGAGCTCAGAACCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCC
CTGCAGAGCAAAAGCCACATCAGGAGTGACTCAGGGGTGGTTCGGGGGAGCTGGAGCCACAGCCCTGGTCTTCTGT
TCTTCTCGCTCATCTTCTGTTAGTGAGGTCCTGCAGGAAGAAATCGGCAAGGCCAGCAGCGGGCTGGGAGAT
ACGGGATAGAGGATGCAAAAGCCTGTGAGGGGTTAGCCCTCTCAGGGGCCCTGACTGAACCTTGGGCAGAAGAC
AGTCCCCCAGACCAGCCTCCCCAGCTTCTGCCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTC
AGCTTCCAGATGGTGAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATC
CACAGATGAGAAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCCTCCAGGCAAGGGAGAAGTCAGAGGC
TGATTCTTGTAGAATTAAACAGCCCTCAACGTGATGAGCTATGATAACACTATGAATTATGTGCAGAGTGAAAGC
ACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAATCCACACTGTGCCCTCCCTTTATTTTTTAACTAAAG
ACAGACAAATTCCTTA

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FIGURE 286

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSPSHGWIYPGPVVHGYWFREGANTDQDAPVA
TNNPARAVWEETRDRFHLGDPHTKNCTLSIRDARRSDAGRYFFRMEKGSIKWNYKHHRLSVNVTALHTRPNILI
PGTLESGCPQNLTCSPWACEQGTTPMISWIGTSVSPLDPSTTRSSVLTLPQPQDHGTS LTCQVTFFGASVTTN
KTVHLNVSYPQNLTMTVFQGDGTVSTVLGNGSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPS
NPGVLELPWVHLRDAAEFTCRAQNPLGSQQVYLNVSLSQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRSCRK
KSARPAAGVGDTGIEDANAVRGSASQGPLEPWAEDSPPDQPPPASARSSVGEGELQYASLSFQMKPWDSRGQE
ATDTEYSEIKIHR

Signal peptide:
amino acids 1-15

Transmembrane domain:
amino acids 351-370

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FIGURE 287

CGCGAGCTGAGAGGAGCAGGTAGAGGGGCAGAGGCGGGACTGTCTGCTGGGGGAGCCGCCAGGAGGCTCCTCAG
GCCGACCCACAGACCTGGCTGGCCAGGATGAAGTATCTCCGGCACCCGGCGGCCCAATGCCACCCCTCATTTGCGCC
ATCGGCGCTTTACCCCTCCTCCTCTTCAGTCTGCTAGTGTACCAACCCACCTGCAAGGTCCAGGAGCAGCCACCG
GCGATCCCCGAGGCCCTGGCCTGGCCCACTCCACCCACCCGCCAGCCCCGGCCCCGTGCCATGCCAACACCTCT
ATGGTCACCCACCCGGACTTCGCCACGCAGCCGCAGCACGTTCAAGAACTTCCTCCTGTACAGACACTGCCGCCAC
TTTCCCCTGCTGCAGGACGTGCCCCCTCTAAGTGCAGCGCAGCCGGTCTTCCTGCTGCTGGTGATCAAGTCTCTCC
CCTAGCAACTATGTGCGCCGCGAGCTGCTGCGGCGCACGTGGGGCCGCGAGCGCAAGGTACGGGGTTTGCAGCTG
CGCCTCCTCTTCTGGTGGGCACAGCCTCCAACCCGCACGAGGCCCGCAAGGTCAACCGGTGCTGGAGCTGGAG
GCACAGACTCACGGAGACATCCTGCAGTGGGACTTCCACGACTCCTTCTTCAACCTCACGCTCAAGCAGGTCTCTG
TTCTTACAGTGGCAGGAGACAAGGTGCGCCAACGCCAGCTTCGTGCTCAACGGGGATGATGACGTCTTTGCACAC
ACAGACAACATGGTCTTCTACCTGCAGGACCATGACCCTGGCCGCCACCTCTTCGTGGGGCAACTGATCCAAAC
GTGGGGCCCCATCCGGGCTTTTTGGAGCAAGTACTATGTGCCAGAGGTGGTGAAGTCAAGCGGTACCCACCC
TATTGTGGGGGTGGTGGCTTCTTGCTGTCCCGCTTACGGCCGCTGCCCTGCGCCGTGCTGCCCATGTCTTGGAC
ATCTTCCCCATTGATGATGTCTTCTGGGTATGTGTCTGGAGCTTGAGGGACTGAAGCCTGCCTCCCACAGCGGC
ATCCGCACGTCTGGCGTGCGGGCTCCATCGCAACACCTGTCTCCTTTGACCCCTGCTTCTACCGAGACCTGCTG
CTGGTGCACCGCTTCTTACCTTATGAGATGCTGCTCATGTGGGATGCGCTGAACAGCCCAACCTCACCTGCGGC
AATCAGACACAGATCTACTGAGTCAGCATCAGGGTCCCCAGCCTCTGGGCTCCTGTTTCCATAGGAAGGGGCGAC
ACCTTCTCTCCAGGAAGCTGAGACCTTTGTGGTCTGAGCATAAGGGAGTGCCAGGGAAGGTTTGAGGTTTGATGA
GTGAATATTCTGGCTGGCGAACTCCTACACATCCTTCAAAACCCACCTGGTACTGTTCCAGCATCTTCCCTGGAT
GGCTGGAGGAACTCCAGAAAATATCCATCTTCTTTTGTGGCTGCTAATGGCAGAAGTGCCTGTGCTAGAGTTCC
AACTGTGGATGCATCCGTCCCGTTTGAGTCAAAGTCTTACTTCCCTGCTCTCACCTACTCACAGACGGGATGCTA
AGCAGTGCACCTGCAGTGGTTAATGGCAGATAAGCTCCGTCTGCAGTTCAGGCCAGCCAGAACTCCTGTGTC
CACATAGAGCTGACGTGAGAAATATCTTTCAGCCAGGAGAGAGGGGTCTGATCTTAACCCCTTCTGGGTCTC
AGACAACCTCAGAAGGTTGGGGGGATACCAGAGAGGTGGTGGAAATAGGACCGCCCCCTCCTTACTTGTGGGATCAA
ATGCTGTAATGGTGGAGGTGTGGGCAGAGGAGGGAGGCAAGTGTCTTTGAAAGTTGTGAGAGCTCAGAGTTTCTG
GGGTCTCATTAGGAGCCCCCATCCCTGTGTTCCCCAAGAATTAGAGAACAGCACTGGGGCTGGAATGATCTTT
AATGGGCCCAAGGCCAACAGGCATATGCCTCACTACTGCCTGGAGAAGGGAGAGATTAGGTCTCCAGCAGCCT
CCCTCACCCAGTATGTTTTACAGATTACGGGGGACCGGGTGAGCCAGTGACCCCTGCAGCCCCCAGCTTCAGG
CCTCAGTGTCTGCCAGTCAAGCTTCACAGGCATTGTGATGGGGCAGCCTTGGGGAATATAAAATTTTGTGAAGAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 288

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65413

<subunit 1 of 1, 372 aa, 1 stop

<MW: 42515, pI: 8.92, NX(S/T): 6

MKYLRHRRPNATLILAIGAFILLFSLLVSPPTCKVQEQPPAIPALAWPTPPTRPAPAPCHANTSMVTHPDFAT
QPQHVQNFLLYRHCRRHFLLQDVPPSKCAQPVFLLLVIKSSPSNYVRRELLRRTWGREKVRGLQLRLLFLVGTA
SNPHEARKVNRLLLELEAQTHGDILQWDFHDSFFNLTLKQVLFQWQETRCANASFVLNGDDDVFAHTDNMVFYLQ
DHDPGRHLEFVGQLIQNVGPIRAFWISKYYVPEVVTQNERYPYCGGGGFLLSRFTAAALRRAHVLDIFPIDDVFL
GMCLELEGLKPASHSGIRTSGVRAPSQHLSSFDPCFYRDLLLVRFLPYEMLLMWDALNQPNLTCGNQTQIY

Important features:**Type II transmembrane domain:**

Amino acids 15-34

N-glycosylation sites:

Amino acids 10-14;64-68;184-188;202-206;362-366;367-371

TonB-dependent receptor proteins signature 1:

Amino acids 1-32

N-myristoylation sites:

Amino acids 308-314;316-322

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FIGURE 289A

CGCGCTCCCCGCGCGCCTCCTCGGGCTCCACGCGTCTTGCCCCGAGAGGCAGCCTCCTCCAGGAGCGGGGCCCT
GCACACCAATGCCCCCGGGTGGGCAGGGGTGCGCGCCGCCGTGCGCGCCCGCCTGGCGCTGGCCTTGGCGCTGGC
GAGCGTCTGAGTGGGCCCTCCAGCCGTGCGCTGCCCCACCAAGTGACCTGCTCCGCTGCCAGCGTGGACTGCCA
CGGGCTGGGCCCTCCGCGCGGTTCCTCGGGGCATCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATAATAT
CACCAGGATCACCAGATGGACTTCGCTGGGGCTCAAGAACCTCCGAGTCTTGCACTCTGGAAGACAACCAGGTCAG
CGTCATCGAGAGAGGCGCCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCCTGAACAAGAATAAGCTGCAAGT
CCTTCCAGAATTGCTTTTCCAGAGCACGCCGAAGCTCACCAGACTAGATTTGAGTGAAAACCAGATCCAGGGGAT
CCCGAGGAAGGCGTTCGCGCGCATCACCAGTGTGAAGAACCTGCAACTGGACAACAACCACATCAGCTGCATTGA
AGATGGAGCCTTCCGAGCGCTGCGCGATTTGGAGATCCTTACCCTCAACAACAACAACATCAGTCGCATCCTGGT
CACCAGCTTCAACCACATGCCGAAGATCCGAACCTCTGCGCCTCCACTCCAACCACCTCTACTGCGACTGCCACCT
GGCCTGGCTCTCGGATTGGCTGCGACAGCGACGGACAGTTGGCCAGTTCACACTCTGCATGGCTCCTGTGCATTT
GAGGGGCTTCAACGTGGCGGATGTGCAAGAAGGAGTACGTGTGCCAGCCCCCACTCGGAGCCCCCATCCTG
CAATGCCAACTCCATCTCCTGCCCTTCGCCCTGCACTGTCAGCAATAACATCGTGGACTGTGAGGAAAGGGCTT
GATGGAGATTCTGCCAACTTGCCTGAGGGGCATCGTCGAAATACGCCCTAGAACAAGAACTCCATCAAAGCCATCCC
TGCAGGAGCCTTACCCAGTACAAGAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCGGATATTGCTCC
AGATGCCTTCCAGGGCCTGAAATCACTCACATCGCTGGTCTGTATGGGAACAAGATCACCAGATTGCCAAGGG
ACTGTTTGATGGGCTGGTGTCCCTACAGCTGCTCCTCCTCAATGCCAACAAGATCAACTGCCTGCGGGTGAACAC
GTTTCAGGACCTGCAGAACCTCAACTTGCTCTCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGGCTCTT
CGCCCCCTCTGCAGTCCATCCAGACACTCCACTTAGCCCCAAAACCCATTTGTGTGCGACTGCCACTTGAAGTGGCT
GGCCGACTACCTCCAGGACAACCCCATCGAGACAAGCGGGGCCCGCTGCAGCAGCCCCGCGCCGACTCGCCAACAA
GCGCATCAGCCAGATCAAGAGCAAGAAGTTCGCTGCTCAGGCTCCGAGGATTACCGCAGCAGGTTTCCAGCAGCA
GTGCTTCATGGACCTCGTGTGCCCCGAGAAGTGTGCTGTGAGGGCAGGATTGTGGACTGCTCCAACCAGAAGCT
GGTCCGCATCCCAAGCCACCTCCCTGAATATGTACCGACCTGCGACTGAATGACAATGAGGTATCTGTCTTGGA
GGCCACTGGCATCTTCAAGAAGTTGCCAACCTGCGGAAAATAAATCTGAGTAACAATAAGATCAAGGAGGTGCG
AGAGGGAGCTTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACCAGCTGGAGACCGTGCACGG
GCGCGTGTTCGCTGGCCTCAGTGGCCTCAAAACCTTGATGCTGAGGAGTAACTTGATCAGCTGTGTGAGTAATGA
CACCTTTGCGCGCCTGAGTTCGGTGAGACTGCTGTCCCTCTATGACAATCGGATCACCACCATCACCCCTGGGGC
CTTACCACGCTTGTCTCCCTGTCCACCATAAACCTCCTGTCCAACCCCTTCAACTGCAACTGCCACCTGGCCTG
GCTCGGCAAGTGGTTGAGGAAGAGGCGGATCGTCAGTGGGAACCCCTAGGTGCCAGAAGCCATTTTTCCTCAAGGA
GATTTCCATCCAGGATGTGGCCATCCAGGACTTACCTGTGATGGCAACGAGGAGAGTAGCTGCCAGCTGAGCCC
GCGCTGCCCCGAGCAGTGCACCTGTATGGAGACAGTGGTGCATGCAGCAACAAGGGGCTCCGCGCCCTCCCCAG
AGGCATGCCCAAGGATGTGACCGAGCTGTACCTGGAAGGAAACACCTAACAGCCGTGCCAGAGAGCTGTCCGC
CCTCCGACACCTGACGCTTATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCACTAACAT
GTCTCACCTCTCCACTCTGATCCTGAGCTACAACCGGCTGAGGTGCATCCCCGTCCACGCCCTTCAACGGGCTGCG
GTCCCTGCGAGTGCTAACCTCCATGGCAATGACATTTCCAGCGTTCTTGAAGGCTCCTTCAACGACCTCACATC
TCTTTCCCATCTGGCGCTGGGAACCAACCCACTCCACTGTGACTGCAGTCTTCCGGTGGCTGTGCGAGTGGGTGAA
GGCGGGGTACAAGGAGCCTGGCATCGCCGCTGCAGTAGCCCTGAGCCCATGGCTGACAGGCTCCTGCTCACCAC
CCCAACCCACCGCTTCCAGTGCAAAGGGCCAGTGGACATCAACATTGTGGCCAAATGCAATGCCTGCCTCTCCAG
CCCGTGCAAGAATAACGGGACATGCACCCAGGACCCTGTGGAGCTGTACCGCTGTGCTGCCCC

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FIGURE 289B

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCCTGTCAGCATGGAGGCACC
TGCCACCTGAGTGACAGCCACAAGGATGGGTTCAGCTGCTCCTGCCCTCTGGGCTTTGAGGGGCAGCGGTGTGAG
ATCAACCCAGATGACTGTGAGGACAACGACTGCGAAAACAATGCCACCTGCGTGGACGGGATCAACAACCTACGTG
TGTATCTGTCCGCCTAACTACACAGGTGAGCTATGCGACGAGGTGATTGACCACTGTGTGCCTGAGCTGAACCTC
TGTCAGCATGAGGCCAAGTGCATCCCCCTGGACAAAGGATTGAGCTGCGAGTGTGTCCCTGGCTACAGCGGGAAG
CTCTGTGAGACAGACAATGATGACTGTGTGGCCCAAGTGCCGCCACGGGGCCAGTGCGTGGACACAATCAAT
GGCTACACATGCACCTGCCCCAGGGCTTCAGTGGACCTTCTGTGAACACCCCCACCCATGGTCTTACTGCAG
ACCAGCCCATGCGACCAAGTACGAGTGCCAGAACGGGGCCAGTGATCGTGGTGCAGCAGGAGCCCACCTGCCGC
TGCCCCACAGGCTTCGCCGGCCCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGGCAAAGACTCCTACGTG
GAACTGGCCTCCGCCAAGGTCCGACCCAGGCCAACATCTCCCTGCAGGTGGCCACTGACAAGGACAACGGCATC
CTTCTCTACAAAGGAGACAATGACCCCCCTGGCACTGGAGCTGTACCAGGGCCACGTGCGGGCTGGTCTATGACAGC
CTGAGTTCCCTCCAACCACAGTGTACAGTGTGGAGACAGTGAATGATGGGCAGTTTACAGTGTGGAGCTGGTG
ACGCTAAACCAGACCCTGAACCTAGTAGTGACAAAGGAACTCCAAAGAGCCTGGGGAAGCTCCAGAAGCAGCCA
GCAGTGGGCATCAACAGCCCCCTCTACCTTGGAGGCATCCCCACCTCCACCGGCCTCTCCGCCTTGCGCCAGGGC
ACGGACCGGCCTCTAGGCGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACGAGCTGCAGGACTTCAAG
GCCCTCCCACCACAGTCCCTGGGGGTGTCAACAGGCTGCAAGTCTGCACCGTGTGCAAGCACGGCCTGTGCCGC
TCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCAGGCTGGACCGGCCCACTCTGCGACCAAGGAGGCCCGG
GACCCCTGCCTCGGCCACAGATGCCACCATGGAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCC
GAGGGCTATGGAGGGGACTTGTGTGACAACAAGAATGACTCTGCCAATGCCTGCTCAGCCTTCAAGTGTCAACAT
GGGCAGTGCCACATCTCAGACCAAGGGGAGCCCTACTGCCTGTGCCAGCCCGGCTTTAGCGGCGAGCACTGCCAA
CAAGAGAATCCGTGCCTGGGACAAGTAGTCCGAGAGGTGATCCGCCGCCAGAAAGGTTATGCATCATGTGCCACA
GCCTCCAAGGTGCCCATCATGGAATGTGCTGGGGGCTGTGGGCCCCAGTGCTGCCAGCCCACCCGAGCAAGCGG
CGGAAATACGTCTTCCAGTGCACGGACGGCTCCTCGTTTGTAGAAGAGGTGGAGAGACACTTAGAGTGC GGCTGC
CTCGCGTGTTC**TAA**GGCCCTGCCCGCCTGCCTGCCACCTCTCGGACTCCAGCTTGATGGAGTTGGGACAGCCAT
GTGGGACCCCCTGGTGATTGAGCATGAAGGAAATGAAGCTGGAGAGGAAGGTAAAGAAGAAGAGAATATTAAAGTA
TATTGTAAATAAACAAAAATAGAACTTAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 290

MAPGWAGVGA AVRRLALALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPRNAERLDLDRNNITR
ITKMDFAGLKNLRVLHLEDNQVSVIERGAFQDLKQLERLRNLNKNKLQVLPELLFQSTPKLTRLDLSENQIQGIPR
KA FRGITDVKNLQLDNNHISCIEDGA FRALRDLEILTNNNNNISRLVTSFNHMPKIRTLRLHSNHLYCDCHLAW
LSDWLRQRRTVGQFTLCMAPVHLRGFNVADVQKKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLME
IPANLPEGIVEIRLEQNSIKAIPAGFTQYKKLKRIDISKNQISDIAPDAFQGLKSLTSLVLYGNKITEIAKGLF
DGLVSLQLLLLNANKINCLRVNTFQDLQNLNLLSLYDNKLQTTISKGLFAPLQSIQTLHLAQNPFFVCDCHLKWLD
YLQDNPIETSGARCSSPRRLANKRISQIKSKKFRCSGSEDIRSRFSSECFMDLVCPEKCRCEGTIVDCSNQKLVR
IPSHLPEYVTDLRLNDNEVSVLEATGIFKKLPNLRKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRV
FRGLSGLKTLMLRSNLISCVSNDTFAGLSSVRLLSLYDNRIITITPGAFTTLVSLSTINLLSNPFNCNCHLAWLG
KWLRKRRIVSGNPRCQKPFLLKEIPIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCMETVVRC SNKGLRALPRGM
PKDVTELYLEGNHILTAVPRELSALRHLLTIDLSNNSISMLTNYTFSNMSHLSTLILSYNRLRCIPVHAFNGLRSL
RVLTLLHGNDISSVPEGSFNDLTSLSHLALGTNPLHCDCSLRWLSEWVKAGYKEPGIARCSSPEPMADRLLLTPT
HRFQCKGPVDINIVAKCNACLSSPCKNNGTCTQDPVELYRCACPYSYKGKDCVTPINTCIQNPCQHGGETCHLSDS
HKDGFSCSCPLGFEGQRCEINPDDCEDNDCENNATCVDGINNYVCICPPNYTGELCDEVIDHCVPENLNCQHEAK
CIPLDKGFSCCECVPGYSGKLCETDNDDCVAHKCRHGAQCVDITINGYTCTCPQGFGPFCEHPPPMVLLQTSPCDQ
YECQNGAQCIIVVQOEPTCRCPPGFAGPRCEKLITVNFVGKDSYVELASAKVRPQANISLQVATDKDNGILLYKGD
NDPLALELYQGHVRLVYDSLSSPPTTVYSVETVNDGQFHSVELVTLNQTNLNVVDKGT PKSLGKLQKQPAVGINS
PLYLGGIPTSTGLSALRQGTDRPLGGFHGCIHEVRINNELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDS
VVCECRPGWTGPLCDQEARDPCLGHRCHHGKCVATGTSYMCKCAEGYGGDLCDNKND SANACSAFKCHHGQCHIS
DQGEPLYCLCQPGFSGEHCQQENPCLGQVVREVIRROKGYASCATASKVPTIMECRGGCGPQCCQPTRSKRRKYVFQ
CTDGSSFEVEVERHLECGCLACS

Signal peptide:

amino acids 1-27

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FIGURE 291

GGATGCAGGACGCTCCCCTGAGCTGCCTGTCACCGACTAGGTGGAGCAGTGTTTCTTCCGCAGACTCAACTGAGA
AGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTTTCAGTTCTGTCTCCGGCAGGCTTTGAGGATGAAGGCTG
CGGGCATTCTGACCCTCATTGGCTGCCTGGTCACAGGCGCCGAGTCCAAAATCTACACTCGTTGCAAACCTGGCAA
AAATATTCTCGAGGGCTGGCCTGGACAATTACTGGGGCTTCAGCCTTGAAACTGGATCTGCATGGCATATTATG
AGAGCGGCTACAACACCACAGCCCCGACGGTCCTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCAACA
GCTTCGCGTGGTGACGACGCGGAAAGCTGAAGGAGAACAACCACTGCCATGTGCCTGCTCAGCCTTGATCACTG
ATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGAGACACAAGGAATGAATATTGGCAAGGCT
GGAAGAAACATTGTGAGGGCAGAGACCTGTCCGAGTGGAAAAAGGCTGTGAGGTTTCCTAAACTGGAACCTGGAC
CCAGGATGCTTTGCAGCAACGCCCTAGGATTTGCAGTGAATGTCCAAATGCCTGTGTCTATCTTGTCCCGTTTCCT
CCCAATATTCCTTCTCAAACCTGGAGAGGGGAAAATTAAGCTATACTTTTAAAGAAATAAATATTCCATTTAAATGTC

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FIGURE 292

MKAAGILTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAPTVLDDGSIDYGIF
QINSAWCRRGKLENNHCHVACSALITDDLTDALICARKIVKETQGMNYWQGWKKHCEGRDLSEWKKGCEVS

Signal peptide:
amino acids 1-19

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FIGURE 293

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTGTACCCAAGGAAAG
TGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCCTGCTGTTTCTCATAGCGACCACCAGAGGA
TGGAGTACAGATGAGGCTAATACTTACTTCAAGGAATGGACCTGTTCTTCGTCTCCATCTCTGCCCAGAAGCTGC
AAGGAAATCAAAGACGAATGTCCTAGTGCATTTGATGGCCTGTATTTTCTCCGCACTGAGAATGGTGTTATCTAC
CAGACCTTCTGTGACATGACCTCTGGGGGTGGCGGCTGGACCCCTGGTGGCCAGCGTGCATGAGAATGACATGCGT
GGGAAGTGCACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCCAGAGGGGGACGGCAAC
TGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCGATGACTACAAGAACCCTGGCTACTACGAC
ATCCAGGCCAAGGACCTGGGCATCTGGCACGTGCCCCAATAAGTCCCCCATGCAGCACTGGAGAAACAGCTCCCTG
CTGAGGTACCGCACGGACACTGGCTTCCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCA
GTGAAATATGGAGAAGGAAAGTGTGGACTGACAACGGCCCGGTGATCCCTGTGGTCTATGATTTTGGCGACGCC
CAGAAAACAGCATCTTATTACTCACCCATGAGCCAGCGGGAATTCAGTGCAGGATTTGTTTCTAGTTTCTAGGTTATTT
AATAACGAGAGAGCAGCCAAACGCCTTGTGTGCTGGAATGAGGGTCACCGGATGTAACACTGAGCATCACTGCATT
GGTGGAGGAGGATACTTTCCAGAGGCCAGTCCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATAT
GGAATCATGTTGGTTACAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGTTGAGAGTTT
TGTGGGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAACAACTTACCCAGTAGCTAGA
ATGTTAATGGCAGAAGAGAAAACAATAAATCATATTGACTCAAGAAAAAAA

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FIGURE 294

MNQLSFLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTENGVIYQTFCDMTSG
GGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFGSAEAATSDDYKNPGYYDIQAKDLGIW
HVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGIYQKYPVKYGEKGCWTDNGPVIIPVVYDFGDAQKTASYSP
YQOREFTAGFVQFRVFNNERAANALCAGMRVTGCNTEHHCIGGGGYFPEASFPQCGDFSGFDWSGYGTHVGYSS
REITEAAVLLFYR

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FIGURE 295

CAGGCCATTTGCATCCCCTGTCCTTGTGTTTCGGAGCCAGGCCACACCGTCCTCAGCAGTGTGCATGTGTTAAAAA
CGCCAAGCTGAATATATC**ATG**CCCCCTATTAAAACTTGTACATGGCTCCCCATTGGTTTTTGGAGAAAAGTTC AAG
CTTTTACCTTGGTGTCTGCCTGTATCCCAGTGTTCAGGCTGGCTAGACGGCGGAAGAAGATCCTATTTTACTGT
CACTTCCCAGATCTGCTTCTCACCAAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATA
GAGGAATACACCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTCACAGCTGCTGTTTTTAAAGGAAACA
TTCAAGTCCCTGTCTCACATAGACCCCTGATGTCTCTATCCATCTCTAAATGTCACCAGCTTTGACTCAGTTGTT
CCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCTGTGCTCTCCATCAACAGATACGAAAGGAAG
AAAAATCTGACTTTGGCACTGGAAGCCCTAGTACAGCTGCGTGGAAGATTGACATCCCAAGATTGGGAGAGGGTT
CATCTGATCGTGGCAGGTGGTTATGACGAGAGAGTCTTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATG
GTCCAACAGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTTCTCAGACAAACAGAAAATCTCCCTCCTC
CACAGCTGCACGTGTGTGCTTTACACACCAAGCAATGAGCACTTTGGCATTGTCCCTCTGGAAGCCATGTACATG
CAGTGCCCAAGTCATTGCTGTTAATTCGGGTGGACCTTGGAGTCCATTGACCACAGTGTACAGGGTTTCTGTGT
GAGCCTGACCCGGTGCATTCTCAGAAGCAATAGAAAAGTTTCATCCGTGAACCTTCTTAAAAGCCACCATGGGC
CTGGCTGGAAGAGCCAGAGTGAAGGAAAAATTTTCCCTGAAGCATTACAGAACAGCTCTACCGATATGTTACC
AAACTGCTGGTAT**TAA**TCAGATTGTTTTTAAGATCTCCATTAATGTCATTTTTATGGATTGTAGACCCAGTTTTGA
AACCAAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTTAAAAAATAAACTTGAGTCTTGAATGTGAGCCA
CTTTCCTATATACACACCTCCCTGTCCACTTTTCAGAAAAACCATGTCTTTTATGCTATAATCATTCCAAATTT
TGCCAGTGTAAAGTTACAAATGTGGTGTCAATCCATGTTTCAGCAGAGTATTTTAATTATATTTCTCGGGATTAT
TGCTCTTCTGTCTATAAATTTGAATGATACTGTGCCTTAATTGGTTTTCATAGTTTAAGTGTGTATCATTATCA
AAGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTTCCAGATTCAATCCACCGAAGTGT
TCACTGTCATCTGTTAGGGAATTTTGTGTTGCTCTTTGCCTGGATCCATAGCGAGAGTGCTCTGTATTTTT
TTTAAGATAATTTGTATTTTGCACACTGAGATATAATAAAAGGTGTTTATCATAAAAAAAAAAAAAAAAAAAA

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FIGURE 296

MPLLKLVHGSPLVFGEKFKLETLVSACIPVFR LARRRKKILFYCHFPDLLLLTKRDSFLKRLYRAPIDWIEEYTTG
MADCILVNSQFTA AVFKETFKSLSHIDPDVLYPSLNVT SFDSVVPEKLDDLVPKGKKFLLLSINRYERKKNLTLA
LEALVQLRGRLTSQDWERVHLIVAGGYDERVLENVEHYQELKKMVQQSDLGQYVTF LRSFSDKQKISLLHSCTCV
LYTPSNEHFGIVPLEAMYMOCFVIAVN SGGPLESIDHSVTGFLCEPDPVHFSEAIEKFIREPSLKATMGLAGRAR
VKEKFSPEAFTEQLYRYVTKLLV

Signal peptide:

amino acids 1-15

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FIGURE 297

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACCAATGTTGGACTTCGCGATCTTCGCCGTTACCTTC
TTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCCAGACAAGCTGCAGGAATTCAGGGATTACT
CCAACCTGAAGAAAAAGATGGTAATCTTCCAGATATTGTGAATAGTGAAGTTTGCATGAGTTCCTGGTTAATTTG
CATGAGAGATATGGGCCTGTGGTCTCCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACTGTTGATGTA
CTGAAGCAGCATATCAATCCCAATAAGACATCGGACCCTTTTGAAACCATGCTGAAGTCATTATTAAGGTATCAA
TCTGGTGGTGGCAGTGTGAGTGAAAACCATGAGGAAAAAATTGTATGAAAATGGTGTGACTGATTCTCTGAAG
AGTAACTTTGCCCTCCTCCTAAAGCTTTCAGAAGAATTATTAGATAAATGGCTCTCCTACCCAGAGACCCAGCAC
GTGCCCCCTCAGCCAGCATATGCTTGGTTTTGCTATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTTGAA
GATGATCAGGAAGTCATTGCTTCCAGAAGAATCATGGCACAGTTTGGTCTGAGATTGGAAAAGGCTTTCTAGAT
GGGTCACTTGATAAAAAACATGACTCGGAAAAACAATATGAAGATGCCCTCATGCAACTGGAGTCTGTTTTAAGG
AACATCATAAAAGAACGAAAAGGAAGGAACCTTCAGTCAACATATTTTCATTGACTCCTTAGTACAAGGGAACCTT
AATGACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGGCCAGTTGCATAATAACTGCAAAATTGTGTACC
TGGGCAATCTGTTTTTTAACCACCTCTGAAGAAGTTCAAAAAAATTATATGAAGAGATAAACCAAGTTTTTGGAA
AATGGTCCTGTTACTCCAGAGAAAATTGAGCAGCTCAGATATTGTCAGCATGTGCTTTGTGAAACTGTTCGAACT
GCCAACTGACTCCAGTTTCTGCCCAGCTTCAAGATATTGAAGGAAAAAATTGACCGATTTATTATTCTAGAGAG
ACCCTCGTCCTTTATGCCCTTGGTGTGGTACTTCAGGATCCTAATACTTGGCCATCTCCACACAAGTTTGATCCA
GATCGGTTTGATGATGAATTAGTAATGAAAACCTTTTCTCCTCACTTGGATTCTCAGGCACACAGGAGTGTCCAGAG
TTGAGGTTTGCATATATGGTGACCACAGTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTTCTGTGGAG
GGACAGGTTATTGAAACAAAGTATGAACTGGTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGA
TATTAAAATTTTATACATTTAAAATCATTGTTAAATTGATTGAGGAAAACAACCATTTAAAAAAAATCTATGTTG
AATCCTTTTATAAACAGTATCACTTTGTAATATAAACACCTATTTGTACTTAA

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FIGURE 298

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLDPDIVNSGSLHEFLVNLHERYGPVVSFWFGR
RLVVS LGTV DVLKQHINPNKTS DPFETMLKSLRLRYQSGGGSVSENHMRKKLYENGVTDSLKSNFALLLKLSEELL
DKWLSYPETQHVPLSQHMLGFAMKSVTQMVMGSTFEDDQEVIRFQKNHGTWVSEIGKGFLDGSLDKNMTRKKQYE
DALMQLESVLRNIIKERKGRNFSQHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTWAICFLTTSSEEVQK
KLYEEINQVFGNGPVTPEKIEQLRYCQHVLCE TVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVLYALGVVLQDP
NTWPSPHKFDPDRFDDELVMKTFSSLGFGSGTQECPELRFAYMVTTVLLSVLVKRLHLLSVEGQVIETKYELVTSS
REEAWITVSKRY

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 271-290

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FIGURE 299

CTAGATTGTGCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACTTCCAGCCTCAGAGACCGCCGCCCTT
GTCCCCGAGGGCCATGGGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTCCTGACGCTCCTGGCGCATCTGGTGGT
CGTCATCACCTTATTCTGGTCCCGGGACAGCAACATACAGGCCTGCCTGCCTCTCACGTTACCCCCGAGGAGTA
TGACAAGCAGGACATTCAGCTGGTGGCCGCGCTCTCTGTCACCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTT
CCTCTCAGGAGTCTCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGTGGC
CCTGTCCTTCTTCATATTCGAGCGTTGGGAGTGCCTACGTATTGGTACATTTTTGTCTTCTGCAGTGCCCTTCC
AGCTGTCACTGAAATGGCTTTATTTCGTCACCGTCTTTGGGCTGAAAAAGAAACCTTCTTGATTACCTTCATGACG
GGAACCTAAGGACGAAGCCTACAGGGGCAAGGGCCGCTTCGTATTCCTGGAAGAAGGAAGGCATAGGCTTCGGTT
TTCCCCTCGGAACTGCTTCTGCTGGAGGATATGTGTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATT
GTATTTAGTGCTTTGTAATAAAATATGTTTTGTAGTAACATTAAGACTTATATACAGTTTTAGGGGACAATTAAA
AAAAAAAAA

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FIGURE 300

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLGLFAVELAGFLSGV
SMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVTEMALFVTVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

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FIGURE 301

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACTGACTCGCTGCTGC
TTCGTGTTCTCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGGATGATGGTCCTCCCGGCTCAGAGGAC
CCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCCCGGGTGCCCTCGGAAGCGGGGCCACATCTCACCTAAGTCC
CGCCCCATGGCCAATTCCACTCTCCTAGGGCTGCTGGCCCCGCCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCC
CCCAACCGCCCGAACCACAGCCCCCACCCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTACTCC
AACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAATGGGACCTTCAGCGTC
CACTTCCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCCTCGTGCCCCCAGTAAAGCTGTAGAGTTC
CACCAGGAACAGCAGATCTTCATCGAAGCCAAGGCCTCCAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTA
GAACGGGGCCGCCGGACCTCGCTTTGCACCCACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCA
GCCACCTGGAGCTGCTCCCAGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCACGGACTATCGGCTG
GTCCAGAAGGTGTGCCAGATTACAACCTACCATAGTGATACCCCTACTACCCATCTGGGTGACCCGGGGCAGGC
CACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCTGCCATGCAGGAGACCATCTGGACACCGGGCAGGGAAGGG
GTTGGGCCTCAGGCAGGGAGGGGGGTGGAGACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAG
AGAAAGGGTCCCAAGTGCTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGGAGGAGGAGTG
GGCTCTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCCTGTGGGCAG
GCCGATCAGTGTTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGGTTCTTGCCATCCTGAGGAAAGATA
GCAACAGGGAGGGGGAGATTTCATCAGTGTTGGACAGCCTGTCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAG
GAGCCAGTCAGCAGGGTGGGTGGGGCCAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCCCTGTCT
GTGTGCTGAGCATGGCATGAGGCTGAAGTGGCAACCCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCT
CCAGCCAGGCCACCCCTTTCCAAAATTCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATTGCTGATGGCACA
CCCATCCTTAAGCTAAGACAGGACGATTGTGGTCCTCCCACACTAAGGCCACAGCCCATCCGCGTGCTGTGTGTC
CCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAGCATCCATGTCCCGGAGAGGGGTCCCTCAACAGTCAGCC
TCACCTGTACAGCCGGGGTTCTCCCGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCACGGGTGGGGCGGGGC
CGGGCCGCAGAGCATGTGCTGGATCTGTTCTGTGTGTCTGTCTGTGGGTGGGGGGAGGGGAGGGAAGTCTTGTGA
AACCGCTGATTGCTGACTTTTGTGTGAAGAATCGTGTCTTGGAGCAGGAAATAAAGCTTGCCCCGGGGCA

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FIGURE 302

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521

><subunit 1 of 1, 252 aa, 1 stop

><MW: 28127, pI: 8.91, NX(S/T): 5

MLTRCCFVFLVQGSLLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMANSTLLGLLAPPGEA
WGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNISISLVP
PSKAVEFHQEQQIFIEAKASKIFNCRMWEKVERGRRTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVVCVYIAF
YSTDYRLVQKVC PDYNYHSDTPYYPSG

Important features of the protein:**Signal peptide:**

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

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FIGURE 303

CGGTGGCCATGACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTCGCCCTTTATGTCT
TCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGCTTTCTTCTGGTTGGTGTCTCTACTGA
TTTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTATTGACAACAAAGATGGACCAACACAGAAATATCTGCTGA
TCTTTGGAGCGTTTGTCTCTGTCTATATCCAAGAAATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCA
GTGAAGGTTTGAAGAGTATAAACCAGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCTTGG
GCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGGCCAGGCACAGTGGGCA
TTCATGGAGATTCTCCTCAATTCTTCCTTTATTAGCTTTTCATGACGCTGGTCATTATCTTGCTGCATGTATTCT
GGGGCATTGTATTTTTTGTGGCTGTGAGAAGAAAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGC
TGGTGTGAGCCAGACCTTCATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTATAATCCTGGTGCTCA
TGGGCACCTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAGACAAGA
ACTTTCTTCTTTACAACCAGCGCTCCAGATTAACCTCAGGGAACCAGCACTTCCCAAACCGCAGACTACATCTTTA
GAGGAAGCACAACTGTGCCTTTTTCTGAAAATCCCTTTTTCTGGTGGAATTGAGAAAGAAATAAACTATGCAGATA

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FIGURE 304

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDNKDGPTQKYLLIFG
AFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLAYVSGLGFGIMSGVFSFVNTLSDSLGP GTVGIHG
DSPQFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKWGILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGT
WAFLAAGGSCRSLLKCLLCQDKNFLLYNQSR
```

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

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FIGURE 305

[illegible]

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FIGURE 306

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLFPNQQSNQVFPSLSLIPLTQM
LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTLISSEE
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLEPAGGAGVNPATQGTPAGRLPTPSG
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

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FIGURE 307

CCGGGGGACATGAGGTGGATACTGTTTCATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAAGAAAAATTTTTTG
GGGACCAAGTTTTGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAAATTGAGTCAACTAGTGAATTCAAACA
ACTTGAAGCTCAATTTCTGGAAATCTCCCTCCTCCTTCAATCGGCCTGTGGATGTCCTGGTCCCATCTGTCAATC
TGCAGGCATTTAAATCCTTCCTGAGATCCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTT
TAGACAATGAAGATGATGAAATGCAACACAATGAAGGGCAAGAACGGAGCAGTAATAACTTCAACTACGGGGCTT
ACCATTTCCCTGGAAGCTATTTACCACGAGATGGACAACATTGCCGCAGACTTTCCTGACCTGGCGAGGAGGGTGA
AGATTGGACATTCGTTTGAAAACCGGCCGATGTATGTACTGAAGTTTACGACTGGGAAAGGCGTGAGGCGGCCGG
CCGTTTGGCTGAATGCAGGCATCCATTCCCAGAGTGGATCTCCAGGCCACTGCAATCTGGACGGCAAGGAAGA
TTGTATCTGATTACCAGAGGGATCCAGCTATCACCTCCATCTTGGAGAAAATGGATATTTTCTTGTTCCTGTGG
CCAATCCTGATGGATATGTGTATACTCAAACCTCAAACCGATTATGGAGGAAGACGCGGTCCCGAAATCCTGGAA
GCTCCTGCATTGGTGCTGACCCAAATAGAACTGGAACGCTAGTTTTGCAGGAAAGGGAGCCAGCGACAACCCCTT
GCTCCGAAGTGATCCATGGACCCCAACGCAATTCCGAAGTGAGGTGAAATCAGTGGTAGATTTTCATCCAAAAAC
ATGGGAATTTCAAGGGCTTCATCGACCTGCACAGCTACTCGCAGCTGCTGATGTATCCATATGGGTACTCAGTCA
AAAAGGCCCCAGATGCCGAGGAACTCGACAAGGTGGCGAGGCTTGCGGCCAAAGCTCTGGCTTCTGTGTGGGCA
CTGAGTACCAAGTGGGTCCCACCTGCACCACTGTCTATCCAGCTAGCGGGAGCAGCATCGACTGGGCGTATGACA
ACGGCATCAAATTTGCATTACATTTGAGTTGAGAGATACCGGGACCTATGGCTTCTCTCTGCCAGCTAACCAGA
TCATCCCCACTGCAGAGGAGACGTGGCTGGGGCTGAAGACCATCATGGAGCATGTGCGGGACAACCTCTACTAGG
CGATGGCTCTGCTCTGTCTACATTTATTTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTCTTT
CCTACCTGTGTGAGTCAGAGCCCTCTGGGTTTGTGGAGCACACAGGCCCTGCCCTCTCCAGCCAGCTCCCTGGAG
TCGTGTGTCTGGCGGTGTCCTGCAAGAACTGGTTCTGCCAGCCTGCTCAATTTTGGTCTGTGTTTTTGATG
AGCCTTTTGTCTGTTTCTCTTCCACCCTGCTGGCTGGGCGGCTGCACTCAGCATCACCCCTTCTGGGTGGCAT
GTCTCTCTTACCTCATTTTTAGAACCAAGAACATCTGAGATGATTCTCTACCCTCATCCACATCTAGCCAAGC
CAGTGACCTTGCTCTGGTGGCACTGTGGGAGACACCACTTGTCTTTAGGTGGGTCTCAAAGATGATGTAGAATTT
CCTTTAATTTCTCGCAGTCTTCTGGAAAATATTTTCTTTGAGCAGCAAATCTGTAGGGATATCAGTGAAGGT
CTCTCCCTCCCTCTCTCTGTTTTTTTTTTTTTTTGGAGACAGAGTTTTGCTCTTGTGTGCCAGGCTGGAGTGTGA
TGGCTCGATCTTGGCTCACCACAACCTCTGCCTCCTGGGTTCAAGCAATTTCTCTGCCTCAGCCTCTTGAGTAGC
TTGGTTTATAGGCGCATGCCACCATGCCTGGCTAATTTTGTGTTTTTAGTAGAGACAGGGTTTCTCCATGTTGGT
CAGGCTGGTCTCAAACCTCCCAACCTCAGGTGATCTGCCCTCCTTGGCCTCCCAGAGTGCTGGGATTACAGGTGTG
AGCCACTGTGCGGGGCGGTCCTCCTTTTTTAGGCCTGAATACAAAGTAGAAGATCACTTTCCTTCACTGTGC
TGAGAATTTCTAGATACTACAGTTCTTACTCCTCTCTTCCCTTTGTTATTCACTGTGACCAGGATGGCGGGAGGG
GATCTGTGTCACTGTAGGTACTGTGCCAGGAAGGCTGGGTGAAGTGACCATCTAAATTGCAGGATGGTGAAATTT
ATCCCCATCTGTCTAATGGGCTTACCTCCTCTTTGCCCTTTGAACTCACTTCAAAGATCTAGGCCCTCATCTTAC
AGGTCTTAAATCACTCATCTGGCCTGGATAATCTCACTGCCCTGGCACATTCCCATTGTGCTGTGGTGTATCCT
GTGTTTCTTGTCTGTTTGT
TTTTGTATCCTGGACCACAAGTTCCTAAGTAGAGCAAGAATTCATCAACCAGCTGCCTCTTGTTCATTTACCT
CAGCACGTACCATCTGTCTTTTGT
TCTTAACCTCCTGCCTAGGATTTGTACAGCATCTGGTGTGTGCTTATAAGCCAATAAATATTCAATGTGAAAAA
AAAAAAAAAA

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FIGURE 308

MRWILFIGALIGSSICGQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNRPVDVLVPSVSLQA
FKSFLRSQGLEAYVTIEDLQALLDNEDEMQHNEGQERSNNFNFGAYHSLEAIYHEMDNIAADFPDLARRVKIG
HSFENRPMYVLKFSTGKGVRRPAVWLNAGIHSREWISQATAIWTARKIVSDYQRDPAITSILEKMDIFLLPVANP
DGYVYTQTQNLWRKTRSRNPGSSCIGADPNRNWNASEFAGKGASDNPCSEVYHGPHANSEVEVKSVVDFIQKHGN
FKGFIDLHSYSQLLMYPYGYSVKKAPDAEELDKVARLAAKALASVSGTEYQVGPTCTTVYPASGSSIDWAYDNGI
KFAFTFELRDTGTYGFLLPANQIIPAEETWLGLKTIMEHVRDNL

Signal peptide:
amino acids 1-16

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FIGURE 309

GGCTGACCGTGCTACATTGCCCTGGAGGAAGCCTAAGGAACCCAGGCATCCAGCTGCCCACGCCTGAGTCCAAGAT
TCTTCCCAGGAACACAAACGTAGGAGACCCACGCTCCTGGAAGCACCAGCCTTTATCTCTTCACCTTCAAGTCCC
CTTTCTCAAGAATCCTCTGTTCTTTGCCCTCTAAAGTCTTGGTACATCTAGGACCCAGGCATCTTGCTTTCCAGC
CACAAAGAGACAGATGAAGATGCAGAAAGGAAATGTTCTCCTTATGTTTGGTCTACTATTGCATTTAGAAGCTGC
AACAAATTCCAATGAGACTAGCACCTCTGCCAACACTGGATCCAGTGTGATCTCCAGTGGAGCCAGCACAGCCAC
CAACTCTGGGTCCAGTGTGACCTCCAGTGGGGTCAGCACAGCCACCATCTCAGGGTCCAGCGTGACCTCCAATGG
GGTCAGCATAGTCACCAACTCTGAGTTCATACAACCTCCAGTGGGATCAGCACAGCCACCAACTCTGAGTTCAG
CACAGCGTCCAGTGGGATCAGCATAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCAC
CAACTCTGAGTCCAGCACACCTCCAGTGGGGCCAGCACAGTCCACCAACTCTGGGTCCAGTGTGACCTCCAGTGG
AGCCAGCACTGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAGGGCCAGCACTGCCACCAACTCTGAGTCTAG
CACACTCTCCAGTGGGGCCAGCACAGCCACCAACTCTGACTCCAGCACAACTCCAGTGGGGCTAGCACAGCCAC
CAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTAG
GGCCAGCACTGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCCAGCACAGCCACCAACTCTGAGTCCAG
AACGACCTCCAATGGGGCTGGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCCAGCACAGCCAC
CAACTCTGACTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGG
GGCCAGCACAGCCACCAACTCTGAGTCCAGCACGACCTCCAGTGGGGCTAGCACAGCCACCAACTCTGACTCCAG
CACAACTCCAGTGGGGCCGGCACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTGGGATCAGCACAGTCCAC
CAATTCTGAGTCCAGCACACCTCCAGTGGGGCCAAACACAGCCACCAACTCTGAGTCCAGTACGACCTCCAGTGG
GGCCAAACACAGCCACCAACTCTGAGTCCAGCACAGTGTCCAGTGGGGCCAGCACTGCCACCAACTCTGAGTCCAG
CACAACTCCAGTGGGGTCAGCACAGCCACCAACTCTGAGTCCAGCACAACTCCAGTGGGGCTAGCACAGCCAC
CAACTCTGACTCCAGCACAACTCCAGTGAGGCCAGCACAGCCACCAACTCTGAGTCTAGCACAGTGTCCAGTGG
GATCAGCACAGTCCACCAATTCTGAGTCCAGCACAACTCCAGTGGGGCCAAACACAGCCACCAACTCTGGGTCCAG
GAGTGAGGCAAAGCCTGGTGGGTCCCTGGTGCCGTGGGAAATCTTCTCATCACCTGGTCTCGGTTGTGGCGGC
CGTGGGGCTCTTTGCTGGGTCTTCTTCTGTGTGAGAAACAGCCTGTCCCTGAGAAACACCTTTAACACAGCTGT
CTACCACCTCATGGCCTCAACCATGGCCTTGGTCCAGGCCCTGGAGGGAATCATGGAGCCCCCACAGGCCAG
GTGGAGTCTTAAGTGGTTCTGGAGGAGACAGTATCATCGATAGCCATGGAGATGAGCGGGAGGAACAGCGGGCC
CTGAGCAGCCCCGGAAGCAAGTGCCGCATTCTTCAGGAAGGAAGAGACCTGGGCACCCAAGACCTGGTTTCCTTT
CATTCATCCCAGGAGACCCCTCCAGCTTTGTTTGAGATCCTGAAAATCTTGAAGAAGGTATTCTCACCTTTCT
TGCCTTTTACCAGACACTGGAAGAGAAATACTATATTGCTCATTTAGCTAAGAAATAAATACATCTCATCTAACAC
ACACGACAAAGAGAAGCTGTGCTTGCCCCGGGGTGGGTATCTAGCTCTGAGATGAACTCAGTTATAGGAGAAAAC
CTCCATGCTGGACTCCATCTGGCATTCAAATCTCCACAGTAAAATCCAAAGACCTCAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 310

MKMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATIS
GSSVTSNGVSIIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSESS
TPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSSTTS
SGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTTSNGA
GTATNSESSTTSSGASTATNSDSSTVSSGASTATNSESSTTSSGASTATNSESSTTSSGASTA
TNSDSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGANTATNS
ESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSTTSSEASTATNSESS
TVSSGISTVTNSESSTTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAVSEAKPGGS
LVPWEIFLITLVSVVAAGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGPGPGGNHGAP
HRPRWSPNWFWRFPVSSIAMEMSGRNSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

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FIGURE 311A

CTAAGCCGGAGGATGTGCAGCTGCGGCGGGCGGCCGGCTACGAAGAGGACGGGGACAGGCGCCGTGCGAACCGA
GCCCAGCCAGCCGGAGGACGCGGGCAGGGCGGGACGGGAGCCCGGACTCGTCTGCCGCCCGCGTCTGCGCGCTCG
TGCCCGGCCCGCGTCCCCGCGCGCAGCGGGAGGCCGCCACCTCGCGCCCGAGCCCGCTAGCGCGCGC
CGGGCATGGTCCCTCTTAAAGGCGCAGGCCGCGGGCGGGCGGGGCGGGTGTGCGGAACAAAGCGCCGGCGGGG
CCTGCGGGCGGGCTCGGGGGCCGCGATGGGCGCGGGCGGCCCGCGGGCGGGCGGGCGCTGCCCGGGCGGGGCTCG
CGGCGCTAGGGCGGGCTGGCCTCCGTGGGCGGGGGCAGCGGGCTGAGGGCGCGCGGAGCCTGCGCGGGCGGGCGG
GGCGGGCGGGCGGGCGGCCGGCGGGCGGAGCGGCGGGGCAATGGCCGCGCGCGGGCGGGCGCGCTGGCTCAGCGTGC
TGCTCGGGCTCGTCTTGGCTTCGTGCTGGCCTCGCGGCTCGTCTGCCCGGGGCTTCCGAGCTGAAGCGAGCGG
GCCCAGGGCGCGCGCCAGCCCCGAGGGCTGCCGGTCCGGGAGGCGGGCGGCTTCCAGGCCGGCGGGGCGCGCG
GCGATGCGCGCGGGGCGCAGCTCTGCCCGGCCGGCTCGGACCCAGATGGCGGGCGGGCGCGGACAGGAACCTTCTCT
TCGTGGGAGTCATGACCGCCAGAAATACCTGCAGACTCGGGCCGTGGCCGCTACAGAATGGTCCAAGACAA
TTCCTGGGAAAGTTCAGTTCTTCTCAAGTGAGGGTCTGACACATCTGTACCAATTCAGTAGTCCACTACGGG
GTGTGGACGACTCCTACCCGCCCCAGAAGAAGTCTTCATGATGCTCAAGTACATGCACGACCACTACTTGGACA
AGTATGAATGGTTTATGAGAGCAGATGATGACGTGTACATCAAAGGAGACCGTCTGGAGAACTTCTGAGGAGTT
TGAACAGCAGCGAGCCCCCTTCTTGGGCGAGCAGGCCTGGGCACCACGGAAGAAATGGGAAACTGGCCCTGG
AGCCTGGTGAGAACTTCTGCATGGGGGGGCGCTGGCGTGATCATGAGCCGGGAGGTGCTTCGGAGAAATGGTGCCG
ACATTGGCAAGTGTCTCCGGGAGATGTACACCACCCATGAGGACGTGGAGGTGGGAAGGTGTGTCCGGAGGTTTG
CAGGGGTGCAGTGTGTCTGGTCTTATGAGATGCGGCAGCTTTTTTATGAGAATTACGAGCAGAACAAAAAGGGGT
ACATTAGAGATCTCCATAACAGTAAATTCACCAAGCTATCACATTACACCCCAACAAAAACCCACCTACCAGT
ACAGGCTCCACAGCTACATGCTGAGCCGCAAGATATCCGAGCTCCGCCATCGCACAAATACAGCTGCACCGCGAAA
TTGTCTGATGAGCAAATACAGCAACACAGAAATTCATAAAGAGGACCTCCAGCTGGGAATCCCTCCCTCTCTCA
TGAGGTTTTCAGCCCCGCCAGCGAGAGGAGATTCTGGAATGGGAGTTTCTGACTGGAAATACTTGTATTTCGGCAG
TTGACGGCCAGCCCCCTCGAAGAGGAATGGACTCCGCCAGAGGGAAGCCTTGACGACATTGTATGCAGGTCA
TGGAGATGATCAATGCCAACGCCAAGACCAGAGGGCGCATCATGACTTCAAAGAGATCCAGTACGGCTACCGCC
GGGTGAACCCCATGTATGGGGCTGAGTACATCCTGGACCTGCTGCTTCTGTACAAAAAGCACAAAGGGGAAGAAAA
TGACGGTCCCTGTGAGGAGGCACGCGTATTTACAGCAGACTTTCAGCAAATCCAGTTTGTGGAGCATGAGGAGC
TGGATGCACAAGAGTTGGCCAAGAGAATCAATCAGGAATCTGGATCCTTGTCTCTCAAATCCCTGAAGA
AGCTCGTCCCCTTTCAGCTCCCTGGGTGGAAGAGTGAAGAGAACCCAAAGATAAAAAGATAAACATACTGA
TTCCTTGTCTGGGCGTTTCGACATGTTTGTGAGATTTATGGGAAACTTTGAGAAGACGTGTCTTATCCCCAATC
AGAAGTCAAGCTCGTGGTCTGCTTTTCAATTCTGACTCCAACCCTGACAAGGCCAAACAAGTTGAACGTGATGA
GAGATTACGCATTAAGTACCCTAAAGCCGACATGCAGATTTTGCCTGTGTCTGGAGAGTTTTCAAGAGCCCTGG
CCCTGGAAGTAGGATCCTCCAGTTTAAACAATGAATCTTTGCTCTTCTTCTGCGACGTGACCTCGTGTTTACTA
CAGAAATCCTTCAGCGATGTCGAGCAAATACAGTCTTGGGCCAACAAATATATTTTCAATCATCTTCAGCCAGT
ATGACCCAAAGATTGTTTATAGTGGGAAAGTTCCAGTGACAACCATTTTGCCTTTACTCAGAAAACCTGGCTTCT
GGAGAAACTATGGGTTTGGCATCACGTGTATTTATAAGGGAGATCTTGTCCGAGTGGGTGGCTTTGATGTTTCCA
TCCAAGGCTGGGGGCTGGAGGATGTGGACCTTTTCAACAAGGTTGTCCAGGCAGGTTTGAAGACGTTTAGGAGCC
AGGAAGTAGGAGTAGTCCACGTCCACCATCCTGTCTTTGTGATCCCAATCTTGACCCCAACAGTACAAAATGT
GCTTGGGTCCAAAGCATCGACCTATGGGTCCACCCAGCAGCTGGCTGAGATGTGGCTGGAAAAAATGATCCAA
GTTACAGTAAAAGCAGCAATAATAATGGCTCAGTGAGGACAGCCTAATGTCCAGCTTTGCTGGAAAAGACGTTTT
TAATTATCTAATTTATTTTTCAAAAATTTTTGTATGATCAGTTTTTGAAGTCCGTATACAAGGATATATTTTAC
ACATCTTCTTGTGAACATTATGTAGCAGACCTGCTTAACCTTTGACTTGAATGTACCTGATGAACAAAACCTTT
TTTAAAAAATGTTTTCTTTTGAGACCTTTGCTCCAGTCCATGGCAGAAAACGTGAACATTCCTGCAAAGTAT
TATTGTAACAAAACACTGTAACCTCTGTTAAATGTTCTGTTGTGATTGTTAAACATTCCACAGATTCTACCTTTTGT
GTTTTGTTTTTTTTTTTACAATTGTTTTAAAGCCATTTTCATGTTCCAGTTGTAAGATAAGGAAATGTGATAATA
GCTGTTTCATCATTGTCTTCAGGAGAGCTTTCCAGAGTTGATCATTTCTCATGGTACTCTGCTCAGCATGGC
CAGTAGGTTTTTTGTTTGTGTTTTGTTCTTTTTTGGACGGAGTCTCACTCTGTTACCCAGGCTGGAATG
CAGTGGCGCAATCTTGGCTCACTTTAACCTCCACTTCCCTGGTTCAAGCAATCCCCGCTTTGCTCCCGAGT
AGCTGGGATTACAGGCACACACCACCGCCAGNTAGTTTTTTTGTATTTTGTAGAGACGGGGTTTTACCAT
GCAAGCCCAGCTGGCCACGTAGGTTTTTAAAGCAAGGGGCGTGAAGAAGGCACAGTGAGGTATGTGGCTGTTCTCG
TGGTAGTTTCATTCGGCTAAATAGACCTGGCATTAAATTTCAAGAAGGATTGGCATTCTCTTCTTGACCCTT
CTCTTTAAAGGGTAAAAATATTAATGTTTGAAGTGAACAAGATGAATTATTACAATAAATCTGATGTACACAGACT
GAAACATACACACATACCCCTAATCAAAACGTTGGGGAAAAATGTATTTGGTTTTGTTCTTCTTCTGCTGTCTG
TGTATGTGGGTGGAGATGGTTTTTCACTTCTTCACTTGTGTTTTATCCTTTGTATCTGAAATACCTTTAA

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FIGURE 311B

TTTATTTAATATCTGTTGTTTCAGAGCTCTGCCATTTCTTGAGTACCTGTTAGTTAGTATTATTTATGTGTATCGG
GAGTGTGTTTAGTCTGTTTTATTTGCAGTAAACCGATCTCCAAAGATTTCCTTTTGGAAACGCTTTTCCCCTCC
TTAATTTTATATTCTTACTGTTTTACTAAATATTAAGTGTTCCTTGACAATTTGGTGCTCATGTGTTTTGGG
GACAAAAGTGAAATGAATCTGTCATTATACCAGAAAGTTAAATTCTCAGATCAAATGTGCCTTAATAAATTTGTT
TTCATTTAGATTTCAAACAGTGATAGACTTGCCATTTTAATACACGTCATTGGAGGGCTGCGTATTTGTAAATAG
CCTGATGCTCATTTGGAAAAATAAACAGTGAACAATATTTTCTATTGTACTTTTCGAACCATTTTGTCTCATT
ATTCCTGTTTAGCTGAAGAATTGTATTACATTTGGAGAGTAAAAAACTTAAACACGAAAAA

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FIGURE 312

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836

><subunit 1 of 1, 802 aa, 1 stop

><MW: 91812, pI: 9.52, NX(S/T): 3

MAARGRRAWLSVLLGLVLGFVLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGARG
DARGAQLWPPGSDPDGGPRDRNFLFVGVMTAQKYLQTRAVAAYRTWSKTIPGKVQFFSSEGSD
TSVPIPVVPLRGVDDSYPPQKKSFMLKYMHDHYLDKYEFMRADDDVYIKGDRLLENFLRSLN
SSEPLFLGQTGLGTTEEMGKLALEPGENFCMGGPGVIMSREVLRRMVPHIGHKCLREMYTTHE
VEVGRCVRRFAGVQCVWSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPPYQYRL
HSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFQPRQREEILEWEE
LTGKYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQYGYRRVNP
MYGAEYILDLLLLLYKKHKGKKMTVPVRRHAYLQOTFSKIQFVEHEELDAQELAKRINQESGSL
SFLSNSLKKLVFPQLPGSKSEHKEPKDKKINILIPLSGRFDMFVRFMGNFEKTCLIPNQNVKL
VVLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQFNNESLLFFC
DVDLVFETTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFTQKTGFWRNYGF
GITCIYKGD LVRVGGFDVSIQGWGLEVDL FNKVQAGLKTFERSQEVGVVHVHHPVFCDPNLD
PKQYKMCLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA

Signal peptide:

amino acids 1-23

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FIGURE 313

GGCCGGACGCCTCCGCGTTACGGGATGAATTAACGGCGGGTTCCGCACGGAGGTTGTGACCCC
TACGGAGCCCCAGCTTGCCACGCACCCCACTCGGCGTCGCGCGGCGTGCCCTGCTTGTGACA
GGTGGGAGGCTGGAACATATCAGGCTGAAAAACAGAGTGGGTACTCTCTTCTGGGAAGCTGGCA
ACAAATGGATGATGTGATATATGCATTCCAGGGGAAGGGAAATTGTGGTGCTTCTGAACCCAT
GGTCAATTAACGAGGCAGTTTCTAGCTACTGCACGTACTTCATAAAGCAGGACTCTAAAAGCT
TTGGAATCATGGTGTGATGAAAGGGATTACTTTATACTGACTCTGTTTTGGGGAAGCTTTT
TTGGAAGCATTTTTCATGCTGAGTCCCTTTTACCTTTGATGTTTGTAACCCATCTTGGTATC
GCTGGATCAACAACCGCCTTGTGGCAACATGGCTCACCTACCTGTGGCATTATTGGAGACCA
TGTTTGGTGTAAGTGATTATACTGGGGATGCATTTGTTCTGGAGAAAGAAGTGTGATTA
TCATGAACCATCGGACAAGAATGGACTGGATGTTCTGTGGAATTGCCTGATGCGATATAGCT
ACCTCAGATTGGAGAAAATTTGCCTCAAAGCGAGTCTCAAAGGTGTTCTGGATTGTGGTGGG
CCATGCAGGCTGCTGCCTATATCTTCATTCATAGGAAATGGAAGGATGACAAGAGCCATTTTCG
AAGACATGATTGATTACTTTTGTGATATTCACGAACCACTTCAACTCCTCATATTTCCAGAAG
GGACTGATCTCACAGAAAACAGCAAGTCTCGAAGTAATGCATTTGCTGAAAAAATGGACTTC
AGAAATATGAATATGTTTTACATCCAAGAACTACAGGCTTTACTTTTGTGGTAGACCGTCTAA
GAGAAGGTAAGAACCCTTGATGCTGTCCATGATATCACTGTGGCGTATCCTCACACATTCCTC
AATCAGAGAAGCACCTCCTCCAAGGAGACTTTCCCAGGGAAATCCACTTTCACGTCCACCGGT
ATCCAATAGACACCTCCCCACATCCAAGGAGGACCTTCAACTCTGGTGCCACAAACGGTGGG
AAGAGAAAGAAGAGAGGCTGCGTTCCTTCTATCAAGGGGAGAAGAATTTTATTTTACCGGAC
AGAGTGTCAATCCACCTTGCAAGTCTGAACTCAGGGTCCTTGTGGTCAAATTGCTCTCTATAC
TGTATTGGACCCTGTTTCAGCCCTGCAATGTGCCTACTCATATATTTGTACAGTCTTGTTAAGT
GGTATTTTATAATCACCATTGTAATCTTTGTGCTGCAAGAGAGAATATTTGGTGGACTGGAGA
TCATAGAACTTGCATGTTACCGACTTTTACACAAACAGCCACATTTAAATTCAAAGAAAAATG
AGTAAGATTATAAGGTTTGCCATGTGAAAACCTAGAGCATATTTTGGAAATGTTCTAAACCTT
TCTAAGCTCAGATGCATTTTTCATGACTATGTGCAATATTTCTTACTGCCATCATTATTTGT
TAAAGATATTTTGCACCTTAATTTTGTGGGAAAAATATTGCTACAATTTTTTTTAAATCTCTGAA
TGTAATTCGATACTGTGTACATAGCAGGAGTGATCGGGGTGAAATAACTTGGGCCAGAATA
TTATTAAACAATCATCAGGCTTTTAAA

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FIGURE 314

MHSRGREIVVLLNPWSINEAVSSYCTYFIKQDSKSFSGIMVSWKGIYFILTLFWGSFFGSIFML
SPFLPLMFVNPSWYRWINNRLVATWLTLPVALLETMFGVKVIITGDAFVPGERSVIIMNHRTR
MDWMFLWNCLMRYSYLRLEKICLKASLKGVPFGFGWAMQAAAYIFIHRKWKDDKSHFEDMIDYF
CDIHEPLQLLI FPEGTDLTENSKSRNAFAEKNGLQKYEYVLHPRTTGFTFVVDRLREGKNLD
AVHDITVAYPHNIPQSEKHLLOGDFPREIH FHVHRYPIDTLPTSKEDLQLWCHKRWEEKEERL
RSFYQGEKNFYFTGQSVIPPCKSELRVLVVKLLSILYWTLFSPAMCLLIYLYSLVKWYFIITI
VIFVLQERIFGGLEIIELACYRLLHKQPHLNSKKNE

Important features of the protein:

Signal peptide:

amino acids 1-22

Transmembrane domains:

amino acids 44-63, 90-108, 354-377

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FIGURE 315

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTGA
CCTCCAAATCATCCATCCACCCCTGCTGTCTATCTGTTTTCATAGTGTGAGATCAACCCACAGG
AATATCC**ATGG**CCTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACAGTG
GCAAGTCACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCTCCTG
CTCCCTCTTTCTGAGACCAGTGCAGAGGCTATGGAAGTGCGGTTCTTCAGGAATCAGTTCCA
TGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACAGTATCG
AGGGAGAACTGAGTTTGTGAAGGACTCCATTGCAGGGGGGGCGTGTCTCTAAGGCTAAAAAA
CATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTTCAGTTCCAGATTTACGATGAGGA
GGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCCTCTCATTTCCATCGTGGGATA
TGTTGACGGAGGTATCCAGTTACTCTGCCTGTCTCAGGCTGGTTCCCCCAGCCACAGCCAA
GTGGAAGGTCCACAAGGACAGGATTTGTCTTCAGACTCCAGAGCAAATGCAGATGGGTACAG
CCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAATGCTGGGAGCATATTGTGTTCCAT
CCACCTTGCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAGAGACGTTTTTCCA
GCCCTCACCTTGGCGCCTGGCTTCTATTTTACTCGGGTTACTCTGTGGTGCCCTGTGTGGTGT
TGTCATGGGGATGATAATTGTTTTCTTCAAATCCAAAGGGAAAATCCAGGCGGAAGTGGACTG
GAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACACGCAGTGGAGGTGACTCT
GGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAAGTGAACCCATAGAAA
AGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCTTCTCA
GGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGACAAAATGTAGGGTGGTATGT
GGGAGTGTGTCGGGATGACGTAGACAGGGGGAAGAACAATGTGACTTTGTCTCCCAACAATGG
GTATTGGGTCCTCAGACTGACAACAGAACATTTGTATTTACATTTCAATCCCCATTTTATCAG
CCTCCCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCCTGGACTATGAGGGTGGGACCAT
CTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACCCTGCTGACATGTCAGTTTGAAGG
CTTGTTGAGACCCTATATCCAGCATGCGATGTATGACGAGGAAAAGGGGACTCCCATATTAT
ATGTCCAGTGTCTTGGGGAT**TG**AGACAGAGAAGACCCTGCTTAAAGGGCCCCACACCACAGACC
CAGACACAGCCAAGGGAGAGTGCTCCCGACAGGTGGCCCCAGCTTCCTCTCCGGAGCCTGCGC
ACAGAGAGTCACGCCCCCACTCTCCTTTAGGGAGCTGAGGTTCTTCTGCCCTGAGCCCTGCA
GCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGATTGGCCTGACCCTGTGGGAGTCAGAAGCC
ATGGCTGCCCTGAAGTGGGGACGGAATAGACTCACATTAGGTTTAGTTTGTGAAAAGTCCATC
CAGCTAAGCGATCTTGAACAAGTCACAACCTCCCAGGCTCCTCATTTGCTAGTCACGGACAGT
GATTCCTGCCTCACAGGTGAAGATTAAAGAGACAACGAATGTGAATCATGCTTGCAGGTTTGA
GGGCACAGTGTTTGTCTAATGATGTGTTTTTATATTATACATTTTCCCACCATAAACTCTGTTT
GCTTATTCCACATTAATTTACTTTTCTCTATACCAAATCACCCATGGAATAGTTATTGAACAC
CTGCTTTGTGAGGCTCAAAGAATAAAGAGGAGGTAGGATTTTCACTGATTCTATAAGCCCAG
CATTACCTGATACCAAAACCAGGCAAAGAAAACAGAAGAAGAGGAAGGAAAAGTACAGGTCCA
TATCCCTCATTAACACAGACACAAAATTTCTAAATAAAATTTTAACAAATTAAGTAAACAAT
ATATTTAAAGATGATATATACTACTCAGTGTGGTTTGTCCCAAAATGCAGAGTTGGTTTAA
TATTTAAATATCAACCAGTGTAATTCAGCACATTAATAAAGTAAAAAGAAAACCATAAAAAA
AAAAA

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FIGURE 316

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866

><subunit 1 of 1, 466 aa, 1 stop

><MW: 52279, pI: 6.16, NX(S/T): 2

MAFVLILVLSFYELVSGWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHAV
VHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEEAT
WELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGYSLY
DVEISIIIVQENAGSILCSIHAEQSHEVESKVLIGETFFQSPWRLASILLGLLCGALCGVVM
GMIIIVFFKSKGKIQAELDWRKKGQAELRDARKHAVEVTLPETAHPKLCVSDLKTVTHRKAP
QEVPHSEKRFRTRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLSPNNGYW
VLRLTTEHLYFTFNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLLTCQFEGLL
RPYIQHAMYDEEKGTPIFICPVSWG

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

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FIGURE 317

GCACCTGCGACCACCGTGAGCAGTC**ATG**GCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTTC
TGGGCTTGTCCTGGCTCTGTGCTGCTGCTGCCAAGGCCTTCCTGTCCCGCGGGAAGCGGCA
GGAGCCGCCGCGACACCTGAAGGAAAATTGGGCCGATTTCCACCTATGATGCATCATCACCA
GGCACCCCTCAGATGGCCAGACTCCTGGGGCTCGTTTTCCAGAGGTCTCACCTTGCCGAGGCATT
TGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGGAAGAGGTCTGATGGG
GCAGATTATTCCAATCTACGGTTTTGGGATTTTTTTTATATATACTGTACATTCTATTTAAGGT
AAGTAGAATCATCCTAATCATATTACATCAAT**TGA**AAATCTAATATGGCGATAAAAATCATTTGT
CTACATTAAAACCTTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTAAATCCTGC
CTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTCAGTTTCACATAAGAATGTTTACTCAA
TGTTTAAGTGTTTTGCCCCAAAATTCACAATAACAAGGCAGAACTAGGACTTGAACATGGAT
CTTTTGGTTCTTAATCCAGTGAGTGATACAATTCAATGCACTCCCCTGCCA

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FIGURE 318

MAYSTVQRVALASGLVLALSLLLPKAFLSRGKRQEPPTPEGKLGRFPPMMHHHQAPSDGQTF
GARFQRSHLAEAFKAKGSGGGAGGGGSGRGLMGQIIPYGFIFLYILYILFKVSRILIILHQ

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FIGURE 319

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTAG
GAAAAGAGTTTGTGGGAACCTGGGTTATCGGCCTCGTCATCTTCATATCCCTGATTGTCTT
GGCAGTGTGCATTGGACTCACTGTTTATTATGTGAGATATAATCAAAGAAGACCTACAATTA
CTATAGCACATTGTCATTTACAACCTGACAACTATATGCTGAGTTTGGCAGAGAGGCTTCTAA
CAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAAAAATGCATTTTATAAATCTCC
ATTAAGGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGGAGTGTT
GGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGAAACTGTAGATAAAAT
TGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTAGATCCTCA
CTCAGTTAAAATTAAAAAATCAACAAGACAGAAACAGACAGCTATCTAAACCATTGCTGCGG
AACACGAAGAAGTAAACTCTAGGTCAGAGTCTCAGGATCGTTGGTGGGACAGAAGTAGAAGA
GGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGTGGAGCAACCTT
AATTAATGCCACATGGCTTGTGAGTGCTGCTCACTGTTTTACAACATATAAGAACCCTGCCAG
ATGGACTGCTTCCTTTGGAGTAACAATAAAACCTTCGAAAATGAAACGGGGTCTCCGGAGAAT
AATTGTCCATGAAAAATACAAACACCCATCACATGACTATGATATTTCTCTTGCAGAGCTTTC
TAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGATGCATCCTATGAGTT
TCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAAATGATGGTTACAGTCA
AAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAACCTGCAATGAACCTCAAGC
TTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTTAGAAGGAAAAACAGATGC
ATGCCAGGGTGACTCTGGAGGACCACTGGTTAGTTCAGATGCTAGAGATATCTGGTACCTTGC
TGGAATAGTGAGCTGGGGAGATGAATGTGCGAAACCCAACAAGCCTGGTGTTTATACTAGAGT
TACGGCCTTGCGGGACTGGATTACTTCAAAAACCTGGTATCTAAGAGACAAAAGCCTCATGGAA
CAGATAACATTTTTTTTTTGTTTTTTGGGTGTGGAGGCCATTTTTAGAGATACAGAATTGGAGA
AGACTTGCAAAACAGCTAGATTTGACTGATCTCAATAAACTGTTTGCTTGATGCATGTATTTT
CTTCCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTGCCAGATCAACTCTGTCATCTGTGA
GCAATAGTTGAAACTTTATGTACATAGAGAAATAGATAAATAAATATTACATTACAGCCTGTA
TTCATTTGTTCTCTAGAAGTTTTGTGAGAATTTTGAAGTTGTTGACATAAATTTGTAATGCATA
TATACAATTTGAAGCACTCCTTTTCTTCAGTTCCCTCAGCTCCTCTCATTTTCAGCAAATATCCA
TTTTCAAGGTGCAGAACAAGGAGTGAAAGAAAATATAAGAAGAAAAAATCCCCTACATTTTA
TTGGCACAGAAAAGTATTAGGTGTTTTTCTTAGTGGAATATTAGAAATGATCATATTCATTAT
GAAAGGTCAAGCAAAGACAGCAGAATACCAATCACTTCATCATTTAGGAAGTATGGGAACATA
GTTAAGGAAGTCCAGAAAGAAGCCAAGATATATCCTTATTTTCATTTCCAACAACACTACTATG
ATAAATGTGAAGAAGATTCTGTTTTTTTGTGACCTATAATAATTATACAAACTTCATGCAATG
TACTTGTTCTAAGCAAATTAAAGCAAATATTTATTTAACATTGTTACTGAGGATGTCAACATA
TAACAATAAAATATAAATCACCCA

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FIGURE 320

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871

><subunit 1 of 1, 423 aa, 1 stop

><MW: 47696, pI: 8.96, NX(S/T): 3

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYYSTLSFTTDK
LYAEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICRFH
STEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTLGQS
LRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFGVTIK
PSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSVPYTNVHRVCLPDASYEFQPGDVMFVTG
FGALKNDGYSQNHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGDSGGPLV
SSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

Transmembrane domain:

amino acids 21-40 (type II)

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FIGURE 321

CCGGGCTCCTGGGTGAGGCCGGCAAGTTTGGAGCGTGGTCAGACAATAGGGGCGTGGCTACGG
CTCGCGGAGCGCAACCAACGCTCTAGACCAGACCTGGGCTCGAGACCATAACTGTTTGGCTTT
AACAGTACGTGGGCGGCCGGAATCCGGGAGTCCGGTGACCCGGGCTGTGGTCTAGCATAAAGG
CGGAGCCCAGAAGAAGGGGCGGGGTATGGGAGAAGCCTCCCCACCTGCCCCCGCAAGGCGGCA
TCTGCTGGTCCTGCTGCTGCTCCTCTCTACCCTGGTGATCCCCCTCCGCTGCAGCTCCTATCCA
TGATGCTGACGCCCAAGAGAGCTCCTTGGGTCTCACAGGCCTCCAGAGCCTACTCCAAGGCTT
CAGCCGACTTTTTCCTGAAAGGTAACCTGCTTCGGGGCATAGACAGCTTATTCTCTGCCCCCAT
GGACTTCCGGGGCCTCCCTGGGAATAACCAAAAGAGGAGAACCAGGAGCACCAGCTGGGGAA
CAACACCCCTCTCCAGCCACCTCCAGATCGACAAGATGACCGACAACAAGACAGGAGAGGTGCT
GATCTCCGAGAATGTGGTGGCATCCATTCAACCAGCGGAGGGGAGCTTCGAGGGTGATTTGAA
GGTACCCAGGATGGAGGAGAAGGAGGCCCTGGTACCCATCCAGAAGGCCACGGACAGCTTCCAC
ACAGAACTCCATCCCCGGGTGGCCTTCTGGATCATTAAGCTGCCACGGCGGAGGTCCCACCAG
GATGCCCTGGAGGGCGGCCACTGGCTCAGCGAGAAGCGACACCGCCTGCAGGCCATCCGGGAT
GGACTCCGCAAGGGGACCCACAAGGACGTCCTAGAAGAGGGGACCGAGAGCTCCTCCCACTCC
AGGCTGTCCCCCGAAAGACCCACTTACTGTACATCCTCAGGCCCTCTCGGCAGCTGTAGGGG
TGGGGACCGGGGAGCACCTGCCTGTAGCCCCATCAGACCCTGCCCCAAGCACCATATGGAAA
TAAAGTTCTTTCTTACATCTAAAAA

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FIGURE 322

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68879
><subunit 1 of 1, 242 aa, 1 stop
><MW: 27007, pI: 8.68, NX(S/T): 2
MGEASPPAPARRHLLVLLLLLSTLVIPSAAAPIHDADAQESSLGLTGLQSLQGF SRLFL
KGNLLRGIDSLFSAPMDFRGLPGNYHKEENQEHQLGNNTLSSHLQIDKMTDNKTGEVLIS
ENVVASIQPAEGSFEGDLKVPRMEEKEALVPIQKATDSFHTELHPRVAFWIILPRRRSH
QDALEGGHWLSEKRHRLQAIRDGLRKGTHKDVLEEGTESSSHSRLSPRKTHLLYILRPSR
QL
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Important features of the protein:**Signal peptide:**

Amino acids 1-30

N-glycosylation sites:

Amino acids 97-101;112-116

N-myristoylation sites:

Amino acids 80-86;132-138;203-209;216-222

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FIGURE 323

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCCC
TGCCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCGGGCGTGGGGCACC GGCC
CAGCGCCGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGCTTC
TCCCTTACGGGGCTCACAATGGCCAGAGAAGATTCGGTGAAGTGTCTGCGCTGCCTGCTCTAC
GCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGATGAGG
GACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTTG
ACTTACTTTTCTGTGGTTCATCCGGTCATGATTGCTGTTTGTGCTGTTTCTTATCATTTGTGGGG
ATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTTGCATGGTACTTTTGAAGT
TTGCTTGTCATTTTCTGTGTAGAACTGGCTTGTGGCGTTTGGACATATGAACAGGAACCTTATG
GTTCCAGTACAATGGTCAGATATGGTCACTTTGAAAGCCAGGATGACAAATTATGGATTACCT
AGATATCGGTGGCTTACTCATGCTTGGAAATTTTTTTTCAGAGAGAGTTTAAAGTGTGTGGAGTA
GTATATTTCACTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCCAGATTCCTGCTGTGTT
AGAGAATTCCCAGGATGTTCCAAACAGGCCACCAGGAAGATCTCAGTGACCTTTATCAAGAG
GGTGTGGGAAGAAAATGTATTCCTTTTTTGAGAGGAACCAACAACCTGCAGGTGCTGAGGTTT
CTGGGAATCTCCATTGGGGTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTGG
GCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAAATGATGTCCTTGAAGAATGACAAC
TCTCAGCACCTGTATGTCCCTCAGTAGAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAA
CACACATCCATGGCAAACAGCTTTAATACACACTTTGAGATGGAGGAGTTATAAAAAGAAATG
TCACAGAAGAAAACCACAACTTGTTTTATTGGACTTGTGAATTTTTGAGTACATACTATGTG
TTTCAGAAATATGTAGAAATAAAAATGTTGCCATAAAATAACACCTAAGCATATACTATTCTA
TGCTTTAAATGAGGATGGAAAAGTTTCATGTCATAAGTCACCACCTGGACAATAATTGATGC
CCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGCCTGTGTATGACTTTTACTGAAC
ACAGTTATGTTTTGAGGCAGCATGGTTTTGATTAGCATTTCGCGATCCATGCAAACGAGTCACA
TATGGTGGGACTGGAGCCATAGTAAAGGTTGATTTACTTCTACCACTAGTATATAAAGTACT
AATTAAATGCTAACATAGGAAGTTAGAAAATACTAATAACTTTTATTACTCAGCGATCTATTC
TTCTGATGCTAAATAAATTATATATCAGAAAACCTTCAATATTGGTGACTACCTAAATGTGAT
TTTTGCTGGTTACTAAAATATTCTTACCCTTAAAAGAGCAAGCTAACACATTGTCTTAAGCT
GATCAGGGATTTTTTGTATATAAGTCTGTGTAAATCTGTATAATTCAGTCGATTTTCAGTTCT
GATAATGTTAAGAATAACCATTATGAAAAGGAAAATTTGTCCTGTATAGCATCATTATTTTTA
GCCTTTCTCTGTTAATAAAGCTTTACTATTCTGTCTTGGGCTTATATTACACATATAACTGTTA
TTTAAATACTTAACCACTAATTTTGAAAATTACCAGTGTGATACATAGGAATCATTATTCAGA
ATGTAGTCTGGTCTTTAGGAAGTATTAATAAGAAAATTTGCACATAACTTAGTTGATTCAGAA
AGGACTTGATGCTGTTTTTCTCCCAAATGAAGACTCTTTTTGACACTAAACACTTTTTAAAA
AGCTTATCTTTGCCTTCTCCAAACAAGAAGCAATAGTCTCCAAGTCAATATAAATTCTACAGA
AAATAGTGTCTTTTTCTCCAGAAAATGCTTGTGAGAATCATTAACATGTGACAATTTAG
AGATTCTTTGTTTTATTTCACTGATTAATATACTGTGGCAAATTACACAGATTATTAATTTT
TTTACAAGAGTATAGTATATTTATTTGAAATGGGAAAAGTGCATTTTACTGTATTTTGTGTAT
TTTGTTTATTTCTCAGAATATGGAAAGAAAATTAATGTGTCAATAAATATTTTCTAGAGAG
TAA

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FIGURE 324

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880

><subunit 1 of 1, 305 aa, 1 stop

><MW: 35383, pI: 5.99, NX(S/T): 0

MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPVV
HPVMIAVCCFLIIVGMLGYCGTVKRNLLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWS
DMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTENDWPPDSCCVREFPGC
SKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWALYYDR
REPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

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FIGURE 325

AGCAGTGCATTGCTGGAGCGAGGAGAAGCTCACGAATCAGCTGCAGGTCTCTGTTTTGAAAAA
GCAGAGATACAGAGGCAGAGGAAAAGGGTGGACTCCTATGTGACCTGTTCTTAGAGCAAGACA
ATCACCATCTGAATTCCAGAAGCCCTGTTTCATGGTTGGGGATATTTTCTCGACTGCATGGAAT
CAGAAAGAAGCAAAAGGATGGGAAATGCCTGCATTCCCCTGAAAAGAATTGCTTATTTCCCTAT
GTCTCTTATCTGCGCTTTTGTGCTGACTGAGGGGAAGAAACCAGCGAAGCCAAAATGCCCTGCCG
TGTGTACTTGTACCAAAGATAATGCTTTATGTGAGAATGCCAGATCCATTCCACGCACCGTTC
CTCCTGATGTTATCTCATTATCCTTTGTGAGATCTGGTTTTACTGAAATCTCAGAAGGGAGTT
TTTTATTCACGCCATCGCTGCAGCTCTTGTTATTCACATCGAACTCCTTTGATGTGATCAGTG
ATGATGCTTTTATTGGTCTTCCACATCTAGAGTATTTATTCATAGAAAACAACAACATCAAGT
CAATTTCAAGACATACTTTCCGGGGACTAAAGTCATTAATTCACCTTGAGCCTTGCAAACAACA
ATCTCCAGACACTCCCAAAGATATTTTCAAAGGCCTGGATTCTTTAACAAATGTGGACCTGA
GGGGTAATTCATTTAATTGTGACTGTAACTGAAATGGCTAGTGGAATGGCTTGGCCACACCA
ATGCAACTGTTGAAGACATCTACTGCGAAGGCCCCCAGAATACAAGAAGCGCAAAATCAATA
GTCTCTCCTCGAAGGATTTTCGATTGCATCATTACAGAATTTGCAAAGTCTCAAGACCTGCCTT
ATCAATCATTGTCCATAGACACTTTTTCTTATTTGAATGATGAGTATGTAGTCATCGCTCAGC
CTTTTACTGGAAAATGCATTTTCCTTGAATGGGACCATGTGGAAAAGACCTTCCGGAATTATG
ACAACATTACAGGCACATCCACTGTAGTATGCAAGCCTATAGTCATTGAACTCAGCTCTATG
TTATTGTGGCCCAGCTGTTTGGTGGCTCTCACATCTATAAGCGAGACAGTTTTGCAAATAAAT
TCATAAAAATCCAGGATATTGAAATTCTCAAAATCCGAAAACCCAATGACATTGAAACATTCA
AGATTGAAAACAACTGGTACTTTGTTGTTGCTGACAGTTCAAAAGCTGGTTTTACTACCATTTAC
AAATGGAACGGAAACGGATTCTACTCCCATCAATCCTTACACGCGTGGTACAGGGACACTGAT
GTGGAATATCTAGAAATAGTCAGAACACCTCAGACACTCAGAACGCCTCATTTAATTCTGTCT
AGTAGTTCCCAGCGTCCTGTAATTTATCAGTGGAAACAAAGCAACACAATTATTCACTAACCAA
ACTGACATTCCTAACATGGAGGATGTGTACGCAGTGAAGCACTTCTCAGTGAAAGGGGACGTG
TACATTTGCTTGACAAGATTCATTGGTGATTCCAAAGTCATGAAATGGGGAGGCTCCTCGTTC
CAGGATATTCAGAGGATGCCATCGCGAGGATCCATGGTGTTCAGCCTCTTCAAATAAATAAT
TACCAATATGCAATTCTTGGAAGTGATTACTCCTTTACTCAAGTGATAACTGGGATGCAGAG
AAAGCCAAATTTGTGAAATTTTCAGGAATTAAATGTTTCAGGCACCAAGATCATTACACATGTG
TCCATTAATAAGCGTAATTTTCTTTTGTCTCCAGTTTTAAGGGAAATACACAGATTTACAAA
CATGTACATAGTTGACTTAAGCGCATGAGACACCAAATTCCTGTGGCTGCCATCAGAAATTTTCT
ACAGTACATGACCCGGATGAACTCAATGCATGATGACTCTTCTTATCACACTTGCAAATGAAT
GCCTTTCAAACATTGAGACTGCTAGAACCAAGCACTACCAGTATCTCCATCCTTAAGTGTCCA
GTCCAGTGATGTGGGAAGTTACCTTTTATAAGACAAAATTTAATTGTGTAAGTGTCTTTGCA
GTGAAGATGTGTAAATAAGCGTTTAAATGGTATCTGTTACTCCAAAAAGAAATATTAATATGTA
CTTTTCCATTTATTTATTCATGTGTACAGAAACAACTGCCAAATAAATGTTTACATTTTCTT
TCATA

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FIGURE 326

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68882
><subunit 1 of 1, 557 aa, 1 stop
><MW: 63818, pI: 8.61, NX(S/T): 3
MESERSKRMGNACIPLKRIAYFLCLLSALLLTEGKKPAKPKCPAVCTCTKDNALCENARS
IPRTVPPDVISLSFVRSGFTEISEGSFLFTPSLQLLLFTSNSFDVISDDAFIGLPHLEYL
FIENNNIKSISRHTFRGLKSLIHLSLANNNLQTLPKDIFKGLDSL TNVDLRGNSFNCDCK
LKWLVEWLGHGTNATVEDIYCEGPPEYKKRKINSLSSKDFDCIITEFAKSQDLPLYQSLSID
TFSYLNDEYVVIAQPFTGKCIFLEWDHVEKTFERNYDNITGTSTVVCKPIVIETQLYVIVA
QLFGGSHIYKRDSFANKFIKIQDIEILKIRKPNDIETFKIENNWFV VADSSKAGFTTIY
KWNNGFGFYSHQSLHAWYRDTDVEYLEIVRTPQTLRTPHLILSSSSQRPVIYQWNKATQLF
TNQTDIPNMEDVYAVKHFSVKGDVYICLTRFIGDSKVMKWGGSSFQDIQRMP SRGSMVFQ
PLQINNYQYAILGSDYSFTQVYNWDAEKAKFVKFQELNVQAPRSFTHVSINKRNF LFASS
FKGNTQIYKHVIVDLA
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Important features of the protein:**Signal peptide:**

Amino acids 1-34

Transmembrane domain:

Amino acids 281-306

N-glycosylation sites:

Amino acids 192-196;277-281;422-426

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 310-314

Tyrosine kinase phosphorylation sites:

Amino acids 228-235;378-385

N-myristoylation sites:

Amino acids 172-178;493-499

Amidation site:

Amino acids 33-37

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FIGURE 327

CCAAGGCCAGAGCTGTGGACACCTTATCCCACTCATCCTCATCCTCTTCCTCTGATAAAGCCC
CTACCAGTGCTGATAAAGTCTTTCTCGTGAGAGCCTAGAGGCCTTAAAAAAAAAAGTGCTTGA
AAGAGAAGGGGACAAAGGAACACCAGTATTAAGAGGATTTTCCAGTGTTTCTGGCAGTTGGTC
CAGAAGGATGCTCCTCCATTCTGCTTCTCACCTGCCTCTTCATCACAGGCACCTCCGTGTCACC
CGTGGCCCTAGATCCTTGTTCTGCTTACATCAGCCTGAATGAGCCCTGGAGGAACACTGACCA
CCAGTTGGATGAGTCTCAAGGTCTCCTCTATGTGACAACCATGTGAATGGGGAGTGGTACCA
CTTCACGGGCATGGCGGGAGATGCCATGCCTACCTTCTGCATACCAGAAAACCACTGTGGAAC
CCACGCACCTGTCTGGCTCAATGGCAGCCACCCCTAGAAAGGCGACGGCATTGTGCAACGCCA
GGCTTGTGCCAGCTTCAATGGGAACCTGCTGTCTCTGGAACACCACGGTGGAAGTCAAGGCTTG
CCCTGGAGGCTACTATGTGTATCGTCTGACCAAGCCCAGCGTCTGCTTCCACGTCTACTGTGG
TCATTTTTATGACATCTGCGACGAGGACTGCCATGGCAGCTGCTCAGATAACCAGCGAGTGCAC
ATGCGCTCCAGGAACTGTGCTAGGCCCTGACAGGCAGACATGCTTTGATGAAAATGAATGTGA
GCAAAACAACGGTGGCTGCAGTGAGATCTGTGTGAACCTCAAAAACCTCCTACCGCTGTGAGTG
TGGGGTTGGCCGTGTGCTAAGAAAGTGATGGCAAGACTTGTGAAGACGTTGAAGGATGCCACAA
TAACAATGGTGGCTGCAGCCACTCTTGCCCTGGATCTGAGAAAGGCTACCAGTGTGAATGTCC
CCGGGGCCTGGTGTCTGTCTGAGGATAACCACACTTGCCAAGTCCCTGTGTTGTGCAAATCAAA
TGCCATTGAAGTGAACATCCCCAGGGAGCTGGTTGGTGGCCTGGAGCTCTTCCTGACCAACAC
CTCCTGCCCAGGAGTGTCCAACGGCACCCTGTCAACATCCTCTTCTCTCAAGACATGTGG
TACAGTGGTCGATGTGGTGAATGACAAGATTGTGGCCAGCAACCTCGTGACAGGTCTACCCAA
GCAGACCCCGGGGAGCAGCGGGGACTTCATCATCCGAACCAGCAAGCTGCTGATCCCGGTGAC
CTGCGAGTTTCCACGCCTGTACACCATTTCTGAAGGATACGTTCCCAACCTTCGAAACTCCCC
ACTGGAAATCATGAGCCGAAATCATGGGATCTTCCCATTCACTCTGGAGATCTTCAAGGACAA
TGAGTTTGAAGAGCCTTACCGGGAAGCTCTGCCCACCCTCAAGCTTCGTGACTCCCTCTACTT
TGGCATTGAGCCCGTGGTGCACGTGAGCGGCTTGGAAGCTTGGTGGAGAGCTGCTTTGCCAC
CCCCACCTCCAAGATCGACGAGGTCTGAAATACTACCTCATCCGGGATGGCTGTGTTTCAGA
TGACTCGGTAAAGCAGTACACATCCCGGGATCACCTAGCAAAGCACTTCCAGGTCCCTGTCTT
CAAGTTTGTGGGCAAAGACCACAAGGAAGTGTCTGCACTGCCGGGTCTTGTCTGTGGAGT
GTTGGACGAGCGTTCCCGCTGTGCCAGGGTTGCCACCGGCGAATGCGTCGTGGGGCAGGAGG
AGAGGACTCAGCCGGTCTACAGGGCCAGACGCTAACAGGCGGCCCGATCCGCATCGACTGGGA
GGACTAGTTTCGTAGCCATACCTCGAGTCCCTGCATTGGACGGCTCTGCTCTTTGGAGCTTCTC
CCCCACCGCCCTCTAAGAACATCTGCCAACAGCTGGGTTTCAGACTTCACACTGTGAGTTCAG
ACTCCCAGCACCACTCACTCTGATTCTGGTCCATTCACTGGGACAGGTACAGCACTGCTG
AACAAATGTGGCCTGGGTGGGGTTTCATCTTTCTAGGGTTGAAAATAAACTGTCCACCCAGAA
AGACACTACCCCATTTCCCTCATTTCTTTCCTACACTTAAATACCTCGTGTATGGTGAATC
AGACCACAAAATCAGAAGCTGGGTATAATATTTCAAGTTACAAACCCTAGAAAAATTAAACAG
TTACTGAAATTATGACTTAAATACCAATGACTCCTTAAATATGTAAATTATAGTTATACCTT
GAAATTTCAATTCAAATGCAGACTAATTATAGGGAATTTGGAAGTGTATCAATAAAACAGTAT
ATAATTTT

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FIGURE 328

MPPFLLLTCLFITGTSVSPVALDPCSAYISLNEPWRNTDHQLDESQGPPLCDNHVNGEWYHFT
GMAGDAMPTFCIPENHCGTHAPVWLNGSHPLEGDGIVQRQACASFNGNCCLWNTTVEVKACPG
GYVYRLTKPSVCFHVYCGHFYDICDEDEDCHGSCSDTSECTCAPGTVLGPDRQTCFDENECEQN
NGGCSEICVNLKNSYRCECGVGRVLRSDGKTCEDEVEGCHNNNGGCSHSLGSEKGYQCECPRG
LVLSEDNHTCQVPVLCKSNAIEVNI PRELVGGLELFLNTSCRGVSNNGTHVNI LFSLKTCGTV
VDVVNDKIVASNLVTGLPKQTPGSSGDFIIRTSKLLIPVTCEFPRLYTISEGYVPNLRNSPLE
IMSRNHGIFPFTLEIFKDNEFEOPYREALPTLKL RDSLYFGIEPVVHVSGLES LVESCFATPT
SKIDEVLKYYLIRDGCVSDDSVKQYTSRDHLAKHFQVPVFKFVGVGDHKEVFLHCRVLVCGVLD
ERSRCAQGCHRRMRRGAGGEDSAGLQGQTLTGGP I RIDWED

Important features of the protein:**Signal peptide:**

amino acids 1-16

N-glycosylation sites.

amino acids 89-93, 116-120, 259-263, 291-295, 299-303

Tyrosine kinase phosphorylation sites.

amino acids 411-418, 443-451

N-myristoylation sites.amino acids 226-232, 233-239, 240-246, 252-258, 296-302, 300-306,
522-528, 531-537**Aspartic acid and asparagine hydroxylation site.**

amino acids 197-209

ZP domain proteins.

amino acids 431-457

Calcium-binding EGF-like proteins.

amino acids 191-212, 232-253

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FIGURE 329

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCCT
GCACTCGGGCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGACC
TGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACC
GGGAGGATCACAGAGCCAGC**ATG**TTACAGGATCCTGACAGTGATCAACCTCTGAACAGCCTCG
ATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGATCCCCA
TCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTTGTGGTTGTCCTCATCAAGGTGATTC
TGGATAAATACTACTTCCTCTGCGGGCAGCCTCTCCACTTCATCCCGAGGAAGCAGCTGTGTG
ACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTCCCCGAAG
GGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCCACTGCAGGTGCTGGACTCGGCCA
CAGGGAAGTGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAGACAGCCTGTA
GGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGATGTTGTTGAAA
TCACAGAAAAACAGCCAGGAGCTTCGCATGCGGAACTCAAGTGGGCCCTGTCTCTCAGGCTCCC
TGGTCTCCCTGCACTGTCTTGCTGTGGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGTGGGG
AGGAGGCCTCTGTGGATTCTTGCCCTTGGCAGGTCAGCATCCAGTACGACAAACAGCACGTCT
GTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCACGGCAGCCCACTGCTTCAGGAAACATA
CCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAACTGGGCAGCTTCCCATCCCTGG
CTGTGGCCAAGATCATCATATTGAATTCAACCCCATGTACCCCAAAGACAATGACATCGCCC
TCATGAAGCTGCAGTTCCCACTCACTTTCTCAGGCACAGTCAGGCCCATCTGTCTGCCCTTCT
TTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGATGGGGCTTTACGAAGCAGA
ATGGAGGGAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCAGGTCATTGACAGCACACGGT
GCAATGCAGACGATGCGTACCAGGGGGGAAGTCACCGAGAAGATGATGTGTGCAGGCATCCCGG
AAGGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGGCCCTGATGTACCAATCTGACCAGT
GGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGGGGGCCCGAGCACCCCAGGAGTAT
ACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATGTCTGGAAGGCTGAGCTG**TAAT**GCT
GCTGCCCCCTTTCAGTGCTGGGAGCCGCTTCCTTCCTGCCCTGCCACCTGGGGATCCCCCAA
AGTCAGACACAGAGCAAGAGTCCCCTTGGGTACACCCCTCTGCCCACAGCCTCAGCATTTCTT
GGAGCAGCAAAGGGCCTCAATTCTGTAAGAGACCCCTCGCAGCCCAGAGGCGCCCAGAGGAAG
TCAGCAGCCCTAGCTCGGCCACACTTGGTGCTCCCAAGCATCCCAGGGAGAGACACAGCCCACT
GAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAAGGAACCTTCCCACACTACTGAATGGAAGC
AGGCTGTCTTGTAAGGCCAGATCACTGTGGGCTGGAGAGGAGAAGGAAAGGGTCTGCGCCA
GCCCTGTCCGTCTTCACCCATCCCCAAGCCTACTAGAGCAAGAAACCAGTTGTAATATAAAAT
GCACTGCCCTACTGTTGGTATGACTACCGTTACCTACTGTTGTCATTGTTATTACAGCTATGG
CCACTATTATTAAAGAGCTGTGTAACATCTCTGGCAAAAAAAAAAAAA

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FIGURE 330

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47644, pI: 5.18, NX(S/T): 2
MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALLSLASIIIVVVLIKVILDKYYFL
CGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLDSATGNWFSA
CFDNFTEALAETACRQMGYSRAVEIGPDQDLDVVEITENSQELMRNSSGPCLSGSIVSLHCL
ACGKSLKTFRVVGEEASVDSWPWQVSIQYDKQHVC GGSILDPHWVLTAAHCFRKHTDVFNWK
VRAGSDKLGSFPSLAVAKIIIIIEFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFDEELTP
ATPLWIIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGGVDTC
QGDSGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWKAEL
```

Transmembrane domain:

amino acids 32-53 (typeII)

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FIGURE 331

AGTGGTTCGATGGGAAGGATCTTTCTCCAAGTGGTTCCTCTTGAGGGGAGCATTCTGCTGGC
TCCAGGACTTTGGCCATCTATAAAGCTTGGCAATGAGAAATAAGAAAATTCTCAAGGAGGACG
AGCTCTTGAGTGAGACCAACAAGCTGCTTTTCACCAAATTGCAATGGAGCCTTTGAAATCA
ATGTTCCAAAGCCCAAGAGGAGAAATGGGGTGAACCTCTCCCTAGCTGTGGTGGTCATCTACC
TGATCCTGCTCACCGCTGGCGCTGGGCTGCTGGTGGTCCAAGTTCTGAATCTGCAGGCGCGGC
TCCGGGTCCTGGAGATGTATTTCTCAATGACACTCTGGCGGCTGAGGACAGCCCGTCCTTCT
CCTTGCTGCAGTCAGCACACCCTGGAGAACACCTGGCTCAGGGTGCATCGAGGCTGCAAGTCC
TGCAGGCCCAACTCACCTGGGTCCGCGTCAGCCATGAGCACTTGCTGCAGCGGGTAGACAAC
TCACTCAGAACCCAGGGATGTTTCAAGTCAAAGGTGAACAAGGCGCCCGAGGTCTTCAAGGTC
ACAAGGGGGCCATGGGCATGCCTGGTGCCCTGGCCCGCCGGGACCACCTGCTGAGAAGGGAG
CCAAGGGGGCTATGGGACGAGATGGAGCAACAGGCCCTCGGGACCCCAAGGCCACCGGGAG
TCAAGGGAGAGGCGGGCCTCCAAGGACCCAGGGTGCTCCAGGGAAGCAAGGAGCCACTGGCA
CCCCAGGACCCCAAGGAGAGAAGGGCAGCAAAGGCGATGGGGGTCTCATTTGGCCCAAAAGGG
AAACTGGAACAAAGGGAGAGAAAGGAGACCTGGGTCTCCAGGAAGCAAAGGGGACAGGGGCA
TGAAAGGAGATGCAGGGGTCTGGGGCCTCCTGGAGCCCAGGGGAGTAAAGGTGACTTCGGGA
GGCCAGGCCCACCAGGTTTGGCTGGTTCCTGGAGCTAAAGGAGATCAAGGACAACCTGGAC
TGCAGGGTGTTCGGGGCCCTCCTGGTGAGTGGGACACCCAGGTGCCAAGGGTGAGCCTGGCA
GTGCTGGCTCCCCTGGGCGAGCAGGACTTCCAGGGAGCCCCGGGAGTCCAGGAGCCACAGGCC
TGAAAGGAAGCAAAGGGGACACAGGACTTCAAGGACAGCAAGGAAGAAAAGGAGAATCAGGAG
TTCCAGGCCCTGCAGGTGTGAAGGGAGAACAGGGGAGCCAGGGCTGGCAGGTCCCAAGGGAG
CCCCTGGACAAGCTGGCCAGAAGGGAGACCAGGGAGTGAAAGGATCTTCTGGGGAGCAAGGAG
TAAAGGGAGAAAAAGGTGAAAGAGGTGAAACTCAGTGTCCGTGAGGATTGTCGGCAGTAGTA
ACCGAGGCCGGGCTGAAGTTTACTACAGTGGTACCTGGGGGACAATTTGCGATGACGAGTGGC
AAAATTCTGATGCCATTGTCTTCTGCCGATGCTGGGTACTCCAAAGGAAGGGCCCTGTACA
AAGTGGGAGCTGGCACTGGGCAGATCTGGCTGGATAATGTTTCAAGTGTGCGGGCACGGAGAGTA
CCCTGTGGAGCTGCACCAAGAATAGCTGGGGCCATCATGACTGCAGCCACGAGGAGGACGCAG
GCGTGGAGTGCAGCGTCTGACCCCGAAACCCTTTCACTTCTCTGCTCCCGAGGTGTCCTCGGG
CTCATATGTGGGAAGGCAGAGGATCTCTGAGGAGTCCCTGGGGACAACCTGAGCAGCCTCTGG
AGAGGGGCCATTAATAAAGCTCAACATCATTGA

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FIGURE 332

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA68886
><subunit 1 of 1, 520 aa, 1 stop
><MW: 52658, pI: 9.16, NX(S/T): 3
MRNKKILKEDELLSETQQAAFHQIAMEPFEINVPKPKRRNGVNFSLAVVVIYLILLTAGAGLL
VVQVLNLQARLRVLEMYFLNDTLAAEDSPSFSLLQSAHPGEHLAQGASRLQVLQAQLTWVRVS
HEHLLQRVDNFTQNPGMFRIKGEQGAPGLQGHKGAMGMPGAPGPPGPPAEKGAKGAMGRDGAT
GPSGPQGPPGVKGEAGLQGPQGAPGKQGATGTPGPQGEKGSKGDGGLIGPKGETGTKGEKGD
GLPGSKGDRGMKGDAGVMGPPGAQGSKGDFGRPGPPGLAGFPGAAGDQGGPGLQGVPPGAV
GHPGAKGEPGSAGSPGRAGLPGSPGSPGATGLKGSKGDGTGLQGGQGRKGESGVPGPAGVKGEQ
GSPGLAGPKGAPGQAGQKGDQGVKGSSGEQGVKGEKGERGENSVSVRIVGSSNRGRAEVYYSG
TWGTICDDEWQNSDAIVFCRMLGYSKGRALYKVGAGTGQIWL DNVQCRGTESTLWSCTKNSWG
HHDCSHEEDAGVECSV

Transmembrane domain:

amino acids 47-66 (type II)

N-glycosylation sites.

amino acids 43-47, 83-87, 136-140

Tyrosine kinase phosphorylation site.

amino acids 432-440

N-myristoylation sites.amino acids 41-47, 178-184, 253-259, 274-280, 340-346, 346-352,
400-406, 441-447, 475-481, 490-496, 515-521**Amidation site.**

amino acids 360-364

Leucine zipper pattern.

amino acids 56-78

Speract receptor repeat

amino acids 422-471, 488-519

Clq domain proteins.

amino acids 151-184, 301-334, 316-349

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FIGURE 333

GGGCTGTTGATTTGTGGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCTG
CCTCTGGCATATGCACACACTCACACATTCTGTACACCCGTCACACACACATACCATGTTCT
CCATCCCCCAGGTCCAGCCCTCAGTGCTGTCCCATCCAGCAGGGCTACCCTGAAGCTCTGGC
TGCAGCCCTCCCGTCCAGTGGGCAGGCGGCTTCATCCCTCCTTTCTCTCCCAAAGCCCAACTG
CTGTCACTGCATGCTCTGCCAAGGAGGAGGGAAGTGCAGTGACAGCAGGAGTAAGAGTGGGAG
GCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTCAGCGAGCCTAGAGAGGGCAGACTA
TCAGGGTGCCGGCGGTGAGAATCCAGGGAGAGGAGCGGAAACAGAAGAGGGGCAGAAGACCGG
GGCACTTGTGGGTTGCAGAGCCCCTCAGCC**ATG**TTGGGAGCCAAGCCACACTGGCTACCAGGT
CCCCTACACAGTCCCGGGCTGCCCTTGTTCTGGTGCTTCTGGCCCTGGGGGCCGGGTGGGCC
CAGGAGGGGTGAGAGCCCGTCCCTGCTGGAGGGGGAGTGCCTGGTGGTCTGTGAGCCTGGCCGA
GCTGCTGCAGGGGGGCCCGGGGAGCAGCCCTGGGAGAGGCACCCCTGGGCGAGTGGCATT
GCTGCGGTCCGAAGCCACCACCATGAGCCAGCAGGGGAAACCGCAATGGCACCAGTGGGGCC
ATCTACTTCGACCAGGTCCTGGTGAACGAGGGCGGTGGCTTTGACCGGGCCTCTGGCTCCTTC
GTAGCCCCGTCCGGGGTGTCTACAGCTTCCGGTTCCATGTGGTGAAGGTGTACAACCGCCAA
ACTGTCCAGGTGAGCCTGATGCTGAACACGTGGCCTGTCACTCTCAGCCTTTGCCAATGATCCT
GACGTGACCCGGGAGGCAGCCACCAGCTCTGTGCTACTGCCCTTGGACCCTGGGGACCGAGTG
TCTCTGCGCTGCGTCGGGGGAATCTACTGGGTGGTTGGAAATACTCAAGTTTCTCTGGCTTC
CTCATCTTCCCTCTCT**TG**AGGACCCAAGTCTTTCAAGCACAGAATCCAGCCCCTGACAACTTT
CTTCTGCCCTCTCTTGCCCCAGAAACAGCAGAGGCAGGAGAGAGACTCCCTCTGGCTCCTATC
CCACCTCTTTGCATGGGACCCTGTGCCAAACACCCAAGTTTAAGAGAAGAGTAGAGCTGTGGC
ATCTCCAGACCAGGCCTTTCCACCCACCCACCCCAAGTTACCCTCCCAGCCACCTGCTGCATC
TGTTCTCTGCTGCTCCTCCGGTTCCCCACCCAGCTTCTGCTCAATGCTGATCAGGGACAGG
TGGCGCAGGTGAGCCTGACAGGCCCCACAGGAGCCAGATGGACAAGCCTCAGCGTACCCTG
CAGGCTTCTTCTGTGAGGAAAGCCAGCATCACGGATCTCAGCCAGCACCGTCAGAAGCTGAG
CCAGCACCGTATGGGCTAGGGTGGGAGGCTCAGCCACAGGCAGAAGGGTGGGAAGGGCCTGGA
GTCTGTGGCTGGTGAGGAAGGAAGGAGGGTGTATTGTCTAGACTGAACATGGTACACATTCTG
CATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCTGGCTGTCTTCTATGCTGGATCCCAGAT
GGA CTCTGGCCCTTACCTCCCCACCTGAGATTAGGGTGAGTGTGTTTGCTCTGGCTGAGAGCA
GAGCTGAGAGCAGGTATACAGAGCTGGAAGTGGACCATGGAAAACATCGATAACCATGCATCC
TCTTGCTTGGCCACCTCCTGAAACTGCTCCACCTTTGAAGTTTGAACCTTTAGTCCCTCCACAC
TCTGACTGCTGCCTCCTTCCCTCCCAGCTCTCTCACTGAGTTATCTTCACTGTACCTGTTCCAG
CATATCCCCACTATCTCTCTTTCTCCTGATCTGTGCTGTCTTATTCTCCTCCTTAGGCTTCT
ATTACCTGGGATTCCATGATTCACTTCTTCAGACCTCTCCTGCCAGTATGCTAAACCTCCC
TCTCTCTTTCTTATCCCGCTGTCCCATTTGGCCAGCCTGGATGAATCTATCAATAAAACAACT
AGAGAATGGTGGTCAGTGAGACACTATAGAATTACTAAGGAGAAGATGCCTCTGGAGTTTGA
TCGGGTGTTACAGGTACAAGTAGGTATGTTGCAGAGGAAAATAAATATCAAAGTGTATACTAA
AATTAAAA

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FIGURE 334

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180
><subunit 1 of 1, 205 aa, 1 stop
><MW: 21521, pI: 7.07, NX(S/T): 1
MLGAKPHWLPGPLHSPGLPLVLVLLALGAGWAQEGSEPVLLERGECLVVCEPGRAAAGGPGGAA
LGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVYSF
RFHVVKVYNRQTVQVSLMLNTWPVISAFANDPDVTREAAATSSVLLPLDPGDRVSLRLRRGNLL
GGWKYSSFSGFLIFPL
```

Signal peptide:
amino acids 1-32

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FIGURE 336

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop
><MW: 43831, pI: 9.64, NX(S/T): 3
MKTLLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRSK
VEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLI AVL YFTWLVFDWNTPKKGRRSQW
VRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGYHPHGIMGLGAF CNFSTEATEVSKKFPGIR
PYLATLAGNFRMPVLR EYLMMSGGICPVSRDTIDYLLSKNGSGNAIIIVVGGAESLSSMPGKN
AVTLRNRKGFVKLALRHGADLVPIYSFGENEVYKQVIFEEGSWGRWVQKKFQKYIGFAPCI FH
GRGLFSSDTWGLVPYSKPITTVVGEPITIPKLEHPTQQDIDLYHTMYMEALVKLFDKHKTKEG
LPETEVLEVN
```

Important features of the protein:**Transmembrane domain:**

amino acids 76-97

N-glycosylation sites.

amino acids 60-63, 173-176, 228-231

N-myristoylation sites.

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

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FIGURE 337

GGGCGGCGGGATGGGGGCCGGGGCGGGCGGGCGCCGACTCGCTGAGGCCCGACGCGAGGGCCGGGGCCGGGCCCCA
GGGCCGAGGAGCGCGGGCGGCCAGAGCGGGGGCGCGGAGGCGACGCCGGGGACGCCCGCGCGACGAGCAGGTGGCG
GCGGCTGCAGGCTTGTCCAGCCGGAAGCCCTGAGGGCAGCTGTTCCCACTGGCTCTGCTGACCTTGTGCCTTGGA
CGGCTGTCTCAGCGAGGGGCGGTGCACCCGCTCCTGAGCAGCGCCATGGGCGCTGCTGGCCTTCTGAAGACCCA
GTTCTGTCTGCACCTGCTGGTGGCTTTGTCTTCGTGGTGGTGGTCTGGTTCATCAACTTCGTCCAGCTGTGCAC
GCTGGCGCTCTGGCCGGTCAGCAAGCAGCTCTACCGCCGCTCAACTGCCGCTCGCTACTCACTCTGGAGCCA
ACTGGTCATGCTGTGGAGTGGTGGTCTCTGCACGGAGTGTACACTGTTACGGACACGGCCACGGTAGAGCGCTT
TGGGAAGGAGCACGCAGTCATCATCTCAACCACAACCTTCGAGATCGACTTCTCTGTGGGTGGACCATGTGTGA
GCGCTTCGGAGTGTGGGGAGCTCCAAGGTCTCGCTAAGAAGGAGCTGCTCTACGTGCCCTCATCGCTGGAC
GTGGTACTTTCTGGAGATTGTGTTCTGCAAGCGGAAGTGGGAGGAGACCGGGACACCGTGGTGAAGGGCTGAG
GCGCTGTGCGACTACCCCGAGTACATGTGTTCTCCTGTACTGCGAGGGGACCGCTTCACGGAGACCAAGCA
CCGCGTTAGCATGGAGGTGGCGGCTGCTAAGGGGCTTCTGTCTCAAGTACCACCTGCTGCCGCGGACCAAGGG
CTTCACCACCGCAGTCAAGTGCCTCCGGGGGACAGTCGAGCTGTCTATGATGTAACCTTCACTTCAAGGAAA
CAAGAACCCGCTCCCTGCTGGGGATCCTCTACGGGAAGAAGTACGAGCGGACATGTGCGTGAGGAGATTTCTCT
GGAAGACATCCCGCTGGATGAAAAGGAAGCAGCTCAGTGGCTTCATAAACTGTACCAGGAGAAGGACGCGCTCCA
GGAGATATATAATCAGAAGGGCATGTTTCCAGGGGAGCAGTTTAAAGCCTGCCCGGAGGCGCTGGACCTCCTGAA
CTTCCTGTCTGGGCCACCATTTCTCTGTCTCCCTCTTCAGTTTTGTCTTGGGCGCTTTGCCAGCGGATCACC
TCTCTGATCCTGACTTTCTTGGGGTTTGTGGGAGCAGCTTCTTTGGAGTTCGCAGACTGATAGGAGAATCGCT
TGAACCTGGGAGGTGGAGATTGCAGTGAAGCTGAGATGGCATCACTGTACTCCAGCCTAGGCAACAGAGCAAGACT
CAGTCTCAAAAAAAAAAAAAAAAAACAAAAACCCAGAAATCTGGAGTTGAACTGTGTAGTTACTGACATGAAAA
ATTCAGTAGAGGCTGAACAGCAGATTTGAGCAGGCAGAAAAAATCAGCAAGCTTGAAGATGGTACCTTGAGATT
TTTCAGGCTAATGAAAAAGAATGAAGGAAAATTAACAGCCTCAGAGACCCATGGTGCACCGTCACACAAATCAA
CATATGCATGATGAGAGTCCAGAGGAGAGAGAGAAAGGTCAGAAAGAATGGCCACAAGCTGATGAAAAACA
GTAACCTACCCACTCAGGAAGCTCAGTGAACCTCAATGAGGATGAATATCAGAGATCCACACCTAGATATTTTCA
AATCAAAGTGTCAAATGACAAAGAATCTTGAAAGCAGCAAGAGATGAGCAACTTATCTTGTCAAAGGATCTTTG
ATCAGATTACAGCTCATTTCTCTCAGAAATCATGGGAGCCAGGAGATAGTGGGATGAACACTGTTGAAGGCAA
AACCTTCAACTGTAATTATTGGACTTTTGAGTCTTAGATGGTCTGACCTCTTGTCTTCAGGGACAGTTTTTCA
ATTTAATCCCTAATAACAATTAGTCAAGCTTCTTGACCTGTAGGAAGGCCTGTCTTTAGGCCGGGCACAGTGGC
TTACACCTGTAATCCAGCACTTTGGGAGGCCAGACGGGTGGATCATTTGGGGTCAGGCTGATCTCAAACCTCCT
GAGTTCAGGTGATCTGCCCGCTCAGCCTCCCAAAGTGTGTGATTGCAGGCGTGAGCCACTGCGCCTGGCCGGA
ATTTCTTTTAAAGGCTGAATGATGGGGGCCAGGCACGATGGCTCACGCCTGTGATCCCAAGTAGCTTGATTGTA
AACATGCACCCACATGCCTGGCTAATTTTTGTATTTTAGTAGAGACGTGTTAGCCAGGCTGGTCTCGATCTCCT
GACCTCAAGTGACCACCTGCCTCAGCCTCCCAAAGTACTGGGATTACAGGCGTGAGCCACTGTGCCTGGCCTTGA
GCATCTTGIGATGTGCTTATTGGCCATTTGTATATCTTCTATCTTCTTTGGGAAATGCTGTTCAGTCTCTTG
CCTTTTTTAAATTTTATTATTTATTTATTTATTTATTTTGGAGACAGGCTTGTGTTCTGTTGCCAGGCTGGAGTA
CAGTGGCACAGTCTTGGCTCACTGCAGCCTCGACCTCCTGGGCTGCAGTGATCCTCCACCTCAGCCTCCCTTGT
AGCTGTATTTTTTGTATTTTGTATTTGTAGCTGTAGTTTTTGTATTTTTTGTGGAGACAGATTTACCATGA
TGCCAGGCTGGTCTTGAACCTCTGAGCTCAAGTGATCTGCCTGCTTCAGCCTCCCAAAGTGCTGGGATTACAGA
CATGAGCCACTGCACCTGGCAAACCTCCCAAATTCACACACACACACAAAAACCACCTGATTCAAATGGGCA
GAGGGGCCGGGTGTGGCCCCAACTACCAGGGAGACTGAAGTGGGAGGATCGCTTGGGCATGAGAAGTCGAGGCTG
CAGTGAGTCGAGGTTGTGCGACTGCATTCCAGCCTGGACAACAGAGTGAGACCCTGTCTC

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FIGURE 338

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop
><MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLKTQFVLHLLVGFFVVSGLVINQVQLCTLALWPVSKQLYRRRLNCRLAYSLWSQLVM
LLEWWSCTECTLFQDQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFGVLGSSKVLAKKEL
LYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHRVSM
EVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVDVTLNFRGNKNPSLLGILYGKKYEAD
MCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLNFLSWA
TILLSPLFSFVLGVFASGSPLLILTF LGFVGAASFGVRRRLIGESLEPGRWRLQ
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 307-323, 335-352

Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169

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FIGURE 339

GATATTCTTTATTTTAAAGAATCTGAAGTACTATGCATCACTCCCTCCAATGTCCTGGGGCAG
CCACCAGGCATATTCATCTTTGTGTGTGTTTTCTTTGCTTTAGCACTGGGGCACTTCTTGC
TTATTTCTTTGGTAGGAAAGGGGCTCAGTTTGTCTTGTGGGGTTGGTGGCAGGCAGGCCGGCT
TACGCCTGATACGGCCCTGGGTTAGAAGGGAAGGGAAGATAAACTTTTATACAAATGGGGATA
GCTGGGGTCTGAGACCTGCTTCCTCAGTAAAATTCTTGGGATCTGCCTATACCTTCTTTTCTC
TAACCTGGCATAACCTGCTTAAAGCCTCTCAGGGCTTCTCTCTGTTCTTAGGATCAAAGTATT
TAGAGCTACAAGAGCCCTCATGGTCTGGCCCTGCCCCCTGGCCAGCTTCATTGTACATGTG
GTGTTCTCTTGTCTTCTGTAATGTGGTATGCCATGGGGTCTTGCACAAGCCTTTCCTCTT
TGGCTGGACACTGTTCCCTGCCCCCCCCATACTCTTCCTACTTAATATGTAGTCATCCTGCAG
ATTTCAATTCTAACATCATTTTCTCCAGGGATCCTGGCCTGACAGAATCTCATCTTGTTTAAT
GCTCTCATAAGACCACTTGTTTCCCTTTTGCAGCACTTGCCACTCAGTTGTATCTTTATGTGC
GTTTGTGGTTGTATGGGTTGTGTCTGTTCCCCAGAATGCCAGCTCTGAGCTGCGTGAGGGTC
AAGGGCATTGCTGTGCCTGCCAGGTATAGTGCCTACATGTGGTGGGTGCTCATGTTTTAGAGA
CTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCAGATGGTGTAGGGCC
CAGCATTGTAAATTCACACGTTGACTGTGCTTGTGAATTATCTGGGGATGCAGGTCCCTGATTC
AGTAGGCCCAGGTTGGGCATCTCTAACAACTCCACGTGATGCTGATGCTGGTCCTATGAAC
TATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGCTCACACCTATGATCCCA
GCACTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATTTCAAGACTAGCCTGGCCA
ACATGGTGGAAACCCCATCTGTACTAAAAATACACAAATTAGCTGGGCATGGTGGCACATGCCT
GTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTGAACCTGGGAGGCGGAGGTTG
CAGTGAGCCGAGATCAGGCCACTGTATTCCAACCAGGGTGACAGAGTGAGACTCTATGTCCAA
AAAAAAAAAA

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FIGURE 340

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234
><subunit 1 of 1, 143 aa, 1 stop
><MW: 15624, pI: 9.58, NX(S/T): 0
MHHSLQCPGAATRHHLCVCFSEFALALGHFLLISLVGKGLSLSCGVGGRQAGLRLIRPWVRE
GKINFYTNNGDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSFLGSKYLELQEPSWSGP
CPPGQLHCTCGVLLSFL

Important features of the protein:

Signal peptide:

amino acids 1-28

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FIGURE 341

CGCCATGGCCGGGCTATCCCGCGGGTCCGCGCGCGCACTGCTCGCCGCCCTGCTGGCGTCGACG
CTGTTGGCGCTGCTCGTGTGCGCCGCGCGGGGTGCGGGCGGGCCGGGACCACGGGGACTGGGAC
GAGGCCTCCCGGCTGCCGCGCTACCACCCCGCGAGGACGCGGCGCGCGTGGCCCGCTTCGTG
ACGCACGTCTCCGACTGGGGCGCTCTGGCCACCATCTCCACGCTGGAGGCGGTGCGCGGCCGG
CCCTTCGCCGACGTCCTCTCGCTCAGCGACGGGCCCCCGGGCGCGGGCAGCGGCGTGCCCTAT
TTCTACCTGAGCCCGCTGCAGCTCTCCGTGAGCAACCTGCAGGAGAATCCATATGCTACACTG
ACCATGACTTTGGCACAGACCAACTTCTGCAAGAAACATGGATTGATCCACAAAGTCCCCTT
TGTGTTACATAATGCTGTCAGGAACCTGTGACCAAGGTGAATGAAACAGAAATGGATATTGCA
AAGCATTGCTTATTCATTCGACACCCTGAGATGAAAACCTGGCCTTCCAGCCATAATTGGTTC
TTTGCTAAGTTGAATATAACCAATATCTGGGTCTGGACTACTTTGGTGGACCAAAAATCGTG
ACACCAGAAGAATATTATAATGTCACAGTTCAGTCAAGCAGACTGTGGTGAATTTAGCAACAC
TTATGAAGTTTCTTAAAGTGGCTCATACACACTTAAAAGGCTTAATGTTTCTCTGGAAAGCGT
CCCAGAATATTAGCCAGTTTTCTGTC

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FIGURE 342

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71269
><subunit 1 of 1, 220 aa, 1 stop
><MW: 24075, pI: 7.67, NX(S/T): 3
MAGLSRGSARALLAALLASTLLALLVSPARGRGGRDHGDWDEASRLPPLPPREDAARVAR
FVTHVSDWGALATISTLEAVRGRPFADVLSLSDGPPGAGSGVPYFYLSPLQLSVSNLQEN
PYATLTMTLAQTNFCKKHGFD PQSPLCVHIMLSGTVTKVNETEMDIAKHSLFIRHPMKT
WPSSHNWFFAKLNITNIWVLDYFGGPKIVTPEEYYNVTVQ
```

Important features of the protein:**Transmembrane domain:**

Amino acids 11-29

N-glycosylation sites:

Amino acids 160-164;193-197;216-220

N-myristoylation sites:

Amino acids 3-9;7-13;69-75;97-103

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FIGURE 343

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGAT
TATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTTTCAGCAACTAAAAAGCCACAG
GAGTTGAACTGCTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTACATT
AAAATCTGTTTTTTGTTCTCTTGTAACTAGCCTTTACCTTCCTAACACAGAGGATCTGTCACT
GTGGCTCTGGCCCCAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCACACCGT
CCCCTCGAAGCCGGGGACAGCCTCACCTTGTGGCCTCTCGCTGGAGCAGTGCCCTCACCAAC
TGTCTCACGTCTGGAGGCACTGACTCGGGCAGTGCAAGGTAGCTGAGCCTCTTGGTAGCTGCGG
CTTTCAAGGTGGGCCTTGCCCTGGCCGTAGAAGGGATTTGACAAGCCCGAAGATTTTCATAGGCG
ATGGCTCCCACTGCCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGGCCAGGACGG
GCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCCGCCCATCTAACCTTTT
CATGTCCTGCACATCACCTGATCCATGGGCTAATCTGAACTCTGTCCCAAGGAACCCAGAGCT
TGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTTTATGTGACAGGA
CTTGCAATTCTCCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCAGGGAAGGAACTTG
TGCCAAATTATGGGTCAGAAAAGATGGAGGTGTTGGGTATCACAAGGCATCGAGTCTCCTGC
ATTCAGTGGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACTCGGGACTCACCTCTG
GGGCCATCAGACAGCCGTTTCCGCCCCGATCCACGTACCAGCTGCTGAAGGGCAACTGCAGGC
CGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCAAGCCAGGGGCAGCCGTCTG
GGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCCCCTCCTTCCCTCTGAGAGGGCCCTCCTATGT
CCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGGCTAATGGCTCAGTGTTGGCCCAGGA
GGTCAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCTGTGCGAACACGGAAATGCCTCCAGT
AAGCACAGGCTGCAAAATCCCCAGGCAAAGGACTGTGTGGCTCAATTTAAATCATGTTCTAGT
AATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGTTCAAATGATCTCCAAGGGCCCT
TATACCCCAGGAGACTTTGATTTGAATTTGAAACCCCAAATCCAAACCTAAGAACCAGGTGCA
TTAAGAATCAGTTATTGCCGGGTGTGGTGGCCTGTAATGCCAACATTTTGGGAGGCCGAGGCG
GGTAGATCACCTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCCCTGTCTC
TACTAAAAATACAAAAAACTAGCCAGGCATGGTGGTGTGTGCCTGTATCCCAGCTACTCGGG
AGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGTGAAGGAGGCTGAGACAGGAGAATCACT
TCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGAAAAAATAAAAAAGAATTATGGTTATTT
GTAA

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FIGURE 344

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277
><subunit 1 of 1, 109 aa, 1 stop
><MW: 11822, pI: 8.63, NX(S/T): 0
MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTAS
PCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD .
```

Signal peptide:
amino acids 1-15

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FIGURE 345

[illegible]

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FIGURE 346

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286

><subunit 1 of 1, 671 aa, 1 stop

><MW: 74317, pI: 7.61; NX(S/T): 0

MPHAFKPGDLVFAKMKGYPHWPARIDDIADGAVKPPPKNKYPIFFFGTHETAFLGPKDLFPYDK
CKDKYGKPNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDDDEDRGVM
AVTAVTATAASDRMESDSDSDKSSDNSGLKRKTPALKMSVSKRARKASSDLDQASVSPSEEN
SESSSESEKTSQDFTPEKKA AVRAPRRGPLGGRKKKKAPSASDSDSKADSDGAKPEPVAMAR
SASSSSSSSSSSSDSDSVKKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSDEVDRISE
WKRRDEARRRELEARRRREQEEELRRLREQEKEEKERRRERADRGEAERGSGGSSGDELREDD
EPVKKRGRKGRGRGPPSSSDSEPEAELEAREAKKSAKKPQSSSTEPARKPGQKEKRV RPEEKQQ
AKPVKVERTRKRSEGFSMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRCLNALEELG
TLQVTSQILQKNTDVVATLKKIRRYKANKDVMKAAEVYTRLKSRVLGPKIEAVQKVNKAGME
KEKAEKLAGEEELAGEEAPQEKAEDKPDLSAPVNGEATSQKGESAEDKEHEEGRDSEEGPR
CGSSEDLHDSVREGPDLDRPGSDRQERERARGDSEALDEES

Signal peptide:

amino acids 1-13

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FIGURE 347

GTTGGTTCTCCTGGATCTTCACCTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATTAATTA
ACACCATTGAAAGAGAACATTGTTTTTCATCATGAATGCTAATAAAGATGAAAGACTTAAAGCCAGAAGCCAAGA
TTTTACCTTTTTCTGCTTTGATGATGCTAAGCATGACCATGTTGTTTCTTCCAGTCACTGGCAGCTTTGAAGCA
AAATATTCCAAGACTCAAGCTAACCTACAAAGACTTGCTGCTTTCAAATAGCTGTATTCCTTTTTGGGTTTCATC
AGAAGGACTGGATTTTCAAACCTCTCTCTTAGATGAGGAAAGAGGCAGGCTGCTCTGGGAGCCAAAGACCACAT
CTTTCTACTCAGTCTGGTTGACTTAAACAAAATTTTAAAGAAGATTTATTGGCCTGCTGCAAAGGAACGGGTGGA
ATTATGTAAATTAGCTGGGAAAGATGCCAATACAGAATGTGCAAATTTTCATCAGAGTACTTCAGCCCTATAACAA
AACTCACATATATGTGTGTGGAACCTGGAGCATTTCATCCAATATGTGGGTATATTGATCTTGGAGTCTACAAGGA
GGATATTATATTCAAACCTAGACACACATAATTTGGAGTCTGGCAGACTGAAATGTCTTTTCGATCCTCAGCAGCC
TTTTGCTTCAGTAATGACAGATGAGTACCTCTACTCTGGAACAGCTTCTGATTTTCTTGGCAAAGATACTGCATT
CACTCGATCCCTTGGGCCTACTCATGACCACCTACATCAGAAGTACATTTTCAGAGCACTACTGGCTCAATGG
AGCAAAATTTATTGGAACCTTTCTTCATACCAGACACCTACAATCCAGATGATGATAAAATATATTTCTTCTTTCTG
TGAATCATCTCAAGAAGGCAGTACCTCCGATAAAACCATCCTTTCTCGAGTTGGAAGAGTTTGTAAGAATGATGT
AGGAGGACAACGCAGCCTGATAAAACAGTGGACGACTTTTCTTAAGGCCAGACTGATTTGCTCAATTCCTGGAG
TGATGGGGCAGATACTTACTTTGATGAGCTTCAAGATATTTATTACTCCCCACAAGAGATGAAAGAAATCCTGT
AGTATATGGAGTCTTTACTACAACCAGCTCCATCTTCAAAGGCTCTGCTGTTTGTGTGTATAGCATGGCTGACAT
CAGAGCAGTTTTTAATGGTCCATATGCTCATAAGGAAAGTGCAGACCATCGTTGGGTGCAGTATGATGGGAGAAAT
TCCTTATCCACGGCCTGGTACATGTCCAAGCAAACCTATGACCCACTGATTAAGTCCACCCGAGATTTTCCAGA
TGATGTCATCAGTTTCATAAAGCGGCACTCTGTGATGTATAAGTCCGTATACCCAGTTGCAGGAGGACCACGTT
CAAGAGAATCAATGTGGATTACAGACTGACACAGATAGTGGTGGATCATGTTCATTGCAGAAGATGGCCAGTACGA
TGTAATGTTTCTTGGAACAGACATTGGAACCTGTCTCAAAGTTGTGAGCATTTCAAAGGAAAAGTGGAAATATGGA
AGAGGTAGTCTGGAGGAGTTGCAGATATTCAAGCACTCATCAATCATCTTGAACATCTTGAACATTTGTCTCTGAAGCA
GCAACAATTGTACATTGGTTCCCGAGATGGATTAGTTTCAGCTCTCCTTGCACAGATGCGACACTTATGGGAAAGC
TTGCGCAGACTGTTGTCTTGCCAGAGACCCCTACTGTGCTTGGGATGGAATGCATGCTCTCGATATGCTCTTAC
TTCTAAAAGGAGAGCTAGACGCCAAGATGTAAATATGGCGACCCCAATCACCCAGTGCTGGGACATCGAAGACAG
CATTAGTCATGAACTGCTGATGAAAAGGTGATTTTTGGCATTGAATTTAACTCAACCTTTCTGGAATGTATACC
TAAATCCCAACAAGCACTATTAATGGTATATCCAGAGGTGAGGGGATGAGCATCGAGAGGAGTTGAAGCCCGA
TGAAAGAATCATCAAAACGGAATATGGGCTACTGATTTCGAAGTTTGCAGAAGAAGGATTCTGGGATGTATTACTG
CAAAGCCCAGGAGCACACTTTCATCCACACCATAGTGAAGCTGACTTTGAATGTTCATTGAGAATGAACAGATGGA
AAATACCCAGAGGGCAGAGCATGAGGAGGGGCAGGTCAAGGATCTATTGGCTGAGTCACGGTTGAGATACAAAGA
CTACATCCAAATCCTTAGCAGCCCCAACTTCAGCCTCGACCAGTACTGCGAACAGATGTGGCACAGGGAGAAGCG
GAGACAGAGAAACAAGGGGGGCCAAAGTGAAGCACATGCAGGAAATGAAGAAGAAACGAAATCGAAGACATCA
CAGAGACCTGGATGAGCTCCCTAGAGCTGTAGCCACGTTAGTTTTCTACTTAATTTAAAGAAAAGAAATCCTTACC
TATAAAACCTATTGCCTTCTGTTTTGTATATCCCTTATCCCTTAATTCATAAATGCTTCCCATTGGAGTTTTGTGAAGG
CACAAGACAATAATCTGAATAAGACAATATGTGATTAATATAAGAAAGGGCAAAAAATTCATTTGAACCGATTTT
CCAAGAACAATCTGCACAAGCAAAGTATAAGAATTATCCTAAAAATAGGGGGTTTTACAGTTGTAAATGTTTTTA
TGTTTTGAGTTTTTGGAAATTTATTGTTCATGTTAAATAGTTGAGCTAAGCAAGCCCCGAATTTGATAGTGTATAAGGT
GCTTTATTCCCTCGAATGTCCATTAAGCATGGAATTTACCATGCAGTTGTGCTATGTTCTTATGAACAGATATAT
CATTCTATTGAGAACCAGTACCTTGTGGTAGGGAATAAGAGGTCAGACACAAATTAAGACAACCTCCCATATC
AACAGGAACTTTTCTCAGTGAGCCATTCACTCCTGGAGAATGGTATAGGAATTTGGAGAGGTGCATTATTTCTTTT
TGGCCACTGGGGTTAAATTTAGTGTACTACAACATTGATTTTACTGAAGGGCACTAATGTTTTCCCCCAGGATTTCT
ATTGACTAGTCAGGAGTAACAGGTTTACAGAGAGAAGTTGGTGCTTAGTTATGTGTTTTTTAGAGTATATACTAA
GCTCTACAGGGACAGAATGCTTAATAAATACTTTAATAAGATATGGGAAAATATTTTAAATAAAACAAGGAAAACA
TAATGATGTATAATGCATCCTGATGGGAAGGCATGCAGATGGGATTTGTTAGAAGACAGAAGGAAAGACAGCCAT
AAATTCTGGCTTTGGGAAAACCTCATATCCCCTGAAAAGGAAGAACAATCACAAATAAAGTGAGAGTAATGTAA
TGGAGCTCTTTTCACTAGGGTATAAGTAGCTGCCAATTTGTAATTCATCTGTTAAAAAAATCTAGATTATAACA
AAGTCTAGCAAAATCTGAGGAACATAAATTTCTTCTGAAGAATCATAGGAAGAGTAGACATTTTATTATAAACC
AATGATATTTTCAGTATATATTTTCTCTTTTAAAAAATATTTATCATACTCTGTATATTATTTCTTTTTACTGC
CTTTATTCTCTCCTGTATATTGGATTTTGTGATTATATTGAGTGAATAGGAGAAAACAATATATAACACACAGA
GAATTAAGAAAATGACATTTCTGGGGAGTGGGGATATATATTTGTTGAATAACAGAACGAGTGTAAAATTTTAAC
AACGGAAGGGTTAAATTAACCTTTTGACATCTTCACTCAACCTTTTCTCATTGCTGAGTTAATCTGTTGTAATT
GTAGTATTGTTTTGTAATTTAACAATAAATAAGCCTGCTACATGT

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FIGURE 348

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883

><subunit 1 of 1, 777 aa, 1 stop

><MW: 89651, pI: 7.97, NX(S/T): 3

MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNIPLRLKLTYSKDLLLSNSCIPFLG
SSEGLDFQTLTLLDEERGRLLLGAKDHIFFLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDANT
ECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFDPPQ
PFASVMTDEYLYSGTASDFLGKDTAFTRSLGPTHDDHHYIRTDISEHYWLNGAKFIGTFFIPDT
YNPDDDKIYFFFRESSQEGSTSDKTILSRVGRVCKNDVGGQRS LINKWTTFLKARLICSIPGS
DGADTYFDELQDIYLLPTRDERNPVVYGVFTTTSSIFKGSACVYSMA DIRAVFNGPYAHKES
ADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDVISFIKRHSVMYKSVYPVAGGPTEK
RINV DYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVSISKEKWNMEEVVLEELQIFKHSS
IILNMELSLKQQQLYIGSRDGLVQLSLHRCDTYGKACADCCLARDPYCAWDGNACSRYAPTSK
RRARRQDVKYGDPITQCWDIEDSISHETADEKVI FGIEFNSTFLECIPKSQQATIKWYIQRSG
DEHREELKPDERIIKTEYGLLIRSLQKKDSGMYECKAQEHTFIHTIVKLTLNVIENEQMENTQ
RAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRNKG GPKWKHMQEM
KKKRNRNRHHRDLDELPRAVAT

Important features of the protein:**Signal peptide:**

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

FIGURE 349

[illegible]

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FIGURE 350

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401
><subunit 1 of 1, 370 aa, 1 stop
><MW: 40685, pI: 4.53, NX(S/T): 0
MQLAKYQSHSKSCPTVFPPTPVLCLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRAQ
VSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPATAEDAELSDF
EECEETGELFEPPAPQALATRALPCPAHVVFQYQAGREDELTITEGEWLEVIEEGDADEWVKA
RNQHGEVGFVPERYLNFPDLSLPESQSDNPGAEPTAFLAQALYSYTGQSAEELSFPEGAL
IRLLPRAQDGVDDGFWRGEFGGRVGVFPSLLVEELLGPPGPPPELSDPEQMLPSPSPPSFSPPA
PTSVLDGPPAPVLPQDKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHPDPLT
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FIGURE 351A

CACAGGGAGACCCACAGACACATATGCACGAGAGAGACAGAGGAGGAAAGAGACAGAGACAAAGGCACAGCGGAA
GAAGGCAGAGACAGGGCAGGCACAGAAGCGGCCAGACAGAGTCTACAGAGGGAGAGGCCAGAGAAGCTGCAGA
AGACACAGGCAGGGAGAGACAAAGATCCAGGAAAGGAGGGCTCAGGAGGAGAGTTTGGAGAAGCCAGACCCCTGG
GCACCTCTCCCAAGCCCAAGGACTAAGTTTTCTCCATTTCTTTAACGGTCTCAGCCCTTCTGAAAACCTTTGCC
TCTGACCTTGGCAGGAGTCCAAGCCCCCAGGCTACAGAGAGGAGCTTTCCAAAGCTAGGGTGTGGAGGACTTGGT
GCCCTAGACGGCCTCAGTCCCTCCCAGCTGCAGTACCAGTGCCATGTCCCAGACAGGCTCGCATCCCGGGAGGGG
CTTGGCAGGGCGCTGGCTGTGGGGAGCCCAACCCTGCCTCCTGCTCCCCATTGTGCCGCTCTCCTGGCTGGTGTG
GCTGCTTCTGCTACTGCTGGCCTCTCTCCTGCCCTCAGCCCCGCTGGCCAGCCCCCTCCCCGGGAGGAGGAGAT
CGTGTTCAGAGAAGCTCAACGGCAGCGTCTCTGCTGGCTCGGGCGCCCCCTGCCAGGCTGTGTGTGCCGCTTGCA
GGCCTTTGGGGAGACGCTGCTACTAGAGCTGGAGCAGGACTCCGGTGTGCAGGTCGAGGGGCTGACAGTGCAGTA
CCTGGGGCAGGCGCCTGAGCTGCTGGGTGGAGCAGAGCCTGGCACCTACCTGACTGGCACCATCAATGGAGATCC
GGAGTCGGTGGCATCTCTGCACTGGGATGGGGGAGCCCTGTAGCGCTGTTACAATATCGGGGGGCTGAACTCCA
CCTCCAGCCCCCTGGAGGGAGGCACCCCTAAGCTGCTGGGGGACCTGGGGCTCACATCCTACGCCGGAAGAGTCC
TGCCAGCGGTCAAGGTCCCATGTGCAACGTCAAGGCTCCTCTTGAAGCCCCAGCCCCAGACCCGAAGAGCCAA
GCGCTTTGCTTCACTGAGTAGATTTGTGGAGACACTGGTGGTGGCAGATGACAAGATGGCCGCATTCCACGGTGC
GGGGCTAAAGCGCTACCTGCTAACAGTGATGGCAGCAGCAGCCAAGGCCTTCAAGCACCAAGCATCCGCAATCC
TGTCAGCTTGGTGGTGACTCGGCTAGTGATCCTGGGGTCAGGCGAGGAGGGGCCCCAAGTGGGGCCAGTGTCTGC
CCAGACCCCTGCGCAGCTTCTGTGCTGGCAGCGGGGCCCTCAACACCCCTGAGGACTCGGGCCCTGACCACTTTGA
CACAGCCATTCTGTTTACCCGTGAGGACCTGTGTGGAGTCTCCACTTGCACACGCTGGGTATGGCTGATGTGGG
CACCGTCTGTGACCCGGCTCGGAGCTGTGCCATTGTGGAGGATGATGGGCTCCAGTCAGCCTTCACTGCTGCTCA
TGAAGTGGGTGATGTCTTCAACATGCTCCATGACAACCTCAAGCCATGCATCAGTTTGAATGGGCCTTTGAGCAC
CTCTCGCCATGTGATGGCCCCCTGTGATGGCTCATGTGGATCCTGAGGAGCCCTGGTCCCCCTGCAGTGCCCGCTT
CATCACTGACTTCTGGACAATGGCTATGGGCACTGTCTCTTAGACAAACCAGAGGCTCCATGCACTGCTGCTGT
GACTTTCCCTGGCAAGGACTATGATGCTGACCCGCTGACCTGACCTTCCGGGCCCTGACGCCATTGTCTCC
ACAGCTGCCCGCCCTGTGCTGCCCTCTGGTGTCTGGCCACCTCAATGGCCATGCCATGTGCCAGACCAAAACA
CTCGCCCTGGGCCGATGGCACACCCTGCGGGCCCGCACAGGCTGCATGGGTGGTGCCTGCCATGGACCA
GCTCCAGGACTTCAATATTCACAGGCTGGTGGCTGGGGTCCCTGGGGACCATGGGGTACTGCTCTCGGACCTG
TGGGGGTGGTGTCCAGTTCTCCTCCCAGACTGCACGAGGCTGTCCCCCGGAATGGTGGCAAGTACTGTGAGGG
CCGCCGTACCCGCTTCCGCTCCTGCAACACTGAGGACTGCCCACTGGCTCAGCCCTGACCTTCCGCGAGGAGCA
GTGTGCTGCCTACAACCACCGCACCCGACCTCTTCAAGAGCTTCCAGGGCCCATGGACTGGGTTCCTCGCTACAC
AGCGTGGCCCCCAGGACCTGCAAACTCACCTGCCAGGCCCGGGCACTGGGCTACTACTATGTGCTGGAGCC
ACGGGTGGTAGATGGGACCCCTGTCCCCGGACAGCTCCTCGGTCTGTGTCCAGGGCCGATGCATCCATGCTGG
CTGTGATCGCATATTGGCTCCAAGAAGAAGTTTGAAGAAGTGCATGGTGTGCGGAGGGGACGGTTCGGTTGCAG
CAAGCAGTCAGGCTCCTTCAGGAAATTACGGTACGGATACAACAATGTGGTCACTATCCCCGCGGGGGCCACCCA
CATTCTTGTCCGGCAGCAGGGAACCCCTGGCCACCCGAGCATCTACTTGGCCCTGAAGTGCAGATGGCTCCTA
TGCCCTCAATGGTGAATACAGCTGATGCCCTCCCCCAGAGTGTGGTACTGCCTGGGGCAGTCAGCTTGCCTA
CAGCGGGCCACTGCAGCCTCAGAGACACTGTGAGGCCATGGGCCACTGGCCAGCCTTTGACACTGCAAGTCTT
AGTGGCTGGCAACCCCCAGGACACAGCCTCCGATACAGCTTCTTCGTGCCCCGGCCGACCCCTTCAACGCCACG
CCCCACTCCCAGGACTGGCTGCACCGAAGAGCACAGATTCTGGAGATCCTTCGGCGGCGCCCCCTGGGCGGGCAG
GAAATAACCTCACTATCCCGGCTGCCCTTTCTGGGCACCGGGGCTCGGACTTAGCTGGGAGAAAGAGAGAGCTT
CTGTTGCTGCCTCATGCTAAGACTCAGTGGGGAGGGGCTGTGGGCGTGAGACCTGCCCCCTCTCTGCCCTAAT
GCGCAGGCTGGCCCTGCCCTGGTTTCTGCCCTGGGAGGAGTGTGGGTAGTGGATGGAAGGGGCTGACAGAC
AGCCCTCCATCTAAACTGCCCCCTCTGCCCTGCGGGTCACAGGAGGGAGGGGAAGGCAGGGAGGGCTGGGCCC
CAGTTGTATTTATTTAGTATTTATTCACTTTTTATTTAGCACAGGGAAGGGGACAAGGACTAGGGTCTGGGGAA
CCTGACCCCTGACCCCTCATAGCCCTCACCTGGGGCTAGGAAATCCAGGGTGGTGGTATAGGTATAAGTGGTG
TGTGTATGCGTGTGTGTGTGTGTGTGAAAATGTGTGTGTGCTTATGTATGAGGTACAACCTGTTCTGCTTTCTCT
TTCCTGAATTTTATTTTTTGGGAAAAGAAAAGTCAAGGGTAGGGTGGGCCTTCAGGGAGTGAGGGATTATCTTTT
TTTTTTTTTCTTTCTTTCTTTCTTTTCTTTTGGAGACAGAATCTCGCTCTGTGCGCCAGGCTGGAGTGCAATG
GCACAATCTCGGCTCACTGCATCCTCCGCCTCCCGGGTCAAGTGATTCTCATGCTCAGCCTCCTGAGTAGCTG
GGATTACAGGCTCCTGCCACCACGCCCAGCTAATTTTTGTTTTGTTTTGTTTGGAGACAGAGTCTCGCTATTGTC
ACCAGGGCTGGAATGATTTCACTCACTGCAACCTTCGCCACCTGGGTTCAGCAATTCTCTGCCCTCAGCCTCC
CGAGTAGCTGAGATTATAGGCACCTACCACCACGCCCCGCTAATTTTTGTATTTTTTAGTAGAGACGGGGTTTTAC
CATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTTAGGTGATCCACTCGCCTTCATCTCCAAAGTGCTGGGATT
ACAGGCGTGAGCCACCGTGCCTGGCCACGCCCCAATAATTTTTGTATTTTTAGTAGAGACAGGGTTTACCATGT
TGGCCAGGCTGCTCTTGAACCTGACCTCAGGTAATCGACCTGCCTCGCCCTCCCAAAGTGCTGGGATTACAGG

FIGURE 351B

[illegible]

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FIGURE 352

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492

><subunit 1 of 1, 837 aa, 1 stop

><MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPGRGLAGRWLWGAQPCLLLPVPLSWLVWLLLLLLASLLPSARLASPLPREEEIVF
PEKLNGSVLPGSGAPARLLCRLQAFGETLLLELEQDSGVQVEGLTVQYLGQAPELLGGAEPGT
YLTGTINGDPESVASLHWDGGALLGVLYRGAEHLQLPLEGGTPNSAGGPGAHILRRKSPASG
QGPMC NVKAPLGSPSPRRRAKRFASLSRFVETLVVADDKMAAFHGAGLKRYLLTVMAAAKA
FKHPSIRNPVSLVVTRLVILGSGEEGPQVGPSAAQTLRSFCAWQRGLNTPEDSGPDHFDTAIL
FTRQDL CGVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAHELGHVFNMLHDNSKPCI
SLNGPLSTSRHVMA PVMAHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHLPVTFPGK
DYDADRQCQLTFGPDSRHCPQLPPPCAALWCSGHLNGHAMCQTKHSPWADGTPCGPAQACMGG
RCLHMDQLQDFNIPQAGGWGPWGPWGDCSRTC GGGVQFSSRDCTRVPVRNGGKYCEGRTRFR
SCNTEDCPTGSALTFREEQCAAYNHRTDLFKSFPGMDWVPRYTGVAPQDQCKLTCQARALGY
YYVLEPRVVDGTPCSPDSSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGGDGSGCSKQSGSFR
KFRYGYNNVVTIPAGATHILVRQQGNPGHRSIYLALKLPDGSYALNGEYTLMPSPTDVVLPGA
VSLRYSGATAASETL SGHGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPTPSTPRPTPQDWLH
RRAQILEILRRRPWAGRK

Important features of the protein:**Signal peptide:**

amino acids 1-48

N-glycosylation site.

amino acids 68-71

Glycosaminoglycan attachment site

amino acids 188-191, 772-775

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

Tyrosine kinase phosphorylation site.

amino acids 730-736

N-myristoylation sites.

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-582, 679-684, 682-687, 763-768

Amidation sites.

amino acids 560-563, 834-837

Leucine zipper pattern.

amino acids 17-38, 24-45

Neutral zinc metalloproteinases, zinc-binding region signature.

amino acids 358-367

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FIGURE 353

GCGGAACTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCCGAGGGCCCAGGGAGCTGCCC
GGCTGGCCTAGGCAGGCAGCCGCACCATGGCCAGCACGGCCGTGCAGCTTCTGGGCTTCCTGC
TCAGCTTCCTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGACAG
CGCACGTGGGCACCAACATCCTCACGGCCGTGTCCTACCTGAAAGGGCTCTGGATGGAGTGTG
TGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCCCCAAG
ACCTCCAGGCTGCCCCGCGCCCTCATGGTCATCTCCTGCCTGCTCTCGGGCATAGCCTGCGCCT
GCGCCGTCATCGGGATGAAGTGCACGCGCTGCGCCAAGGGGCACACCCGCCAAGACCACCTTTG
CCATCCTCGGCGGCACCCTCTTCATCCTGGCCGGCCTCCTGTGCATGGTGGCCGTCTCCTGGA
CCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCAGCGGCATGAAGTTTGAGA
TTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGTGGCACCCCTGC
TTTGCCCTGTCTGCCAGGACGAGGCACCCTACAGGCCCTACCAGGCCCCGCCAGGGCCACCA
CGACCACTGCAAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAGACAATCGGGCCC
CCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTGTGAGTCCCCACAG
CCTGCTTCTCCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTCAATGGAGGCAGGGG
TTCCAGCACAAAGTTTACTTCTGGGCAATTTTTGTATCCAAGGAAATAATGTGAATGCGAGGA
AATGTCTTTAGAGCACAGGGACAGAGGGGGAAATAAGAGGAGGAGAAAGCTCTCTATACCAA
GACTGAAAAAAAAAATCCTGTCTGTTTTTGTATTTATTATATATATTTATGTGGGTGATTTGA
TAACAAGTTTAATATAAAGTGACTTGGGAGTTTGGTCAGTGGGGTTGGTTTGTGATCCAGGAA
TAAACCTTGCGGATGTGGCTGTTTATGAAAAAAAAAAAAA

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FIGURE 354

MASTAVQLLGFLLSFLGMVGTLLITTLPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIYQ
CQIYRSLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAKGTPAKTTFAILGGTLFI
LAGLLCMVAVSWTTNDVVQNFYNPLPSGMKFEIGQALYLGFISSLSLIGGTLLCLSCQDEA
PYRPYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-103, 115-141, 160-182

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FIGURE 355

GAGCTCCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCGC
AGGCGGCAGGGCGGGCGGCCAGGAT**CATG**TCCACCACCACATGCCAAGTGGTGGCGTTCCCTCC
TGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGCACCCAGG
ACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGCGTGA
GGCAGAGTTTCAGGCTTCACCGAATGCAGGCCCTATTTACCACATCCTGGGACTTCCAGCCATGC
TGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCCTGGGTGCCATTGGCCTCCTGGTAT
CCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCCAACATGA
CACTGACCTCCGGGATCATGTTCAATTGTCTCAGGTCTTTGTGCAATTGCTGGAGTGTCTGTGT
TTGCCAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCGGCATGGGTG
GGATGGTGCAGACTGTTTCAGACCAGGTACACATTTGGTGGCGCTCTGTTTCGTGGGCTGGGTG
CTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGGCCTGGCACCAG
AAGAAACCAACTACAAAGCCGTTTCTTATCATGCCTCAGGCCACAGTGTTGCCTACAAGCCTG
GAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAAACAAGAAGATATACGATGGAG
GTGCCCCGACAGAGGACGAGGTACAATCTTATCCTTCCAAGCACGACTATGT**GTAA**TGCTCTA
AGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCACCCAAAAACAAGGAGATCCCA
TCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGCCTCGATTTTCATCTTTG
GAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCCACCATAAAACAGCTGAG
TTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTATTTCTTTTTTAAATATAA
CTTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCACATTTTGATGATTTAGACAG
ACTCCCCCTCTTCCTCCTAGTCAATAAACCCATTGATGATCTATTTCCAGCTTATCCCCAAG
AAAACCTTTTGAAGGAAAGAGTAGACCCAAAGATGTTATTTTCTGCTGTTTGAATTTTGTCTC
CCCACCCCCAACTTGGCTAGTAATAAACACTTACTGAAGAAGAAGCAATAAGAGAAAGATATT
TGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTGTGATCTTAAAAGTTACCAAACCA
AAGTCATTTTCAGTTTGAGGCAACCAAACCTTTCTACTGCTGTTGACATCTTCTTATTACAGC
AACACCATTCTAGGAGTTTCTGAGCTCTCCACTGGAGTCCTCTTTCTGTCGCGGGTCAGAAA
TTGTCCCTAGATGAATGAGAAAATTATTTTTTTTAAATTTAAGTCCTAAATATAGTTAAAATAA
ATAATGTTTTAGTAAAATGATACACTATCTCTGTGAAATAGCCTCACCCCTACATGTGGATAG
AAGGAAATGAAAAAATAATTGCTTTGACATTGTCTATATGGTACTTTGTAAAGTCATGCTTAA
GTACAAATTCATGAAAAGCTCACACCTGTAATCCTAGCACTTTGGGAGGCTGAGGAGGAAGG
ATCACTTGAGCCCAGAAGTTCGAGACTAGCCTGGGCAACATGGAGAAGCCCTGTCTCTACAAA
ATACAGAGAGAAAAAATCAGCCAGTCATGGTGGCATAACCTGTAGTCCCAGCATTCCGGGAG
GCTGAGGTGGGAGGATCACTTGAGCCCAGGGAGGTTGGGGCTGCAGTGAGCCATGATCACACC
ACTGCACTCCAGCCAGGTGACATAGCGAGATCCTGTCTAAAAAAATAAAAAATAAATAATGGA
ACACAGCAAGTCCTAGGAAGTAGGTTAAAACCTAATTCTTTAA

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FIGURE 356

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734

><subunit 1 of 1, 261 aa, 1 stop

><MW: 27856, pI: 8.50, NX(S/T): 1

MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVVFQYEGLRSCVRQSSGFTEC
RPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIMFI
VSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTLIGG
VMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTEDEVQ
SYPSKHDYV

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

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FIGURE 357

GGAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCGG
AGTCCAGCTGGCTAAAACTCATCCCAGAGGATA**ATG**GCAACCCATGCCTTAGAAATCGCTGGG
CTGTTTCTTGGTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGGAGA
GTGTCGGCCTTCATTGAAAACAACATCGTGGTTTTTGAAGAACTTCTGGGAAGGACTGTGGATG
AATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAGAAATCTATGATTCCCTGCTGGCTCTT
TCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCTTCTTGGCT
TTCATGATGGCCATCCTTGGCATGAAATGCACCAGGTGCACGGGGGACAATGAGAAGGTGAAG
GCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGTCTATCCCT
GTGAGCTGGGTTGCCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAATGTTGCCCAA
AAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCACGGCACTGGTGTGATTGTTGGA
GGAGCTCTGTTCTGCTGCGTTTTTTGTTGCAACGAAAAGAGCAGTAGCTACAGATACTCGATA
CCTTCCCATCGCACAAACCCAAAAAAGTTATCACACCGGAAAGAAGTCACCGAGCGTCTACTCC
AGAAGTCAGTATGTG**TAG**TTGTGTATGTTTTTTAACTTTACTATAAAGCCATGCAATGACA
AAAATCTATATTACTTTCTCAAAATGGACCCCAAAGAACTTTGATTTACTGTTCTTAACTGC
CTAATCTTAATTACAGGAAGTGTGCATCAGCTATTTATGATTCTATAAGCTATTTTCAGCAGAA
TGAGATATTAAACCCAATGCTTTGATTGTTCTAGAAAGTATAGTAATTTGTTTTCTAAGGTGG
TTCAAGCATCTACTCTTTTTATCATTACTTCAAAATGACATTGCTAAAGACTGCATTATTTT
ACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAGTGTAAACATTTATATCTCA
CATAGAGACATGCTTATATGGTTTTATTTAAAATGAAATGCCAGTCCATTACACTGAATAAAT
AGAACTCAACTATTGCTTTTCAGGGAAATCATGGATAGGGTTGAAGAAGGTACTATTAATTG
TTTAAAAACAGCTTAGGGATTAATGTCCTCCATTTATAATGAAGATTAAAATGAAGGCTTTAA
TCAGCATTGTAAAGGAAATTGAATGGCTTTCTGATATGCTGTTTTTTAGCCTAGGAGTTAGAA
ATCCTAACTTCTTTATCCTCTTCTCCCAGAGGCTTTTTTTTTCTTGTGTATTAAATTAACATT
TTTAAAACGCAGATATTTTGTCAAGGGGCTTTGCATTCAAAGTCTTTTCCAGGGCTATACTC
AGAAGAAAGATAAAAAGTGTGATCTAAGAAAAAGTGTGGTTTTAGGAAAGTGAAAATATTTTT
GTTTTTGTATTTGAAGAAGAATGATGCATTTTGACAAGAAATCATATATGTATGGATATATTT
TAATAAGTATTTGAGTACAGACTTTGAGGTTTCATCAATATAAATAAAAGAGCAGAAAAATAT
GTCTTGGTTTTTCATTTGCTTACCAAAAAACAACAACAAAAAAGTTGTCCTTTGAGAACTTC
ACCTGCTCCTATGTGGGTACCTGAGTCAAAATTGTCATTTTTGTTCTGTGAAAAATAAATTTT
CTTCTTGTAACATTTCTGTTTAGTTTTACTAAAATCTGTAAATACTGTATTTTTCTGTTTTATT
CCAAATTTGATGAACTGACAATCCAATTTGAAAGTTTGTGTGACGTCTGTCTAGCTTAAAT
GAATGTGTTCTATTTGCTTTATACATTTATATTAATAAATTGTACATTTTTCTAATT

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FIGURE 358

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735

><subunit 1 of 1, 225 aa, 1 stop

><MW: 24845, pI: 9.07, NX(S/T): 0

MATHALEIAGLFLGGVGMVGTVAVTVMPOWRVSAFIENNIVVFENFW EGLWMNCVRQANIRMQ
CKIYDSL LALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGIIF
IITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVFCCN
EKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

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FIGURE 359

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCTCGCCCTCCTGCTCGCGCCCC
GCCGCCATGGCTGCCTCCCCGCGCGGCCTGCTGTCCTGGCCCTGACCGGGCTGGCGCTGCTC
CTGCTCCTGTGCTGGGGCCCAGGTGGCATAAGTGGAATAAACTCAAGCTGATGCTTCAAAAA
CGAGAAGCACCTGTTCCAATAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGAATTC
CTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCGAGGTGCAGCAG
TGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATCACCTAT
TGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCACTATGAT
GAAGACTCTGCAATTGGTCCCCGGAGCCCCCTACGGCTTTAGGCATGGAGCCAGCGTCAACTAC
GATGACTACTTAACCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATTCTCTTCATGT
ATCTCCTAATGCCTTACACTACTTGGTTTCTGATTTGCTCTATTTTCAGCAGATCTTTTCTACC
TACTTTGTGTGATCAAAAAAGAAGAGTTAAAACAACACATGTAAATGCCTTTTGATATTTTCAT
GGGAATGCCTCTCATTTAAAAATAGAAATAAAGCATTTTGTTAAAAAGA

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FIGURE 360

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742

><subunit 1 of 1, 148 aa, 1 stop

><MW: 17183, pI: 8.77, NX(S/T): 0

MAASPARPAVLALTGLALLLLLCWGPGGISGNKCLKMLQKREAPVPTKTKVAVDENKAKEFLG

SLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRDRNGHEYYGDIYQRHYDED

SAIGPRSPYGFRHGASVNYDDY

Signal peptide:

amino acids 1-30

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FIGURE 362

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746

><subunit 1 of 1, 148 aa, 1 stop

><MW: 16896, pI: 6.05, NX(S/T): 1

MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGLSDWLCIAFVESKFNISKIN
ENADGSFDYGLFQINSHYWCNDYKSYSENLCVDCQDLLNPNNLAGIHCAKRIVSGARGMNNW
VEWRLHCSGRPLSYWLTGCRLR

Signal peptide:

amino acids 1-18

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FIGURE 363

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTCAGCCCTGCTTGACTGAGAACCCAC
CAGCTCATCCCAGACACCTCATAGCAACCTATTTATACAAAGGGGGAAAGAAACACCTGAGCA
GAATGGAATCATTATTTTTTTCCCAAGGAGAAAACCGGGGTAAAGGGAGGGAAGCAATTCAAT
TTGAAGTCCCTGTGAATGGGCTTTCAGAAGGCAATTAAAGAAATCCACTCAGAGAGGACTTGG
GGTGAAACTTGGGTCTGTGGTTTTCTGATTGTAAGTGAAGCAGGTCTTGACACGCTGTTG
GCAAATGTCAGGACCAGGTAAAGTGAAGTGGCAGAAAACTTCCAGGTGGAACAAGCAACCCAT
GTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTAACTTGAACATGACCTGTTGC
ATTTGGCAAGTTCTAGCAACATGCTCCTAAGGAAGCGATACAGGCACAGACCATGCAGACTCC
AGTTCCTCCTGCTGCTCCTGATGCTGGGATGCGTCTGATGATGGTGGCGATGTTGCACCCTC
CCCACCACACCCTGCACCAGACTGTACAGCCCAAGCCAGCAAGCACAGCCCTGAAGCCAGGT
ACCGCCTGGACTTTGGGGAATCCCAGGATTGGGTACTGGAAGCTGAGGATGAGGGTGAAGAGT
ACAGCCCTCTGGAGGGCCTGCCACCCTTTATCTCACTGCGGGAGGATCAGCTGCTGGTGGCCG
TGGCCTTACCCAGGCCAGAAGGAACCAGAGCCAGGGCAGGAGAGGTGGGAGCTACCGCCTCA
TCAAGCAGCCAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGACTGGGGGGCTGATGAGGACG
GGGAGGTGTCTGAAGAAGAGGAGTTGACCCCGTTACAGCCTGGACCCACGTGGCCTCCAGGAGG
CACTCAGTGGCCGCATCCCCCTCCAGAGGGCTCTGCCGAGGTGCGGCACCCACTGTGTCTGC
AGCAGCACCCCTCAGGACAGCCTGCCACAGCCAGCGTCATCCTCTGTTTCCATGATGAGGCCT
GGTCCACTCTCCTGCGGACTGTACACAGCATCCTCGACACAGTGGCCAGGGCCTTCTGAAGG
AGATCATCCTCGTGACGACCTCAGCCAGCAAGGACAACCTCAAGTCTGCTCTCAGCGAATATG
TGGCCAGGCTGGAGGGGGTGAAGTTACTCAGGAGCAACAAGAGGCTGGGTGCCATCAGGGCCC
GGATGCTGGGGGCCACCAGAGCCACCGGGGATGTGCTCGTCTTCATGGATGCCCACTGCGAGT
GCCACCCAGGCTGGCTGGAGCCCCTCCTCAGCAGAATAGCTGGTGACAGGAGCCGAGTGGTAT
CTCCGGTGATAGATGTGATTGACTGGAAGACTTTCCAGTATTACCCCTCAAAGGACCTGCAGC
GTGGGGTGTGGACTGGAAGCTGGATTTCCTGAGGAACTTTGCCAGAGCATGTGAGGAAGG
CCCTCCAGTCCCCCATAAGCCCCATCAGGAGCCCTGTGGTGCCCGGAGAGGTGGTGGCCATGG
ACAGACATTACTTCCAAAACACTGGAGCGTATGACTCTCTTATGTGCTGCGAGGTGGTGAAA
ACCTCGAACTGTCTTTCAAGGCCTGGCTCTGTGGTGGCTCTGTTGAAATCCTTCCCTGCTCTC
GGGTAGGACACATCTACCAAATCAGGATTCCATTCCCCCTCGACCAGGAGGCCACCCTGA
GGAACAGGGTTTCGCATTGCTGAGACCTGGCTGGGGTCATTCAAAGAAACCTTCTACAAGCATA
GCCAGAGGCCTTCTCCTTGAGCAAGGCTGAGAAGCCAGACTGCATGGAACGCTTGACGCTGC
AAAGGAGACTGGGTTGTCGGACATTCCACTGGTTTCTGGCTAATGTCTACCCTGAGCTGTACC
CATCTGAACCCAGGCCAGTTTCTCTGGAAAGCTCCACAACACTGGACTTGGGCTCTGTGCAG
ACTGCCAGGCAGAAGGGGACATCCTGGGCTGTCCATGGTGTGGCTCCTTGCACTGACAGCC
GGCAGCAACAGTACCTGCAGCACACCAGCAGGAAGGAGATTCACTTTGGCAGCCACAGCACC
TGTGCTTTGCTGTGTCAGGCAGGAGCAGGTGATTCTTCAGAACTGCACGGAGGAAGGCCTGGCCA
TCCACCAGCAGCACTGGGACTTCCAGGAGAATGGGATGATTGTCCACATTCTTTCTGGGAAAT
GCATGGAAGCTGTGGTGCAAGAAAACAATAAAGATTTGTACCTGCGTCCGTGTGATGGAAAAG
CCCGCCAGCAGTGGCGATTTGACCAGATAAATGCTGTGGATGAACGATGCAATGTCAATGTCAG
AAGGAAAAGAGAATTTTGGCCATCAAAATCCAGCTCCAAGTGAACGTAAAGAGCTTATATATT
TCATGAAGCTGATCCTTTTGTGTGTGTGCTCCTTGTGTTAGGAGAGAAAAAGCTCTATGAAA
GAATATAGGAAGTTTCTCCTTTTACACCTATTTTCATTGACTGCTGGCTGCTTA

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FIGURE 364

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760

><subunit 1 of 1, 639 aa, 1 stop

><MW: 73063, pI: 6.84, NX(S/T): 2

MLLRKRYRHRPCRLQFLLLLLMLGCVLMMVAMLHPPHHTLHQTVTAQASKHSPEARYRLDFGE
SQDWVLEAEDEGE EYSPL EGLPPFISLREDQLLVAVALPQARRNQSQGRRGGSYRLIKQPRRQ
DKEAPKRDWGADEDEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHPQDS
LPTASVILCFHDEAWSTLLRTVHSILDTVPRAFLKEIILVDDL SQQQLKSALSEYVARLEGV
KLLRSNKRLGAIRARMLGATRATGDVLVFMDAHCECHPGWLEPLLSRIAGDRSRVVS PVIDVI
DWKTFQYYPSKDLQRGVLDWKLD FHWEPLPEHVRKALQSPISPIRSPVVPGEVVAMDRHYFQN
TGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHIIYQNQDSHSPLDQEATLRNRVRIA
ETWLGSFKETFYKHSPEAFSLSKAEKPDCMERLQLQRR LGCRTFWHFLANVPELYPSEPRPS
FSGKLHNTGLGLCADCQAEGDILGCPMVLAPCSDSRQQQYLQHTSRKEIHFGSPQHLCFAVRQ
EQVILQNCTEEGLAIHQHWFQENGMIVHILSGKCMEAVVQENNKDLYLRPCDGKARQQWRF
DQINAVDER

Signal peptide:

amino acids 1-28

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FIGURE 365

GGAGAGAGGCGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCTCGGAGCGCGGCGG
AGCCAGACGCTGACCACGTTCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCCGGC
AGCCGGGAGCC**ATG**CGACCCAGGGCCCCGCGCCTCCCCGCAGCGGCTCCGCGGCCTCCTGC
TGCTCCTGCTGCTGCAGCTGCCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAGCAAA
AGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGGGCCAG
CAGGAGTGCTGGTGCAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTGGGATCC
CAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAGCTTTGAGGAGTCCT
GGACACCCAACTACAAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCTTGGGAAAA
TTGCGGAGTGACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGTTCAGTGGCT
CACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTACATTCAATGGAGCTG
AATGTTTCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAGCCCTGAAATGA
ATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAGGAATTGGTGCTG
GATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTTCAGATTACCCAAAAGGAGATGCTTCTA
CTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAA**TAA**ATGCTTTAATTTT
CATTTGCTACCTCTTTTTTTTATTATGCCTTGGAATGGTTCACTTAAATGACATTTTAAATAAG
TTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGACCAAAGTGTGATTTCA
CACTGTTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAGTGGTTTCAATATTTTTTT
TAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTATAATTTGGAATATTGTTG
TGGTCTTTTGTTTTTTCTCTTAGTATAGCATTTTTTAAAAAATATAAAAGCTACCAATCTTTG
TACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTAAATAAAAATTATTTCCAACA

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FIGURE 366

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGVP
GRDGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAEC
TFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGPLPIEAIYLDQGSPENNSTI
NIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

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FIGURE 367

GTTAACCAGCGCAGTCCTCCGTGCGTCCCGCCCGCCGCTGCCCTCACTCCCGGCCAGG**ATGGC**
ATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCCTGCGGTGCT
CACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCCGTC
GGGAGAAGGCCCCGTGGAGAGCACCAGCCCCGGCCGGGAGCCCGTGGACACCGGTCCCCCAGC
CCCCACCGTCGCGCCAGGACCCGAGGACAGCACCGCGCAGGAGCGGCTGGACCAGGGCGGCGG
GTCGCTGGGGCCCGGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTGCGTGGT
GCTGGCGCTCGTGGTCGTCGCGCTGAGAAAGTTTTCTGCCTCC**TGA**AGCGAATAAAGGGGCCG
CGCCCGCCGCGGCGCGACTCGGCAAAAAAAAAAAAAAA

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FIGURE 368

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVVESTSPGREPVDTGP
PPTVAPGPEDESTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS
```

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 91-110

Glycosaminoglycan attachment site.

amino acids 44-47

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 116-119

N-myristoylation site.

amino acids 91-96

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FIGURE 369

GGCCGTTGGTTGGTGCGCGGCTGAAGGGTGTGGCGCGAGCAGCGTCGTTGGTTGGCCGGCGGC
GGGCCGGGACGGGC**ATG**GGCCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGGCGCTGGCCCACG
GCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGAACT
TCAAGTCCTGGTGGGTGGGCGACATCCCCGTGTCAGGGGCGCTGCTCACCGACTGGAGCGACG
ACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACCCGGGAGAAGCTGGACCAAG
TGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCCCCGGGT
ATTTCCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAACGCCATCA
TCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCCAGGGAGGGACCCAGCC
TAGCACCTGAAGGATCAATGCCATCACCCCGCGGGGACCTCCCC**TAA**GTAGCCCCCAGAGGGCG
CTGGGAGTGTGTCACCGCCCTCCCCTGAAGTTTGTCTCATCTCACGCTGGGGGTCAACCTGG
GGACCCCTTCCCTCCGGGCCATGGACACACATACATGAAAACCAGGCCGCATCGACTGTCAGC
ACCGCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACAACTGCACAGACTCGCACGTCTG
CCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCCGTGCCAGGGCCCTAC
TGTCCCTGGGGTCCCAGGCTCTCCTTGGAGGGGGCTCCCCGCCTTCCACCTGGCTGTCTCGG
GTAGGGCGGGGCCGTGGGTTCAGGGGCGCACCACTTCCAAGCCTGTGTCCACAGGTCTCTCGG
CGCAGTGGAAGTCAGCTGTCCAGGGCCTCCTGAACTACATAAATAACTGGCACAAGTAAGTCC
CCTCCTCAAACCAACACAGGCAGTGTGTGTATGTGAGCACCTCGTGGGTGAGTATGTGTGGGG
CACAGGCTGGCTCCCTCAGCTCCCACGTCTTAGAGGGGGCTCCCGAGGAGGTGGAACCTCAACC
CAGCTCTGCGCAGGAGGCGGGCTGCAGTCCTTTTCTCCCTCAAAGGTCTCCGACCCTCAGCTGG
AGGCGGGCATCTTTCCTAAAGGGTCCCCATAGGGTCTGGTTCCACCCCATCCAGGTCTGTGG
TCAGAGCCTGGGAGGGTTCCCTACGATGGTTAGGGGTGCCCCATGGAGGGGCTGACTGCCCCA
CATTGCCTTTCAGACAGGACACGAGCATGAGGTAAGGCCGCCCTGACCTGGACTTCAGGGGGA
GGGGGTAAAGGGAGAGAGGAGGGGGGGCTAGGGGGTCTCTAGATCAGTGGGGGCACTGCAGGT
GGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTCACCTCTGCAACCACACCCATGTGGTG
GTTTCATGAACAGACCACGCTCCTCTGCCTTCTCCTGGCCTGGGACACACAGAGCCACCCCGG
CCTTGTGAGTGACCCAGAGAAGGGAGGCCTCGGGAGAAGGGGTGCTCGTAAGCCAACACCAGC
GTGCCGCGGCCTGCACACCCTTCGGACATCCCAGGCACGAGGGTGTCGTGGATGTGGCCACAC
ATAGGACCACACGTCCCAGCTGGGAGGAGAGGCCTGGGGCCCCCAGGGAGGGAGGCAGGGGGT
GGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCCCCGCAGCCTGGTATCGCCAGCCTTAAGGT
GTCTGGAGCCCCCACACTTGGCCAACCTGACCTTGGGAAGATGCTGCTGAGTGTCTCAAGCAGC
ACTGACAGCAGCTGGGCCTGCCCCAGGGCAACGTGGGGGCGGAGACTCAGCTGGACAGCCCCT
GCCTGTCACTCTGGAGCTGGGCTGCTGCTGCCTCAGGACCCCCCTCTCCGACCCCGGACAGAGC
TGAGCTGGCCAGGGCCAGGAGGGCGGGAGGGAGGGAATGGGGGTGGGCTGTGCGCAGCATCAG
CGCCTGGGCAGGTCCGCAGAGCTGCGGGATGTGATTAAAGTCCCTGATGTTTCTC

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FIGURE 370

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399

><subunit 1 of 1, 157 aa, 1 stop

><MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCIVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMKE
LHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIIERHL
APGSWGGGQLSREGPSLAPEGSMPSPRGDLP

Signal peptide:

amino acids 1-15

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FIGURE 371

GCCGGCTGTGCAGAGACGCC**ATG**TACCGGCTCCTGTCAGCAGTGACTGCCCGGGCTGCCGCCC
CCGGGGGCTTGGCCTCAAGCTGCGGACGACGCGGGGTCCATCAGCGCGCCGGGCTGCCGCCTC
TCGGCCACGGCTGGGTGCGGGGCTCGGGCTGGGGCTGGCGCTCGGGGTGAAGCTGG
CAGGTGGGCTGAGGGGCGCGGCCCCGGCGCAGTCCCCCGCGGCCCCGACCTGAGGCGTCGC
CTCTGGCCGAGCCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGCAGACCCCGGCGCCGC
CCTGCTCCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGATCAAGG
ATGAGGTGGGCGCACCGGGCATAGTGGTTGGAGTTTCTGTAGATGGAAAAGAAGTCTGGTCAG
AAGGTTTAGGTTATGCTGATGTTGAGAACCGTGTACCATGTAAACCAGAGACAGTTATGCGAA
TTGCTAGCATCAGCAAAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAGCAGGGAAAC
TGGATCTTGATATTCCAGTACAACATTATGTTCCCGAATTCCCAGAAAAAGAATATGAAGGTG
AAAAGGTTTCTGTCACAACAAGATTACTGATTTCCCATTTAAGTGGAATTCGTCATTATGAAA
AGGACATAAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTTGAAGATGATGAAAGAGAATG
TTGCATTTGAGCAAGAAAAAGAAGGCAAAAGTAATGAAAAGAATGATTTTACTAAATTTAAAA
CAGAGCAGGAGAATGAAGCCAAATGCCGGAATTCAAAACCTGGCAAGAAAAAGAATGATTTTG
AACAAGGCGAATTATATTTGAGAGAAAAGTTGAAAATTC AATTGAATCCCTAAGATTATTTA
AAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTGTATTCAACTTTTGGCTATACCC
TACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAAATATTTGGACTATATGCAGAAAATAT
TCCATGACTTGATATGCTGACGACTGTGCAGGAAGAAAACGAGCCAGTGATTTACAATAGAG
CAAGG**TAA**ATGAATACCTTCTGCTGTGTCTAGCTATATCGCATCTTAACACTATTTTATTAAT
TAAAAGTCAAATTTTCTTTGTTTCCATTCCAAAATCAACCTGCCACATTTTGGGAGCTTTTCT
ACATGTCTGTTTTCTCATCTGTAAAGTGAAGGAAGTAAACATGTTTATAAAGTAAAAAAA

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FIGURE 372

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41221, pI: 8.54, NX(S/T): 0

MYRLLSAVTARAAAPGGLASSCGRRGVHQRAGLPPLGHGWVGGGLGLGLGLALGVKLAGGLRGA
APAQSPAAPDPEASPLAEPPEQSLAPWSPQTPAPPCSRCFARAIESSRDLLHRIKDEVGAPG
IVVGVSVDGKEVWSEGLGYADVENRVPCPETVMRIASISKSLTMVALAKLWEAGKLDLDIPV
QHYVPEFPEKEYEGEKVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAFEQEK
EGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKNDPLFF
KPGSQFLYSTFGYTLLAAIVERASGCKYLDYMQKIFHDLDMLTTVQEENEPVIYNRAR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 39-60

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FIGURE 373

GACTACGGGGAGAGAGAGAGAGACCAGGACAGCTGCTGAGACCTCTAAGAAGTCCAGATACTAA
GAGCAAAGATGTTTCAAACCTGGGGGCCCTCATTGTCTTCTACGGGCTGTTAGCCCAGACCATGG
CCAGTTTGGAGGCCTGCCCCGTGCCCTGGACCAGACCCTGCCCTTGAATGTGAATCCAGCCCTG
CCCTTGAGTCCCACAGGTCTTGCAGGAAGCTTGACAAATGCCCTCAGCAATGGCCTGCTGTCT
GGGGGCCTGTTGGGCATTCTGGAAAACCTTCCGCTCCTGGACATCCTGAAGCCTGGAGGAGGT
ACTTCTGGTGGCCTCCTTGGGGGACTGCTTGGAAGTACGTCAGTGATTCCTGGCCTGAAC
AACATCATTGACATAAAGGTCACTGACCCCCAGCTGCTGGAACCTTGGCCTTGTGCAGAGCCCT
GATGGCCACCGTCTCTATGTCACCATCCCTCTCGGCATAAAGCTCCAAGTGAATACGCCCCCTG
GTCGGTGCAAGTCTGTTGAGGCTGGCTGTGAAGCTGGACATCACTGCAGAAATCTTAGCTGTG
AGAGATAAGCAGGAGAGGATCCACCTGGTCCTTGGTGACTGCACCCATTCCCCTGGAAGCCTG
CAAATTTCTCTGCTTGATGGACTTGGCCCCCTCCCCATTCAAGGTCTTCTGGACAGCCTCACA
GGGATCTTGAATAAAGTCCTGCCTGAGTTGGTTCAGGGCAACGTGTGCCCTCTGGTCAATGAG
GTTCTCAGAGGCTTGGACATCACCCCTGGTGCATGACATTGTTAACATGCTGATCCACGGACTA
CAGTTTGTCAATCAAGGTCTTAAGCCTTCCAGGAAGGGGCTGGCCTCTGCTGAGCTGCTTCCCAG
TGCTCACAGATGGCTGGCCCATGTGCTGGAAGATGACACAGTTGCCTTCTCTCCGAGGAACCT
GCCCCCTCTCCTTTCCCACCAGGCGTGTGTAACATCCCATGTGCCTCACCTAATAAAATGGCT
CTTCTTATGCA

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FIGURE 374

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76533
><subunit 1 of 1, 256 aa, 1 stop
><MW: 26713, pI: 5.62, NX(S/T): 0
MFQTGGLIVFYGLLAQTMAQFGGLPVPLDQTLPLNVNPALPLSPTGLAGSLTNALSNGLL
SGLLGILENLPLLDILKPGGGTSGGLLGGLLGKVTSVIPGLNNIIDIKVTDPQLLELGL
VQSPDGHRLYVTIPLGIKLQVNTPLVGASLLRLAVKLDITAEILAVRDKQERIHVLGDC
THSPGSLQISLLDGLGPLPIQGLLDSTGILNKVLPVLVQGNVCPLVNEVLRGLDITLVH
DIVNMLIHGLQFVIKV
```

Important features of the protein:**Signal peptide:**

Amino acids 1-19

Transmembrane domain:

Amino acids 79-97

N-myristoylation sites:

Amino acids 46-52;49-55;58-64;62-68;66-72;80-86;81-87;
82-88;85-91;86-92;89-95;202-208;233-239

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FIGURE 375

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCCTTT
AAAT**ATG**TCAAGATCCAGACTTTTCAGTGTCACCTCAGCGATCTCAACGATAGGGATCTTGTG
TTTGCCGCTATTCCAGTTGGTGCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGTAA
TTATAATGACCAACACCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTGGTGGC
AGCTCTTCTCTGTGGAGCTGTGGTCCTCTGCCTCCAGTGCTGGCTGAGGAGACCCCGAATTGA
TTCTCACAGGCGCACCATGGCAGTTTTTGCTGTTGGAGACTTGGACTCTATTTATGGGACAGA
AGCAGCTGTGAGTCCAACCTGTTGGAATTCACCTTCAAACCTCAAACCCCTGACCTATATCCTGT
TCCTGCTCCATGTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTGTAAAAACAAC
CTGATTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTCAAAAACATCAA
ATTTAGGAATAGTTATTTTCAGTTGTTGGAAATGTCCAGAGATCTATTCATATAGTCTGAGGAA
GGACAATTCGACAAAAGAATGGATGTTGGAAAAAATTTTGGTCATGGAGATGTTTAAATAGTA
AAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGCTACACAACCAAATTAAT
GCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTTTCCATCACATTTA
GGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAAACTCTTTCCTAGCATGGGGTCC
ATAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACATGTCCAGAACCAGAAC
CAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAAGAAAAGTTTGGAGTTG
AAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCTCAGCAAAAACAAGAGGT
TTTATGCCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGAAGGAGATTGCTGAAGATA
TAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCCCTTTTACAGTAATGAATGT
GGCCTCCATAGTCCATAGTGTCTCTGGAGCCTCAGGGCTTGGCATTATTTGCAGCATCATG
CTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGCAGAAGTAGCAATGAGACATCT
TCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGACAAAACATCCATCACAGATGA
CATATGATCTTCAGCTGACAAATTTGTTGAACAAAACAATAAACATCAATAGATATCTAAAAA

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FIGURE 376

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303

><subunit 1 of 1, 146 aa, 1 stop

><MW: 16116, pI: 4.99; NX(S/T): 0

MSRSRLFSVTSAISTIGILCLPLFQLVLSDLPCCEEDEMCVNYNDQHPNGWYIWILLLLVLVAA

LLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYPVP

APCFGPLGSPPPYEEIVKTT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 52-70

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FIGURE 377

CGCGGATCGGACCCAAGCAGGTCGGCGGGCGGGCAGGAGAGCGGCCGGGCGTCAGCTCCTCG
ACCCCCGTGTCGGGCTAGTCCAGCGAGGCGGACGGGCGGGCGTGGGCCC**ATG**GCCAGGCCCGGC
ATGGAGCGGTGGCGCGACCGGCTGGCGCTGGTGACGGGGGGCCTCGGGGGGCATCGGCGCGGCC
GTGGCCCGGGCCCTGGTCCAGCAGGGACTGAAGGTGGTGGGCTGCGCCCGCACTGTGGGCAAC
ATCGAGGAGCTGGCTGCTGAATGTAAGAGTGCAGGCTACCCCGGGACTTTGATCCCCACAGA
TGTGACCTATCAAATGAAGAGGACATCCTCTCCATGTTCTCAGCTATCCGTTCTCAGCACAGC
GGTGTAGACATCTGCATCAACAATGCTGGCTTGGCCCGGCCTGACACCCTGCTCTCAGGCAGC
ACCAGTGGTTGGAAGGACATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTGCACACGGGAA
GCCTACCAGTCCATGAAGGAGCGGAATGTGGACGATGGGCACATCATTAACATCAATAGCATG
TCTGGCCACCGAGTGTTACCCCTGTCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTC
ACTGCGCTGACAGAGGGACTGAGGCAAGAGCTTCGGGAGGCCCAGACCCACATCCGAGCCACG
TGCATCTCTCCAGGTGTGGTGGAGACACAATTCGCCTTCAAACCTCCACGACAAGGACCCTGAG
AAGGCAGCTGCCACCTATGAGCAAATGAAGTGTCTCAAACCCGAGGATGTGGCCGAGGCTGTT
ATCTACGTCCTCAGCACCCCCGCACACATCCAGATTGGAGACATCCAGATGAGGCCACCGGAG
CAGGTGACCT**TAG**TGACTGTGGGAGCTCCTCCTTCCCTCCCCACCCTTCATGGCTTGCCTCCTG
CCTCTGGATTTTAGGTGTTGATTTCTGGATCACGGGATACCACTTCCTGTCCACACCCCGACC
AGGGGCTAGAAAATTTGTTTGAGATTTTTATATCATCTTGTCAAATTGCTTCAGTTGTAAATG
TGAAAAATGGGCTGGGGAAGGAGGTGGTGTCCCTAATTGTTTTACTTGTTAACTTGTTCTTG
TGCCCTGGGCACTTGGCCTTTGTCTGCTCTCAGTGTCTTCCCTTTGACATGGGAAAGGAGTT
GTGGCCAAAATCCCCATCTTCTGCACCTCAACGTCTGTGGCTCAGGGCTGGGGTGGCAGAGG
GAGGCCTTCACCTTATATCTGTGTTGTTATCCAGGGCTCCAGACTTCCTCCTCTGCCTGCCCC
ACTGCACCCTCTCCCCCTTATCTATCTCCTTCTCGGCTCCCCAGCCAGTCTTGGCTTCTTGT
CCCCTCCTGGGGTCATCCCTCCACTCTGACTCTGACTATGGCAGCAGAACACCAGGGCCTGGC
CCAGTGGATTTTCATGGTGATCATTAAGAAAGAAAATCGCAACCAAAAAAAAAAAAA

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FIGURE 378

MARPGMERWRDRLALVTGASGGIGA A VARALVQOGLKVVG CARTVGNIEELAAECKSAGYPGT
LIPYRC DLSNEEDILSMFSAIRSQHSGVDICINNAGLARPD TLLSGSTSGWKDMFN VNV LALS
ICTREAYQSMKERNVDDGHIININSMGHRVLP LSVTHFY SATKYAVTALTEGLRQELREAQT
HIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVLSTPAHIQIGDIQ
MRPTEQVT

Important features of the protein:**Signal peptide:**

amino acids 1-17

N-myristoylation sites.amino acids 18-24, 21-27, 22-28, 24-30, 40-46, 90-96, 109-115,
199-205**Short-chain alcohol dehydrogenase.**

amino acids 30-42, 104-114

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FIGURE 379

GAGCGGAGTAAATCTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGTT
TCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGCAGCTGACGCCCGCTTATTAGC
TCTCGCTGCGTCGCCCCGGCTCAGAAGCTCCGTGGCGGGCGGACCGTGACGAGAAGCCCACG
GCCAGCTCAGTTCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCCTTTTAAACTCCCT
CTTCAAACTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATACAACCTTGCTGAAGATGAA
GAATATACAATATTGAGGATATTTTTTTCTTTTTTTTTCAAGTCTTGATTGTGGCTTACCT
CAAGTTACCATTTTTTCAGTCAAGTCTGTTTGTGTTGCTTCTTCAGAAATGTTTTTACAATCTC
AAGAAAAATATGTCCAGAAATTGAGTTTACTGTTGCTTGATTGTTGGACTCATTTGGGGATT
GATGTTACTGCACTATACTTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTTACGTGAGCA
AATACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAATAAGAACACAGTGG
TGTCGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAATTGCTGTCCTTCT
GGATGACATTTTGCAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATATTGTTGTGAATGG
CTCAGCAGCCAACACCACCAATGGTACTAGTGGGAATTTGGTGCCAGTAACCACAAAATAAAG
AACGAATGTCTCGGGCAGTATCAGATAGCAGTTGAAAATCACCTTGCTGCTCCATCCACTG
TGGATTATATCCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGACAGAGCAATACTTTAC
AATAAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTGCTGGAATCTAATTCTGTACATA
AAAATTTTAAAGTTATTTGTTTGCTTTTCAAGGCAAGTCTGTTCAATGCTGTACTATGTCCTTAA
AGAGAATTTGGTAACTTGGTTGATGTGGTAAGCAGATAGGTGAGTTTTGTATAAATCTTTTGT
GTTTGAGATCAAGCTGAAATGAAAACACTGAAAACATGGATTGCTTCTATAACACATTTAT
TTAAGTATATAACACGTTTTTTGGACAAGTGAAGAATGTTTAAATCATTCTGTGCTTTGTTCTC
AATAGATGTAAGTGTAGACTACGGCTATTTGAAAAATGTGCTTATTGTACTATATTTTGT
ATTCCAATTATGAGCAGAGAAAGGAAATATAATGTTGAAAATAATGTTTTGAAATCATGACCC
AAAGAATGTATTGATTTGCACTATCCTTCAGAATAACTGAAGGTTAATTATTGTATATTTTAA
AAAATTACACTTATAAGAGTATAATCTTGAAATGGGTAGCAGCCACTGTCCATTACCTATCGT
AAACATTGGGGCAATTTAATAACAGCATTAATAAGTTGTAACTCTAATCTTATACTTATTG
AAGAATAAAAGATATTTTTATGATGAGAGTAACAATAAAGTATTCATGATTTTTACATACAT
GAATGTTTCATTTAAAAGTTTAAATCCTTTGAGTGTCTATGCTATCAGGAAAGCACATTATTTCC
ATATTTGGGTAAATTTTGCTTTTATTATATTGGTCTAGGAGGAAGGGACTTTGGAGAATGGAA
CTCTTGAGGACTTTAGCCAGGTGTATATAATAAAGGTACTTTTGTGCTGCATTAAATGCTTG
GAAAGTGTAAACATTATATTATATAAGAGTATCCTTTATGAAATTTTGAATTTGTATAACAGA
TGCATTAGATATTCATTTTATATAATGGCCACTTAAAATAAGAACATTTAAAATATAAACTAT
GAAGATTGACTATCTTTTCAGGAAAAAGCTGTATATAGCACAGGGAACCCTAATCTTGGGTA
ATTCTAGTATAAAAACAAATTATACTTTTATTTAAATTTCCCTTGTAGCAAATCTAATTGCCAC
ATGGTGCCCTATATTTTCATAGTATTTTATTCTCTATAGTAACTGCTTAAGTGCAGCTAGCTTCT
AGATTTAGACTATATAGAATTTAGATATTGTATTGTTTCGTCATTATAATATGCTACCACATGT
AGCAATAATTACAATATTTTATTAATAAATATGTGAAATATTGTTTCATGAAAGACAGATT
TCCAAATCTCTCTTCTCTCTGTACTGTCTACCTTTATGTGAAGAAATTAATTATATGCCA
TTGCCAGGT

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FIGURE 380

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648

><subunit 1 of 1, 140 aa, 1 stop

><MW: 15668, pI: 10.14, NX(S/T): 5

MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE

NKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNLVP

VTTNKRTNVSGSIR

Important features of the protein:**Signal peptide:**

amino acids 1-26

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FIGURE 381

AACTTCTACATGGGCCTCCTGCTGCTGGTGCTCTTCCTCAGCCTCCTGCCGGTGGCCTACACC
ATCATGTCCCTCCCACCCTCCTTTGACTGCGGGCCGTTTCAGGTGCAGAGTCTCAGTTGCCCGG
GAGCACCTCCCCTCCCGAGGCAGTCTGCTCAGAGGGCCTCGGCCCAGAATTCAGTTCTGGTT
TCATGCCAGCCTGTAAAAGGCCATGGAACCTTTGGGTGAATCACCGATGCCATTTAAGAGGGTT
TTCTGCCAGGATGGAAATGTTAGGTCGTTCTGTGTCTGCGCTGTTCAATTCAGTAGCCACCAG
CCACCTGTGGCCGTTGAGTGCTTGAAATTGAGGAAGTGAAGAAATTAATTTCTCATGTATTTTT
CTCATTTATTTATTAATTTTTTAAGTATAGTTGTACATATTTGGGGGTACATGTGATATTTGG
ATACATGTATACAATATATAATGATCAAATCAGGGTAACTGGGATATCCATCACATCAAACAT
TTATTTTTTTATTCTTTTTTAGACAGAGTCTCACTCTGTCAACCAGGCTGGAGTGCAGTGGTGCC
ATCTCAGCTTACTGCAACCTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCTCCACCTCCCAA
GTAGCTGGGACTACAGGCATGCACCACAATGCCCAACTAATTTTTGTATTTTTAGTAGAGACG
GGGTTTTGCCATGTTGCCCAGGCTGGCCTTGAAGTCTGGCCTCAAACAATCCACTTGCCTCG
GCCTCCCAAAGTGTTATGATTACAGGCGTGAGCCACCGTGCCTGGCCTAAACATTTATCTTTT
CTTTGTGTTGGGAACCTTTGAAATTATACAATGAATTATTGTTAACTGTCATCTCCCTGCTGTG
CTATGGAACACTGGGACTTCTTCCCTCTATCTAACTGTATATTTGTACCAAGTTAACCAACCGT
ACTTCATCCCCACTCCTCTCTATCCTTCCCAACCTCTGATCACCTCATTCTACTCTCTACCTC
CATGAGATCCACTTTTTTTAGCTCCCACATGTGAGTAAGAAAATGCAATATTTGTCTTTCTGTG
CCTGGCTTATTTCACTTAACATAATGACTTCCTGTTCCATCCATGTTGCTGCAAATGACAGGA
TTTCGTTCTTAATTTCAATTAAAATAACCACACATGGCAAAA

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FIGURE 382

MGLLLLVLFLSLLPVAYTIMSLPPSFDCGPFRCRVSVAREHLPSRGSLLRGPRPRIPVLVSCQ
PVKGHGTLGESPMPEKRVFCQDGNVRSFCVCAVHFSSHQPPVAVECLK

Important features of the protein:

Signal peptide:

amino acids 1-18

N-myristoylation site.

amino acids 86-92

Zinc carboxypeptidases, zinc-binding region 2 signature.

amino acids 68-79

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FIGURE 383

TTCTGAAGTAACGGAAGCTACCTTGTATAAAGACCTCAACACTGCTGACC**ATG**ATCAGCGCAG
CCTGGAGCATCTTCCTCATCGGGACTAAAATTGGGCTGTTCCCTTCAAGTAGCACCTCTATCAG
TTATGGCTAAATCCTGTCCATCTGTGTGTCGCTGCGATGCGGGTTTCATTTACTGTAATGATC
GCTTTCTGACATCCATTCCAACAGGAATACCAGAGGATGCTACAACCTCTCTACCTTCAGAACA
ACCAAATAAATAATGCTGGGATTCCTTCAGATTTGAAAACTTGCTGAAAGTAGAAAAGAATAT
ACCTATAACCACAACAGTTTAGATGAATTTCCCTACCAACCTCCCAAAGTATGTAAAAGAGTTAC
ATTTGCAAGAAAATAACATAAGGACTATCACTTATGATTCACTTTCAAAAATTC CCTATCTGG
AAGAATTACATTTAGATGACAACCTCTGTCTCTGCAGTTAGCATAGAAGAGGGAGCATTC CGAG
ACAGCAACTATCTCCGACTGCTTTTCCCTGTCCCGTAATCACCTTAGCACAAATTC CCTGGGGTT
TGCCAGGACTATAGAAGAACTACGCTTGGATGATAATCGCATATCCACTATTT CATCACCAT
CTCTTCAAGGTCTCACTAGTCTAAAACGCCTGGTTCTAGATGGAAACCTGTTGAACAATCATG
GTTTAGGTGACAAAGTTTTCTTCAACCTAGTTAATTTGACAGAGCTGTCCCTGGTGC GGAATT
CCCTGACTGCTGCACCAGTAAACCTTCAGGCACAAACCTGAGGAAGCTTTATCTTCAAGATA
ACCACATCAATCGGGTGCCCCAAATGCTTTTTCTTATCTAAGGCAGCTCTATCGACTGGGATA
TGTCCAATAATAACCTAAGTAATTTACCTCAGGGTATCTTTGATGATTTGGACAATATAACAC
AACTGATTCTTCGCAACAATCCCTGGTATTGCGGGTGCAAGATGAAATGGGTACGTGACTGGT
TACAATCACTACCTGTGAAGGTCAACGTGCGTGGGCTCATGTGCCAAGCCCCAGAAAAGGTTT
GTGGGATGGCTATTAAGGATCTCAATGCAGAACTGTTTGATTGTAAGGACAGTGGGATTGTAA
GCACCATTCAGATAACCACTGCAATACCCAACACAGTGTATCCTGCCCCAAGGACAGTGGCCAG
CTCCAGTGACCAAACAGCCAGATATTAAGAACCCCAAGCTCACTAAGGATCAACAAACCACAG
GGAGTCCCTCAAGAAAAACAATTACAATTACTGTGAAGTCTGTCACCTCTGATACCATTCATA
TCTCTTGAAACTTGCTCTACCTATGACTGCTTTGAGACTCAGCTGGCTTAAACTGGGCCATA
GCCCCGCATTTGGATCTATAACAGAAACAATTGTAACAGGGGAACGCAGTGAGTACTTGGTCA
CAGCCCTGGAGCCTGATTCACCCCTATAAAGTATGCATGGTTCCCATGGAAACCAGCAACCTCT
ACCTATTTGATGAAACTCCTGTTTGTATTGAGACTGAAACTGCACCCCTTCGAATGTACAACC
CTACAACCACCCTCAATCGAGAGCAAGAGAAAGAACCTTACAAAAACCCCAATTTACCTTTGG
CTGCCATCATTTGGTGGGGCTGTGGCCCTGGTTACCATTGCCCTTCTTGCTTTAGTGTGTTGGT
ATGTTCATAGGAATGGATCGCTCTTCTCAAGGAACCTGTGCATATAGCAAAGGGAGGAGAAGAA
AGGATGACTATGCAGAAGCTGGCACTAAGAAGGACAACCTCTATCCTGGAAATCAGGGAAACTT
CTTTTCAGATGTTACCAATAAGCAATGAACCCATCTCGAAGGAGGAGTTTGTAATACACACCA
TATTTCCCTCCTAATGGAATGAATCTGTACAAAACAATCACAGTGAAAGCAGTAGTAACCGAA
GCTACAGAGACAGTGGTATTCCAGACTCAGATCACTCACACT**CATGA**TGCTGAAGGACTCACA
GCAGACTTGTGTTTTGGGTTTTTTAAACCTAAGGGAGGTGATGGT

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FIGURE 384

MISAAWSIFLIGTKIGLFLQVAPLSVMAKSCPSVCRCDAGFIYCNDRFLTSIPTGIPEDATTL
YLQNNQINNAGIPSDLKNLLKVERIYLYHNSLDEFPTNLPKYVKELHLQENNIRTITYDSLK
IPYLEELHLDDNSVSAVSIEEGAFRDSNYLRLLFLSRNHLSTIPWGLPRTIEELRLDDNRIST
ISSPSLQGLTSLKRLVLDGNLLNNHGLGDKVFFNLVNLTELSLVRNSLTAAPVNLPGTNLRKL
YLQDNHINRVPPNAFSYLRQLYRLDMSNNNLSNLPQGIFDDLDNITQLILRNNPWYCGCKMKW
VRDWLQSLPVKVNVRGLMCQAPEKVRGMAIKDLNAELFDCKDSGIVSTIQITTAIPNTVYPAQ
GQWPAPVTKQPDIKNPCLTKDQQTTGSPSRKTITITVKSVTSDTIHISWKLALPMTALRLSWL
KLGHSPAFGSITETIVTGERSEYLVTALEPDSPYKVCMPMETSNLYLFEDETPVCIETETAPL
RMYNPTTTLNREQEKEPYKNPNLPLAAIIGGAVALVTIALLALVCWYVHRNGSLFSRNCAYSK
GRRRKDDYAEAGTKKDNSILEIRETSFQMLPISNEPISKEEFVIHTIFPPNGMNLYKNNHSES
SSNRSYRDSGIPDSDHSHS

Important features of the protein:**Signal peptide:**

amino acids 1-28

Transmembrane domain:

amino acids 531-552

N-glycosylation sites.

amino acids 226-229, 282-285, 296-299, 555-558, 626-629, 633-636

Tyrosine kinase phosphorylation site.

amino acids 515-522

N-myristoylation sites.amino acids 12-17, 172-177, 208-213, 359-364, 534-539, 556-561,
640-645**Amidation site.**

amino acids 567-570

Leucine zipper pattern.

amino acids 159-180

Phospholipase A2 aspartic acid active site.

amino acids 34-44

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FIGURE 385

CCGTCATCCCCCTGCAGCCACCCTTCCCAGAGTCCTTTGCCCAGGCCACCCAGGCTTCTTGG
CAGCCCTGCCGGGCCACTTGTCTTCA**ATGT**CTGCCAGGGGGAGGTGGGAAGGAGGTGGGAGGAG
GGCGTGCAGAGGCAGTCTGGGCTTGGCCAGAGCTCAGGGTGCTGAGCGTGTGACCAGCAGTGA
GCAGAGGCCGGCCATGGCCAGCCTGGGGCTGCTGCTCCTGCTCTTACTGACAGCACTGCCACC
GCTGTGGTCCTCCTCACTGCCTGGGCTGGACACTGCTGAAAGTAAAGCCACCATTGCAGACCT
GATCCTGTCTGCGCTGGAGAGAGCCACCGTCTTCCTAGAACAGAGGCTGCCTGAAATCAACCT
GGATGGCATGGTGGGGGTCCGAGTGCTGGAAGAGCAGCTAAAAAGTGTCCGGGAGAAGTGGGC
CCAGGAGCCCCCTGCTGCAGCCGCTGAGCCTGCGCGTGGGGATGCTGGGGGAGAAGCTGGAGGC
TGCCATCCAGAGATCCCTCCACTACCTCAAGCTGAGTGATCCCAAGTACCTAAGAGAGTTCCA
GCTGACCCTCCAGCCCGGGTTTTGGAAGCTCCACATGCCTGGATCCACACTGATGCCTCCTT
GGTGTACCCACGTTCCGGCCCCAGGACTCATTCTCAGAGGAGAGAAGTGACGTGTGCCTGGT
GCAGCTGCTGGGAACCGGGACGGACAGCAGCGAGCCCTGCGGCCTCTCAGACCTCTGCAGGAG
CCTCATGACCAAGCCCGGCTGCTCAGGCTACTGCCTGTCCACCAACTGCTCTTCTTCCTCTG
GGCCAGAATGAGGGGATGCACACAGGGACCACTCCAACAGAGCCAGGACTATATCAACCTCTT
CTGCGCCAACATGATGGACTTGAACCGCAGAGCTGAGGCCATCGGATACGCCTACCCTACCCG
GGACATCTTCATGGAAAACATCATGTTCTGTGGAATGGGCGGCTTCTCCGACTTCTACAAGCT
CCGGTGGCTGGAGGCCATTCTCAGCTGGCAGAAACAGCAGGAAGGATGCTTCGGGGAGCCTGA
TGCTGAAGATGAAGAATTATCTAAAGCTATTCAATATCAGCAGCATTTTTCGAGGAGAGTGAA
GAGGCGAGAAAAACAATTTCCAGATTCTCGCTCTGTTGCTCAGGCTGGAGTACAGTGGCGCAA
TCTCGGCTCACTGCAACCTTTGCCTCCTGGGTTCAAGCAATTCTCTTGCCTCATCCTCCCGAG
TAGCTGGGACTACAGGAGCGTGCCACCATACTGGCTAATTTTTATATTTTTTAGTAGAGAC
AGGGTTTCATCATGTGTGCTCATGCTGGTCTCGAACTCCTGATCTCAAGAGATCCGCCCACCTC
AGGCTCCCAAAGTGTGGGATTAT**TAG**GTGTGAGCCACCGTGTCTGGCTGAAAAGCACTTTCAA
GAGACTGTGTTGAATAAAGGGCCAAGGTTCTTGCCACCCAGCACTCATGGGGGCTCTCTCCCC
TAGATGGCTGCTCCTCCCACAACACAGCCACAGCAGTGGCAGCCCTGGGTGGCTTCCTATACA
TCCTGGCAGAATACCCCCAGCAAACAGAGAGCCACACCCATCCACACCGCCACCACCAAGCA
GCCGCTGAGACGGACGGTTCCATGCCAGCTGCCTGGAGGAGGAACAGACCCCTTTAGTCCTCA
TCCCTTAGATCCTGGAGGGCACGGATCACATCCTGGGAAGAAGGCATCTGGAGGATAAGCAAA
GCCACCCCGACACCCAATCTTGGAAGCCCTGAGTAGGCAGGGCCAGGGTAGGTGGGGGCCGGG
AGGGACCCAGGTGTGAACGGATGAATAAAGTTCAACTGCAACTGAAAAAAAAA

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FIGURE 386

MSARGRWEGGRRACRGSGLARAQGAERVTSSEQRPAMASLGLLLLLLLLLTALPPLWSSSLPG
LDTAESKATIADLILSALERATVFLEQRLPEINLDGMVGVRVLEEQLKSVREKWAQEPLLQPL
SLRVGMLGEKLEAAIQRS LHYLKLSDPKYLREFQLTLQPGFWKLPHAWIHTDASLVYPTFGPQ
DSFSEERSDVCLVQLLGTGTDSSSEPCGLSDLCRSLMTKPGCSGYCLSHQLLFFLWARMRGCTQ
GPLQQSQDYINLFCANMMDLNRRAEAIGYAYPTRDIFMENIMFCGMGGFSDFYKLRWLEAILS
WQKQQEGCGEPDAEDEELSKAIQYQQHFSRRVKRREKQFPDSRSVAQAGVQWRNLGSLQPLP
PGFKQFSCILLPSSWDYRSVPPYLANFYIFLVETGFHHVAHAGLELLISRPPTSGSQSVGL

Important features of the protein:**Signal peptide:**

amino acids 1-26

Transmembrane domain:

amino acids 39-56

Tyrosine kinase phosphorylation sites.

amino acids 149-156, 274-282

N-myristoylation sites.

amino acids 10-16, 20-26, 63-69, 208-214

Amidation site.

amino acids 10-14

Glycoprotein hormones beta chain signature 1.

amino acids 230-237

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FIGURE 387

GGTCTGAGTGCAGAGCTGCTGTCAATGGCGGCCGCTCTGTGGGGCTTCTTTCCCGTCCTGCTGC
TGCTGCTGCTATCGGGGGATGTCCAGAGCTCGGAGGTGCCCGGGGCTGCTGCTGAGGGATCGG
GAGGGAGTGGGGTCGGCATAGGAGATCGCTTCAAGATTGAGGGGCGTGCAAGTGTCCAGGGG
TGAAGCCTCAGGACTGGATCTCGGCGGCCCGAGTGCTGGTAGACGGAGAAGAGCACGTCGGTT
TCCTTAAGACAGATGGGAGTTTTGTGGTTTCATGATATACCTTCTGGATCTTATGTAGTGGAAG
TTGTATCTCCAGCTTACAGATTTGATCCCGTTCGAGTGGATATCACTTCGAAAGGAAAAATGA
GAGCAAGATATGTGAATTACATCAAAACATCAGAGGTTGTCAGACTGCCCTATCCTCTCCAAA
TGAAATCTTCAGGTCCACCTTCTTACTTTATTAAGGGAATCGTGGGGCTGGACAGACTTTC
TAATGAACCCAATGGTTATGATGATGGTTCTTCCTTTATTGATATTTGTGCTTCTGCCTAAAG
TGGTCAACACAAGTGATCCTGACATGAGACGGGAAATGGAGCAGTCAATGAATATGCTGAATT
CCAACCATGAGTTGCCTGATGTTTCTGAGTTCATGACAAGACTCTTCTCTTCAAAATCATCTG
GCAAATCTAGCAGCGGCAGCAGTAAACAGGCAAAAGTGGGGCTGGCAAAGGAGGTAGTCAG
GCCGTCCAGAGCTGGCATTTCACAAAACACGGCAACACTGGGTGGCATCCAAGTCTTGAAAA
CCGTGTGAAGCAACTACTATAAACTTGAGTCATCCCGACGTTGATCTCTTACAACTGTGTATGTT
AACTTTTTAGCACATGTTTTGTACTTGGTACACGAGAAAACCCAGCTTTCATCTTTTGTCTGT
ATGAGGTCAATATTGATGTCACTGAATTAATTACAGTGTCTATAGAAAATGCCATTAATAAA
TTATATGAACACTACTATACATTATGTATATTAATTAACATCTTAATCCAGAAATCAAAAAA
AAAAAAAAAAAAAAAAAAAAA

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FIGURE 388

MAAALWGFFPVLLLLLLLLSGDVQSSEVPGAAAEGSGGSGVGIGDRFKIEGRAVVPGVKPDQWIS
AARVLVDGEEHVGFLKTDGSFVVDIPSGSYVVEVVSPAYRFDVVRVDITSKGKMRARYVNYI
KTSEVVRLPYPLQMKSSGPPSYFIKRESWGWTDFLMNPMVMMMLVPLLI FVLLPKVVNTSDPD
MRREMEQSMNMLNSNHELPDVSEFMTRLFSSKSSGKSSSGSSKTGKSGAGKRR

Important features of the protein:**Signal sequence:**

amino acids 1-23

Transmembrane domain:

amino acids 161-182

N-glycosylation site.

amino acids 184-187

Glycosaminoglycan attachment sites.

amino acids 37-40, 236-239

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 151-154

N-myristoylation sites.

amino acids 33-38, 36-41, 38-44, 229-234

Amidation site.

amino acids 238-241

ATP/GTP-binding site motif A (P-loop).

amino acids 229-236

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FIGURE 389

GTCGTGTGCTTGGAGGAAGCCGCGGAACCCCCAGCGTCCGTCC**ATG**GCGTGGAGCCTTGGGAG
CTGGCTGGGTGGCTGCCTGCTGGTGTGAGCATTTGGGAATGGTACCACCTCCCGAAAATGTCAG
AATGAATTCTGTTAATTTCAAGAACATTCTACAGTGGGAGTCACCTGCTTTTGCCAAAGGGAA
CCTGACTTTTACAGCTCAGTACCTAAGTTATAGGATATTCCAAGATAAATGCATGAATACTAC
CTTGACGGAATGTGATTTTCTCAAGTCTTTCCAAGTATGGTGACCACACCTTGAGAGTCAGGGC
TGAATTTGCAGATGAGCATTGAGACTGGGTAAACATCACCTTCTGTCCTGTGGATGACACCAT
TATTGGACCCCCTGGAATGCAAGTAGAAGTACTTGCTGATTCTTTACATATGCGTTTCTTAGC
CCCTAAAATTGAGAATGAATACGAACTTGGAATGATGAAGAATGTGTATAACTCATGGACTTA
TAATGTGCAATACTGGAAAAACGGTACTGATGAAAAGTTTCAAATTACTCCCCAGTATGACTT
TGAGGTCTCAGAAACCTGGAGCCATGGACAACCTTATTGTGTTCAAGTTCGAGGGTTTCTTCC
TGATCGGAACAAAGCTGGGGAATGGAGTGAGCCTGTCTGTGAGCAAACAACCCATGACGAAAC
GGTCCCCTCCTGGATGGTGGCCGTATCCTCATGGCCTCGGTCTTCATGGTCTGCCTGGCACT
CCTCGGCTGCTTCTCCTTGCTGTGGTGCCTTACAAGAAGACAAAGTACGCCCTTCTCCCCTAG
GAATTCTCTTCCACAGCACCTGAAAGAGTTTTTGGGCCATCCTCATCATAACACACTTCTGTT
TTTCTCCTTTCCATTGTCGGATGAGAATGATGTTTTTGACAAGCTAAGTGTGATTGCAGAAGA
CTCTGAGAGCGGCAAGCAGAATCCTGGTGACAGCTGCAGCCTCGGGACCCCGCCTGGGCAGGG
GCCCCAAAGCT**AG**GCTCTGAGAAGGAAACACACTCGGCTGGGCACAGTGACGTACTCCATCTC
ACATCTGCCCTCAGTGAGGGATCAGGGCAGCAAACAAGGGCCAAGACCATCTGAGCCAGCCCCA
CATCTAGAACTCCAGACCTGGACTTAGCCACCAGAGAGCTACATTTTAAAGGCTGTCTTGGCA
AAAATACTCCATTTGGGAACTCACTGCCTTATAAAGGCTTTCATGATGTTTTCAGAAGTTGGC
CACTGAGAGTGTAATTTTCAGCCTTTTATATCACTAAAATAAGATCATGTTTTAATTGTGAGA
AACAGGGCCGAGCACAGTGGCTCACGCCTGTAATACCAGCACCTTAGAGGTCGAGGCAGGCGG
ATCACTTGAGGTGAGGAGTTCAAGACCAGCCTGGCCAATATGGTGAAACCCAGTCTCTACTAA
AAATACAAAAATTAGCTAGGCATGATGGCGCATGCCTATAATCCCAGCTACTCGAGTGCCTGA
GGCAGGAGAATTGCATGAACCCGGGAGGAGGAGGAGGAGGTTGCAGTGAGCCGAGATAGCGGC
ACTGCACTCCAGCCTGGGTGACAAAGTGAGACTCCATCTCAAAAAAAAAAAAAAAAAAATTGTG
AGAAACAGAAATACTTAAATGAGGAATAAGAATGGAGATGTTACATCTGGTAGATGTAACAT
TCTACCAGATTATGGATGGACTGATCTGAAAATCGACCTCAACTCAAGGGTGGTCAGCTCAAT
GCTACACAGAGCACGGACTTTTGGATTCTTTGCAGTACTTTGAATTTATTTTCTACCTATAT
ATGTTTTATATGCTGCTGGTGTCCATTAAAGTTTTACTCTGTGTTGC

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FIGURE 390

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83551

><subunit 1 of 1, 325 aa, 1 stop

><MW: 37011, pI: 5.09, NX(S/T): 4

MAWSLGSWLGGCLLVSALGMVPPPENVRMNSVNFKNILQWESPAFAKGNLTFTAQYLSYRIFQ
DKCMNTTLTECDFSSLSKYGDHTLRVRAEFADHSDWVNITFCPVDDTIIGPPGMQVEVLADS
LHMRFLAPKIENEYETWTMKNVYNSWTYNVQYWKNGTDEKFQITPOYDFEVLRLNLEPWTTYCV
QVRGFLPDRNKAGEWSEPVEQTTHDETVPSSWMVAVILMASVFMVCLALLGCFSLLWCYKKT
KYAFSPRNSLPQHLKEFLGHPHNTLLFFSFPLSDENDVFDKLSVIAEDSESGKQNP GDSCSL
GTPPGQGPQS

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 222-245

N-glycosylation sites.

amino acids 49-53, 68-72, 102-106, 161-165

N-myristoylation sites.

amino acids 6-12, 316-322

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FIGURE 391

CTGTGCAGCTCGAGGCTCCAGAGGCACACTCCAGAGAGAGCCAAGGTTCTGACGCG**ATG**AGGA
AGCACCTGAGCTGGTGGTGGCTGGCCACTGTCTGCATGCTGCTCTTCAGCCACCTCTCTGCGG
TCCAGACGAGGGGCATCAAGCACAGAATCAAGTGGAACCGGAAGGCCCTGCCAGCACTGCCC
AGATCACTGAGGCCCAGGTGGCTGAGAACCGCCCGGAGCCTTCATCAAGCAAGGCCGCAAGC
TCGACATTGACTTCGGAGCCGAGGGCAACAGGTACTACGAGGCCAACTACTGGCAGTTCCCCG
ATGGCATCCACTACAACGGCTGCTCTGAGGCTAATGTGACCAAGGAGGCATTTGTCACCGGCT
GCATCAATGCCACCCAGGCGGCGAACCAGGGGGAGTTCCAGAAGCCAGACAACAAGCTCCACC
AGCAGGTGCTCTGGCGGCTGGTCCAGGAGCTCTGCTCCCTCAAGCATTGCGAGTTTTGGTTGG
AGAGGGGCGCAGGACTTCGGGTCACCATGCACCAGCCAGTGCTCCTCTGCCTTCTGGCTTTGA
TCTGGCTCATGGT**GAAATAA**GCTTGCCAGGAGGCTGGCAGTACAGAGCGCAGCAGCGAGCAAA
TCCTGGCAAGTGACCCAGCTCTTCTCCCCCAAACCCACGCGTGTTCTGAAGGTGCCCAGGAGC
GGCGATGCACTCGCACTGCAAATGCCGCTCCCACGTATGCGCCCTGGTATGTGCCTGCGTTCT
GATAGATGGGGGACTGTGGCTTCTCCGTCACTCCATTCTCAGCCCCTAGCAGAGCGTCTGGCA
CACTAGATTAGTAGTAAATGCTTGATGAGAAGAACACATCAGGCACTGCGCCACCTGCTTCAC
AGTACTTCCCAACAACCTCTTAGAGGTAGGTGTATTCCCGTTTTACAGATAAGGAAACTGAGGC
CCAGAGAGCTGAAGTACTGCACCCAGCATCACCAGCTAGAAAGTGGCAGAGCCAGGATTCAAC
CCTGGCTTGTCTAACCCAGGTTTTCTGCTCTGTCCAATTCCAGAGCTGTCTGGTGATCACTT
TATGTCTCACAGGGACCCACATCCAAACATGTATCTCTAATGAAATTGTGAAAGCTCCATGTT
TAGAAATAAATGAAAACACCTGA

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FIGURE 392

MRKHLSSWWLATVCMLLFSHL SAVQTRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQG
RKLDIDFGAEGNRYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQAANQGEFQKPDNK
LHQQVLWRLVQELCSLKHCEFWLERGAGLRVTMHQPVLLCLLALIWL MVK

Important features of the protein:

Signal peptide:

amino acids 1-26

Transmembrane domain:

amino acids 157-171

N-glycosylation sites.

amino acids 98-102, 110-114

Tyrosine kinase phosphorylation site.

amino acids 76-83

N-myristoylation sites.

amino acids 71-77, 88-94, 93-99, 107-113, 154-160

Amidation site.

amino acids 62-66

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FIGURE 393

TGAAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGAA
TGGTGAAGGTGCCTGTCTAACTTTTCTGTAAAAAGAACCAGCTGCCTCCAGGCAGCCAGCCCT
CAAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTCGCCAA
TTTAACACCAAGAAGAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTGAGAG
ATGAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCTTCTGCCCTCCTTTG
CTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTTGCCTGGGTTTTACCCTGCTTCTC
TGGAGCCAGGTATCAGGGGCCCAGGGCCAAGAATTCCACTTTGGGCCCTGCCAAGTGAAGGGG
GTTGTTCCCCAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAGCTCAGGAT
AACATCACGAGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTCTCGGATGCTGAGAGC
TGTTACCTTGTCCACACCCTGCTGGAGTTCTACTTGA AAACTGTTTTCAAAAACCACCACAAT
AGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACA ACTTTGTTCTCATC
GTGTCACAACTGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGACAGTGCACACAGG
CGGTTTTCTGCTATTCCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGCTCTGACCAAAGCC
CTTGGGGAAGTGGACATTCTTCTGACCTGGATGCAGAAATCTACAAGCT**CTGA**ATGTCTAGA
CCAGGACCTCCCTCCCCCTGGCACTGGTTTGTTCCTGTGTCATTTCAAACAGTCTCCCTTCC
TATGCTGTTCACTGGACACTTCACGCCCTTGGCCATGGGTCCCATTCTTGGCCCAGGATTATT
GTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAGGTGCCTCTGGATGCTGT
GAAGAGTCTACAGAGAAGATTCTTGTATTTATTACA ACTCTATTTAATTAATGTCAGTATTTT
AACTGAAGTTCTATTTATTTGTGAGACTGTAAGTTACATGAAGGCAGCAGAATATTGTGCCCC
ATGCTTCTTTACCCCTCACAATCCTTGCCACAGTGTGGGGCAGTGGATGGGTGCTTAGTAAGT
ACTTAATAAACTGTGGTGCTTTTTTTTGGCCTGTCTTTGGATTGTTAAAAACAGAGAGGGATG
CTTGGATGTAAAACTGAACTTCAGAGCATGAAAATCACACTGTCTTCTGATATCTGCAGGGAC
AGAGCATTGGGGTGGGGGTAAGGTGCATCTGTTTGAAAAGTAAACGATAAAATGTGGATTAAA
GTGCCCAGCACAAAGCAGATCCTCAATAAACATTTTCA TTTCCCACCCACACTCGCCAGCTCAC
CCCATCATCCCTTTCCCTTGGTGCCCTCCTTTTTTTTTTATCCTAGTCATTCTTCCCTAATCT
TCCACTTGAGTGTCAAGCTGACCTTGCTGATGGTGACATTGCACCTGGATGTACTATCCAATC
TGTGATGACATTCCCTGCTAATAAAAGACAACATAACTCCAAAAAAAAAAAAAAAAAAAAAAAAA
AAAA

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FIGURE 394

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002

><subunit 1 of 1, 206 aa, 1 stop

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRLQSLWTLARPFPCPLLATASQMQMVVLPCLGFTLLLSQVSGAQGQEFHFGPCQVKG
VVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLEVHTLLEFYLKTVFKNHHN
RTVEVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRELLFRRAFKQLDVEAALTKA
LGEVDILLTWMQKFYKL

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

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FIGURE 395

GCCTTGGCCTCCCAAAGGGCTGGGATTATAGGCGTGACCACCATGTCTGGTCCAGAGTCTCAT
TTCCTGATGATTTATAGACTCAAAGAAAAC**TCATG**TTCAGAAGCTCTCTTCTCTTCTGGCCTC
CTCTCTGTCTTCTTTCCCTCTTTCTTCTTATTTTAATTAGTAGCATCTACTCAGAGTCATGCA
AGCTGGAAATCTTTCATTTTGCTTGTGAGTGGGGTAGGTCAGTCTTAGTTTTATTTTT
TGAAATTTCAACTTTCAGATTCAGGGGGTACATGTGAAGGTTTGTTTTATGAGTATATTGCAT
GATGCTGAGGTTTGGGGT

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FIGURE 396

MFRSSLLFWPPLCLLSLFLILISSIYSESKLEIFHFACQWGRSLSLSFYFLKFQLSDSGGT
CEGLFYEYIA

Important features of the protein:

Signal peptide:

amino acids 1-25

N-myristoylation site.

amino acids 62-68

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FIGURE 397

CATGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCCTG
TGTCTCTGGTGGTTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGAATGT
CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATTT
CATATATGGGCAAAAGAAATGGCTGAATAAATCAGAATGCAGAAATATCAATAGAACCTACTG
TGATCTTTCTGCTGAAACTTCTGACTACGAACACCAGTATTATGCCAAAGTTAAGGCCATTTG
GGGAACAAAGTGTTCCAAATGGGCTGAAAGTGGACGGTTCATCCTTTTTTAGAAACACAAAT
TGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGTCCTGACAGCTCC
AGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAATATACTCCAATCT
GAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCCCAGTGTGTGACCAA
CCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGTACACGTGGAGTCCTT
CGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTGCCAGGACTTTGAAAGA
TCAATCATCAGAGTTCAAGGCTAAATCATCTTCTGGTATGTTTTGCCCATATCTATTACCGT
GTTTCTTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCACGTTGGCAAAGAGAAACA
CCCAGCAAATTTGATTTTGATTTATGGAAATGAATTTGACAAAAGATTCTTTGTGCCTGCTGA
AAAAATCGTGATTAACCTTTATCACCTCAATATCTCGGATGATTCTAAATTTCTCATCAGGA
TATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAATGATCCTCAGCCCAGCGGGAA
CCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAGGGTATGCTTCGCATTTGATGGA
AATTTTTTGTGACTCTGAAGAAAACACGGAAGGTACTTCTCTCAGCCAGCAAGAGTCCCTCAG
CAGAACAATACCCCCGGATAAAACAGTCATTGAATATGAATATGATGTCAGAACCACTGACAT
TTGTGCGGGGCCTGAAGAGCAGGAGCTCAGTTTGCAGGAGGAGGTGTCCACACAAGGAACATT
ATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCCGCAAACGTTACAGTACTCATACACCCC
TCAGCTCCAAGACTTAGACCCCCCTGGCGCAGGAGCACACAGACTCGGAGGAGGGGCCGGAGGA
AGAGCCATCGACGACCCTGGTCGACTGGGATCCCCAACTGGCAGGCTGTGTATTCTTTCGCT
GTCCAGCTTCGACCAGGATTCAGAGGGCTGCGAGCCTTCTGAGGGGGATGGGCTCGGAGAGGA
GGGTCTTCTATCTAGACTCTATGAGGAGCCGGCTCCAGACAGGCCACCAGGAGAAAATGAAAC
CTATCTCATGCAATTCATGGAGGAATGGGGGTTATATGTGCAGATGGAAAAC**TGA**TGCCAACA
CTTCCTTTTGCCTTTTGTTTCCTGTGCAAACAAGTGAGTCACCCCTTTGATCCCAGCCATAAA
GTACCTGGGATGAAAGAAGTTTTTTCCAGTTTGTCTAGTGTCTGTGAGAA

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FIGURE 398

MPLPPLLLLLLLAAPWGRAVPCVSGGLPKPANITFLSINMKNVLQWTPPEGLQGKVTYTVQYF
IYGQKKWLNKSECRNINRTYCDLSAETSDYEHQYYAKVKAIWGTKCSKWAESGRFYPPLETQI
GPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQQIYSNLKYNVSVLNTKSNRTWSQCVTN
HTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQCARTLKDQSSEFKAKIIFWYVLPISITV
FLFSVMGYSIYRYIHVGKEKHANLILYGNFEDKRFFVPAEKIVINFITLNISSDDSKISHQD
MSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKHLGYASHLMEIFCDSEENTEGTSLTQQESLS
RTIPDPKTVIEYEYDVRTTDICAGPEEQELSLQEEVSTQGTLLSQALAVLGPQTLQYSYTP
QLQDLDPQAQEHDTSEEGPEEPPSTTLVDWDPQTGRLCIPSLSSFDQDSEGCEPSEGDGLGEE
GLLSRLYEPPAPDRPPGENETYLMQFMEEWGLYVQMEN

Signal sequence:
amino acids 1-18

Transmembrane domain:
amino acids 240-260

N-glycosylation sites.
amino acids 31-34, 72-75, 80-83, 171-174, 180-183, 189-192,
304-307, 523-526

Tyrosine kinase phosphorylation site.
amino acids 385-392, 518-526

N-myristoylation sites.
amino acids 53-58, 106-111, 368-373, 492-497

Tissue factor
amino acids 1-278

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FIGURE 399

CCGGCG**ATG**TCGCTCGTGCTGCTAAGCCTGGCCGCGCTGTGCAGGAGCGCCGTACCCCGAGAG
CCGACCGTTCAATGTGGCTCTGAAACTGGGCCATCTCCAGAGTGGATGCTACAACATGATCTA
ATCCCCGGAGACTTGAGGGACCTCCGAGTAGAACCTGTTACAAC TAGTGTTGCAACAGGGGAC
TATTC AATTTTGATGAATGTAAGCTGGGTACTCCGGGCAGATGCCAGCATCCGCTTGTTGAAG
GCCACCAAGATTTGTGTGACGGGCAAAAGCAACTTCCAGTCCTACAGCTGTGTGAGGTGCAAT
TACACAGAGGCCTTCCAGACTCAGACCAGACCCTCTGGTGGTAAATGGACATTTTCCTACATC
GGCTTCCCTGTAGAGCTGAACACAGTCTATTTCAATTGGGGCCATAATATTCCTAATGCAAAT
ATGAATGAAGATGGCCCTTCCATGTCTGTGAATTTACCTCACCAGGCTGCCTAGACCACATA
ATGAAATATAAAAAAAGTGTGTCAAGGCCGGAAGCCTGTGGGATCCGAACATCACTGCTTGT
AAGAAGAATGAGGAGACAGTAGAAGTGAACCTCACAACCACTCCCCTGGGAAACAGATACATG
GCTCTTATCCAACACAGCACTATCATCGGGTTTTCTCAGGTGTTTGAGCCACACCAGAAGAAA
CAAACGCGAGCTTCAGTGGTGATTCCAGTGACTGGGGATAGTGAAGGTGCTACGGTGCAGCTG
ACTCCATATTTTCCTACTTGTGGCAGCGACTGCATCCGACATAAAGGAACAGTTGTGCTCTGC
CCACAAACAGGCGTCCCTTTCCCTCTGGATAACAACAAAAGCAAGCCGGGAGGCTGGCTGCCT
CTCCTCCTGCTGTCTCTGCTGGTGGCCACATGGGTGCTGGTGGCAGGGATCTATCTAATGTGG
AGGCACGAAAGGATCAAGAAGACTTCCTTTTCTACCACCACACTACTGCCCCCATTAAAGTT
CTTGTGGTTTACCCATCTGAAATATGTTTCCATCACACAATTTGTTACTTCACTGAATTTCTT
CAAAACCATTG CAGAAAGTGAGGTCATCCTTGAAAAGTGGCAGAAAAAGAAAATAGCAGAGATG
GGTCCAGTGCAGTGGCTTGCCACTCAAAGAAGGCAGCAGACAAAGTCGTCTTCCTTCTTTCC
AATGACGTCAACAGTGTGTGCGATGGTACCTGTGGCAAGAGCGAGGGCAGTCCCAGTGAGAAC
TCTCAAGACCTCTTCCCCCTTGCCTTTAACCTTTTCTGCAGTGATCTAAGAAGCCAGATT CAT
CTGCACAAATACGTGGTGGTCTACTTTAGAGAGATTGATACAAAAGACGATTACAATGCTCTC
AGTGTCTGCCCCAAGTACCACCTCATGAAGGATGCCACTGCTTTCTGTGCAGAACTTCTCCAT
GTCAAGCAGCAGGTGTCAGCAGGAAAAAGATCACAAGCCTGCCACGATGGCTGCTGCTCCTTG
TAG

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FIGURE 400

MSLVLLSLAALCRSAVPREPTVQCGSETGPSPEWMLQHDLI PGDLRDLRVEPVTT SVATGDYS
ILMNVS WVL RADASIRLLKATKICVTGKS NFQSYSCVRCNYTEAFQTQTRPSGGKWTFSYIGF
PVELNTVYFIGAHNIPNANMNEDGPSMSVNFTSPGC LDHIMKYKKKCVKAGSLWDPNITACKK
NEETVEVNFTTTPLGNRYMALIQHSTIIGFSQVFEPHQKKQTRASVVIPVTGDSEGATVQLTP
YFPTCGSDCIRHKGT VVLC PQTGVPFPLDNNKSKPGGWLPLLLLSLLVATWVLVAGIYLMWRH
ERIKKTSFSTTTLLPPIKVLVVYPSEICFHHTICYFTEFLQNHCRSEVILEKWQKKKIAEMGP
VQWLATQKKAADKVVFLSNDVNSVCDGTCGKSEGPSSENSQDLFPLAFNLFCSDLRSQIHLH
KYVVVYFREIDTKDDYNALSVCPKYHLMKDATAFCAELLHV KQQVSAGKRSQACHDGCCSL

Important features of the protein:**Signal peptide:**

amino acids 1-14

Transmembrane domain:

amino acids 290-309

N-glycosylation sites.amino acids 67 - 71, 103 - 107, 156 - 160, 183 - 187, 197 - 201
and 283 - 287**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 228 - 232 and 319 - 323

Casein kinase II phosphorylation sites.

amino acids 178 - 182, 402 - 406, 414 - 418 and 453 - 457

N-myristoylation site.

amino acids 116-122

Amidation site.

amino acids 488-452

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FIGURE 401

GGGAACAGGGAACTATCAGCCCCTCGGCCTCCGGGCCCTGCATTCTCTAGCC**ATGG**ACCG
GGACCTTTTGCGGCAGTCGCTAAATTGCCACGGGTCGTCTTTGCTCTCTCTACTTTCGGAG
CGAACAGCAGGACAATCCACACTTCCGTAGCCTCCTGGGGTCGGCCGCCGAGCCAGCCCCG
GGGCCCCGCCGCCAGCACCCGTTGCAGGGCAGAAAAGAGAAGAGAGTTGACAACATCGA
GATACAGAAATTATCTCTCCAAAAAAGCGGATCTGCTTTTTGCACTTTCCTGGAATCAGA
TGCACCTGCAACTTCTGAAATTAATGAAGACAGTGAAGATCATTATGCAATCATGCCACC
TTTAGAGCAATTATGAGATACCTAGTATGGATCGGAGAGAGCTGTTTTTCCGAGATAT
TGAGCGTGGTGATATAGTGATTGGAAGAATTAGTTCTATTTCGGAATTCGGTTTTTTCAT
GGTGTGATCTGTTTAGGAAGTGGTATCATGAGAGATATAGCCCACTTAGAAATCACAGC
TCTTTGTCCCTTAAGAGATGTGCCCTTCTCACAGTAACCATGGGGATCCTTTATCATATTA
CCAAACTGGTGACATCATTCGAGCTGGAATCAAGGATATTGACAGATACCATGAAAAGCT
AGCAGTATCTCTGTATAGCTCTTCTCTTCCACCACACCTATCTGGTATTAAATTAGGTGT
AATTAGCTCTGAAGAGCTTCCCTTATACTACAGGAGAAGTGTGAGCTAAATAGCAATTC
TTTGGAGTCCATGAAAATGTCATGCAGAGTTCCTTGGGATTTGTTAATCCAGGAGTAGT
TGAATTCCTTCTAGAAAACTAGGAATAGATGAATCTAATCCACCATCTTTAATGAGAGG
CCTACAAAGCAAAAATTTCTCTGAAGATGATTTTGCTTCTGCATTGAGAAAAAACAATC
CGCATCTTGGGCTTTAAATGTGTGAAGATCGGAGTTGACTATTTTAAAGTTGGACGCCA
TGTGGATGCTATGAATGAATACAATAAAGCTTTGGAAATAGACAAACAAAACGTGGAAGC
TTTGGTAGCTCGTGGAGCATTATATGCGACAAAAGGAAGTTTGAACAAAGCAATAGAAGA
TTTTGAGCTTGCATTAGAAAATGTCCAACCTCACAGAAATGCAAGAAAATACCTCTGCCA
GACACTTGTAGAGAGAGGAGGACAGTTAGAAGAAGAAGAAAAGTTTTAAATGCTGAAAG
TTACTATAAGAAAGCCTTGGCTTTGGATGAGACTTTTAAAGATGCAGAGGATGCTTTGCA
GAACTTCATAAATATATGCAGAAATCTTTGGAATTAAGAGAAAAACAAGCTGAAAAGGA
AGAAAAGCAGAAAACAAAGAAAATAGAAACAAGTGCAGAAAAGTTGCGTAAGCTCTTAA
AGAAGAGAAGAGGCTAAAGAAGAAAAGAAGAAAATCAACTTCTTCTCAAGTGTTCCTC
TGCTGATGAATCAGTGTCTTCATCATCATCCTCTTCTCTCTGGTCACAAAAGGCATAA
GAAACATAAGAGGAACCGTTCAGAGTCTTCTCGCAGTTCAGAAAGGCATTATCTAGGGC
ATCCTCAAATCAGATAGATCAGAATAGGAAAGATGAGTGCTACCCAGTTCCAGCTAATAC
TTCAGCATCTTTCTTAACCATAAACAAGAAGTGGAGAACTACTGGGGAAGCAGGATAG
GTTACAGTATGAAAAGACACAGATAAAAGAGAAAGATAGATGCCCTCTCTCTCATCTTC
ACTTGAAATACCGGATGATTTTGGAGTGTACTCCTATTTATTTAAAAAGTTAACTATAAA
ACAGCCTCAGGCAGGTCCTTCAGGAGATATTCCAGAAGAGGGCATTGTTATCATAGATGA
CAGCTCCATTATGTTACTGACCCTGAAGACCTTCAAGTGGGACAAGATATGGAGGTGGA
AGACAGTGGTATTGATGATCCTGACCACGGG**TAG**GCTTAGGTTTATGTGTGTGTATGTGT
CTTAGTTTTTAAACAAAAAATTA AAAAGTAAAAAACTAAAAATAGAAAAATGCTTAGAG
AATAAGGATATAAAGAATATTTTGTGCAGTTGAACAATGAGTGCTTAAGCTAAATGTCA
TCACAAAAGAGTAAAAAAATTTTACAAAATTA AAAATGTTTAAAGTTAAAAAGCTCTAGG
AAGCTAAGGTCAATTTATTATTGGAGAAATAAAATTATTTTTATGAATTTACTGT

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FIGURE 402

MDRDLRLQSLNCHGSSLLSLRSEQQDNPHFRSLLGSAEPARGPPPQHPLQGRKEKRVD
NIEIQKFISKKADLLFALSWKSDAPATSEINEDSEDHYAIMPPLEQFMEIPSMRRELEFF
RDIERGDIVIGRISSIREFGFFMVLICLGSGIMRDIAHLEITALCPLRDVPSHSNHGDPL
SYYQTGDIIRAGIKDIDRYHEKLAVSLYSSSLPPHLSGIKLGVISSEELPLYRRSVELN
SNSLESYENVMQSSLGFVNPGVVEFLLEKLGIDESNPPSLMRGLQSKNFSEDDFASALRK
KQSASWALKCVKIGVDYFKVGRHVDAMNEYNKALEIDKQNEALVARGALYATKGS LNKA
IEDFELALENCPTHNRNARKYLCQTLVERGGQLEEEEEKFLNAESYKKALALDETFKDAED
ALQKLHKYMQKSLELREKQAEKEEKQKTKKIETSAEKLRLKLLKEEKRLKKRRRKSTSSSS
VSSADESVSSSSSSSSSGHKRHKHKRNRSESSRRHSSRASSNQIDQNRKDECYPVP
ANTSASFNLHKQEVKLLGKQDRLOQYEKTKIIEKDRCPSSSSLEIPDDFGVSYLFFKKL
TIKQPQAGPSGDIPEEGIVIIDSSIHVTDPEDLQVGQDMEVEDSGIDDPDHG

Important features of the protein:**Signal peptide:**

Amino acids 1-23

Transmembrane domain:

Amino acids 138-155

N-glycosylation sites:

Amino acids 288-292;508-512;542-546

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 300-304;472-476;473-477;517-521;598-602

N-myristoylation sites:

Amino acids 218-224;222-228;271-277;348-354

Amidation site:

Amino acids 52-56

Cell attachment sequence:

Amino acids 125-128

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FIGURE 403

CCGAGGCGGGAGGAGCCCGAGGGGGCGCGAGCCCCGCATGAATCATTGTAGTCAATCATTTTC
CAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAACTGCCAGCTCAGAATA
GGAAAATAACTTGGGATTTTATATTGGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTT
ATGACAAACTTTTCAGAGACTGTTGATTTGGTGAGACAGACCGGCCATCAGTGTGGCATGTCAG
AGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAAAGAATGAACCTCAGAGACCCCCC
CGCAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCA
CTGCCTACTTTGTGATTCAACCTTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTCTGGAGCTC
ACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCCATTGCCAAGAAGTACA
TGTCAGAAAATAAGGGAGTTCTCTGCATGGGGGTGATGAAGACAGACCCTTTCCAGACTTTG
ACCCCTGGTGGACAAACGACTGTGAGCAGAAAGAGTCAGAGCCCATTCCTGCCAACTGCACTG
GCTGTGCCCAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCCCAAGGAAATTTGAGAGGC
TCCATCCACTGGTGATCAAGACGGGAAAGCCCCTGTTGGAGGAAGAGATTCAGCATTTTTTGT
GCCAGTACCCTGAGGCGACAGAAGGCTTCTCTGAAGGGTTTTTCGCAAGTGGTGGCGCTGCT
TTCCTGAGCGGTGGTTCCCATTTCTTATCCATGGAGGAGACCTCTGAACAGATCACAAATGT
TACGTGAGCTTTTTCTGTTTTCACTCACCTGCCATTTCCAAAAGATGCCTCTTTAAACAAGT
GCTCCTTTCTTCACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAGATGCCTGACCTATTTA
TCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCAGTGCCGAAGACATTGTC
AGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCGACACCACCCACTGGAAGG
TCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGATGGAACCGCTTTCTCAGAAC
TGTAGGAAATAGAACTGTGCACAGGAACAGCTTCAGAGCCGAAAACCAGGTTGAAAGGGGAA
AAATAAAAAACAAAAACGATGAAACTGCAAAAA

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FIGURE 404

MDLAANEISIIYDKLSETVDLVRQTGHQCGMSEKAIEKFIRQLLEKNEPQRPPPQYPLLIVVYK
VLATLGLILLTAYFVIQPFSPPLAPEPVLSGAHTWRSLIHHIRLMSLPIAKKYMSENKGVPLHG
GDEDRPFPDFDPWWTNDCEQNESEPIPANCTGCAQKHLKVMILLEDAPRKFERLHPLVIKTGKP
LLEEEIQHFLLCQYPEATEGFSEGFFAKWWRCFPERWFPPYPWRRPLNRSQMLRELFVPVFTHL
PFPKDASLNKCSFLHPEPVVGSKMHKMPDLFIIGSGEAMLQLIPPFQRRHCQSVAMPIEPGD
IGYVDTTHWKVYVIARGVQPLVICDGTAFSEL

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FIGURE 405

TGCCGGGCTGCGGGGCGCCTTGACTCTCCCTCCACCCTGCCTCCTCGGGCTCCACTCGTCTGCCCCCTGGACTCCC
GTCTCCTCCTGTCTCCTCCGGCTTCCCAGAGCTCCCTCCTTATGGCAGCAGCTTCCCGCGTCTCCGGCGCAGCTTCT
CAGCGGACGACCCCTCTCGCTCCGGGGCTGAGCCCAGTCCCTGGATGTTGCTGAAACTCTCGAGATCATGCGCGGG
TTTGGCTGCTGCTTCCCCGCCGGGTGCCACTGCCACCGCCGCCCTCTGCTGCCGCCGTCCGCGGGATGCTCAG
TAGCCCGCTGCCCGGCCCCCGGATCCTGTGTTCTCGGAAGCCGTTTGCTGCTGCAGAGTTGCACGAACTAGTC
ATGGCTGCTGTTGGGAGTCCCCGCGGCAGTGCAGCAGCTGGACACTTTGCGAGGGCTTTTGCTGGCTGCTGCTGCTG
CCCGTCATGCTACTCATCGTAGCCCGCCCGGTGAAGCTCGCTGCTTTCCCTACCTCCTTAAGTGACTGCCAAACG
CCCACCGGCTGGAATTGCTCTGTTATGATGACAGAGAAAATGATCTCTTCTCTGTGACACCAACACCTGTAAA
TTTGATGGGGAATGTTTAAGAATTGGAGACACTGTGACTTGGCTCTGTTCAGTTCAAGTGCAACAATGACTATGTG
CCTGTGTGTGGCTCCAATGGGGAGAGCTACCAGAATGAGTGTTACCTGCGACAGGCTGCATGCAAACAGCAGAGT
GAGATACTTGTGGTGTGAGAAGGATCATGTGCCACAGATGCAGGATCAGGATCTGGAGATGGAGTCCATGAAGGC
TCTGGAGAACTAGTCAAAAGGAGACATCCACCTGTGATATTTGCCAGTTTGGTGCAGAATGTGACGAAGATGCC
GAGGATGCTGGTGTGTGTGTAATATTGACTGTTCTCAAACCAACTTCAATCCCCTCTGCGCTTCTGATGGGAAA
TCTTATGATAATGCATGCCAAATCAAAGAAGCATCGTGTGAGAAACAGGAGAAAATTGAAGTCATGTCTTTGGGT
CGATGTCAAGATAACACAACACTACAACTACTAAGTCTGAAGATGGGCATTATGCAAGAACAGATTATGCAGAGAAT
GCTAACAAATTAGAAGAAAGTGCCAGAGAACACCACATACCTTGTCCGGAACATTACAATGGCTTCTGCATGCAT
GGGAAGTGTGAGCATTCATCAATATGCAGGAGCCATCTTGCAAGGTGTGATGCTGGTTATACTGGACAACACTGT
GAAAAAAGGACTACAGTGTCTATACGTTGTTCCCGGTCCTGTACGATTTCAGTATGTCTTAATCGCAGCTGTG
ATTGGAACAATTGAGATTGCTGTGATCTGTGTGGTGGTCCTCTGCATCACAAGGAAATGCCCCAGAAGCAACAGA
ATTCACAGACAGAAGCAAATACAGGGCACTACAGTTCAGACAATACAACAAGAGCGTCCACGAGGTTAATCTAA
AGGGAGCATGTTTACAGTGGCTGGACTACCGAGAGCTTGGACTACACAATACAGTATTATAGACAAAAGAATAA
GACAAGAGATCTACACATGTTGCCTTGCATTTGTGGTAATCTACACCAATGAAAACATGTACTACAGCTATATTT
GATTATGTATGGATATATTTGAAATAGTATACATTGTCTTGATGTTTTTCTGTAATGTAAATAAACTATTTATA
TCACACAATATAGTTTTTCTTTCCCATGTATTTGTTATATATAATAAATACTCAGTGATGAG

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FIGURE 406

MVLWESPRQCSSWTLCGEFCWLLLLPVMLLIVARPVKLAAPPTSLSDCQTPTGWNC SGY
DDRENDLFLCDTNTCKFDGECLRIGDTVTVCVCQFKCNNDYVPVCGSNGESYQNECYLRQ
AACKQQSEILVVSEGSCATDAGSGSGDGVHEGSGETSQKETSTCDICQFGAECDEDAED
VWCVCNIDCSQTNFNPLCASDGKSYDNACQIKEASCQKQEKIEVMSLGRCQDNTTTTTK
SEDGHYARTDYAENANKLEESAREHHIPCPEHYNGFCMHGKCEHSINMQEPSCRC DAGY
TGQHCEKKDYSVLYVVP GPVRFQYVLIAAVIGTIQIAVICVVVLCITRKCPRSNRIHRQ
KQNTGHYSSDNTTRASTRLI

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FIGURE 407

CTCGCAGCCGAGCGCGGCCGGGGAAGGGCTCTCCTTCCAGCGCCGAGCACTGGGCCCTGGCAG
ACGCCCCAAGATTGTTGTGAGGAGTCTAGCCAGTTGGTGAGCGCTGTAATCTGAACCAGCTGT
GTCCAGACTGAGGCCCATTTGCATTGTTTAACATACTTAGAAAATGAAGTGTTCATTTTTAA
CATTCTCTCCAATTGGTTTAATGCTGAATTACTGAAGAGGGCTAAGCAAACACAGGTGCTT
GCGCTGAGGGCTCTGCAGTGGCTGGGAGGACCCCGGCGCTCTCCCCGTGTCTCTCCACGACT
CGCTCGGCCCTCTGGAATAAAACACCCGCGAGCCCCGAGGGCCCAGAGGAGGCCGACGTGCC
CGAGCTCTCCGGGGTCCCGCCGCGAGCTTTCTTCTCGCCTTCGCATCTCCTCCTCGCGCG
TCTTGAGACATGCCAGGAATAAAAAGGATACTACTGTTACCATTCTGGCTCTCTGTCTTCCAA
GCCCTGGGAATGCACAGGCACAGTGCACGAATGGCTTTGACCTGGATCGCCAGTCAGGACAGT
GTTTAGATATTGATGAATGCCGAACCATCCCCGAGGCCTGCCGAGGAGACATGATGTGTGTTA
ACCAAATGGCGGGTATTTATGCATTCCCCGACAAACCCTGTGTATCGAGGGCCCTACTCGA
ACCCCTACTCGACCCCTACTCAGGTCCGTACCCAGCAGCTGCCCCACCACTCTCAGCTCCAA
ACTATCCCACGATCTCCAGGCCTCTTATATGCCGCTTTGGATACCAGATGGATGAAAGCAACC
AATGTGTGGATGTGGACGAGTGTGCAACAGATTCCCACCAGTGCAACCCCCACCCAGATCTGCA
TCAATACTGAAGGCGGGTACACCTGCTCCTGCACCGACGGATATTGGCTTCTGGAAGGCCAGT
GCTTAGACATTGATGAATGTGCTATGGTTACTGCCAGCAGCTCTGTGCGAATGTTTCTGGAT
CCTATTCTTGTACATGCAACCCTGGTTTTACCCTCAATGAGGATGGAAGGTCTTGCCAAGATG
TGAACGAGTGTGCCACCGAGAACCCTGCGTGCAACCTGCGTCAACACCTACGGCTCTCTCA
TCTGCCGCTGTGACCCAGGATATGAACCTGAGGAAGATGGCGTTCATTGCAGTGATATGGACG
AGTGCAGCTTCTCTGAGTTCCTCTGCCAACATGAGTGTGTGAACCAGCCCCGGCACATACTTCT
GCTCCTGCCCTCCAGGCTACATCCTGCTGGATGACAACCGAAGCTGCCAAGACATCAACGAAT
GTGAGCACAGGAACCACACGTGCAACCTGCAGCAGACGTGCTACAATTTACAAGGGGGCTTCA
AATGCATCGACCCCATCCGCTGTGAGGAGCCTTATCTGAGGATCAGTGATAACCGCTGTATGT
GTCCTGCTGAGAACCCTGGCTGCAGAGACCAGCCCTTTACCATCTTGTACCGGGACATGGACG
TGGTGTGAGGACGCTCCGTTCCCGCTGACATCTTCAAATGCAAGCCACGACCCGCTACCCCTG
GGGCCTATTACATTTTCCAGATCAAATCTGGGAATGAGGGCAGAGAATTTTACATGCGGCAAA
CGGGCCCCATCAGTGCCACCCTGGTGATGACACGCCCCATCAAAGGGCCCCGGGAAATCCAGC
TGGACTTGGAATGATCACTGTCAACACTGTCATCAACTTCAGAGGCAGCTCCGTGATCCGAC
TGCGGATATATGTGTGCGCAGTACCCATTCTGAGCCTCGGGCTGGAGCCTCCGACGCTGCCTCT
CATTGGCACCAAGGGACAGGAGAAGAGAGGAAATAACAGAGAGAATGAGAGCGACACAGACGT
TAGGCATTTCTGCTGAACGTTTCCCGAAGAGTCAGCCCCGACTTCCTGACTCTCACCTGTA
CTATTGCAGACCTGTCACCCTGCAGGACTTGCCACCCCAAGTTCCTATGACACAGTTATCAA
AAGTATTATCATTGCTCCCTGATAGAAGATTGTTGGTGAATTTTCAAGGCCTTCAGTTTATT
TCCACTATTTTCAAAGAAAATAGATTAGGTTTGCGGGGGTCTGAGTCTATGTTCAAAGACTGT
GAACAGCTTGCTGTCACTTCTTACCTCTTCCACTCCTTCTCTCACTGTGTTACTGCTTTGCA
AAGACCCGGGAGCTGGCGGGGAACCCTGGGAGTAGCTAGTTTGCTTTTTCGCTACACAGAGAA
GGCTATGTAAACAAACCACAGCAGGATCGAAGGGTTTTAGAGAATGTGTTTCAAACCATGC
CTGGTATTTTCAACCATAAAAGAAGTTTTCAGTTGTCCTTAAATTTGTATAACGGTTTAAATTCT
GTCTTGTTCAATTTGAGTATTTTAAAAAATATGTCGTAGAATTCCTTCGAAAGGCCTTCAGA
CACATGCTATGTTCTGTCTTCCCAAACCCAGTCTCCTCTCCATTTTAGCCAGTGTTTCTTT
GAGGACCCCTTAATCTTGCTTCTTTAGAATTTTACCCTTGGATTGGAATGCAGAGGTCT
CCAAACTGATTAAATATTTGAAGAGA

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FIGURE 408

MPGIKRILTVTILALCLPSPGNAQAQCTNGFDLDRQSGQCLDIDECRTIPEACRGDMMCVNQNGG
GYLCIPRTNPVYRGPYSNPYSTPYSGPYPAAAPPLSAPNYPTISRPLICRFGYQMDESNQCV
DVDECATDSHQCNPTQICINTEGGYTCSTDGWLLLEGQCLDIDECRYGYCQQLCANVPGSYS
CTCNPGFTLNEDGRSCQDVNECATENPCVQTCVNTYGSLICRCDPGYELEEDGVHCSDMDECS
FSEFLCQHECVNQPGTYFCSCPPGYILLDDNRSCQDINECEHRNHTCNLQQTTCYNLQGGFKCI
DPIRCEEPYLRISDNRCMCPAENPGCRDQPFITILYRDMDVVSGRSVPADIFQMQATTRYPGAY
YIFQIKSGNEGREFYMRQTGPISATLVMTRPIKGPREIQLDLEMITVNTVINFRGSSVIRLRI
YVSQYPF

Important features of the protein:**Signal peptide:**

amino acids 1-25

N-glycosylation sites.

amino acids 283-287, 296-300

N-myristoylation sites.amino acids 21-27, 64-70, 149-155, 186-192, 226-232, 242-248,
267-273, 310-316**Aspartic acid and asparagine hydroxylation sites.**

amino acids 144-156, 181-193, 262-274

Cell attachment sequence.

amino acids 54-57

Calcium-binding EGF-like.

amino acids 131-166, 172-205, 211-245, 251-286

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FIGURE 409

CCCACGCGTCCGCGGACGCGTGGGTGCGACTAGTTCTAGATCGCGAGCGGCCGCCGCGGCTCA
GGGAGGAGCACCGACTGCGCCGCACCCTGAGAGATGGTTGGTGCCATGTGGAAGGTGATTGTT
TCGCTGGTCCTGTTGATGCCTGGCCCTGTGATGGGCTGTTTCGCTCCCTATACAGAAGTGTT
TCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTTCTCACCCCTTACATTGAAGCTGGG
AAGATCCAAAAAGGAAGAGAATTGAGTTTGGTCGGCCCTTTCCAGGACTGAACATGAAGAGT
TATGCCGGCTTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTTCTGGTTCTTCCCA
GCTCAGATACAGCCAGAAGATGCCCCAGTAGTTCTCTGGCTACAGGGTGGGCCGGGAGGTTCA
TCCATGTTTGGACTCTTTGTGGAACATGGGCCTTATGTTGTCACAAGTAACATGACCTTGCGT
GACAGAGACTTCCCCTGGACCACAACGCTCTCCATTGCTTTACATTGACAATCCAGTGGGCACA
GGCTTCAGTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGTAGCACGGGAT
TTATACAGTGCATAATTGAGTTTTCAGATATTTCTGAATATAAAAAATAATGACTTTTAT
GTCAGTGGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTCATCCATTCCCTC
AACCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGATGGATATTCTGAT
CCCGAATCAATTATAGGGGGCTATGCAGAATTCCTGTACCAAATTGGCTTGTTGGATGAGAAG
CAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATCAGGAAGCAGAACTGG
TTTGAGGCCTTTGAAATACTGGATAAACTACTAGATGGCGACTTAACAAGTGATCCTTCTTAC
TTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTTGCGGTGCACGGAACCTGAGGAT
CAGCTTTACTATGTGAAATTTTTGTCACTCCCAGAGGTGAGACAAGCCATCCACGTGGGGAAT
CAGACTTTTAATGATGGAACATAGTTGAAAAGTACTTGCGAGAAGATACAGTACAGTCAGTT
AAGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGATCTACAATGGCCAACTGGAC
ATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTTGATGGGCATGGACTGGAAAGGATCCCGAG
GAATACAAGAAGGCAGAAAAAAAGTTTGGAAGATCTTTAAATCTGACAGTGAAGTGGCTGGT
TACATCCGGCAAGCGGGTGACTTCCATCAGGTAATTATTCGAGGTGGAGGACATATTTTACCC
TATGACCAGCCTCTGAGAGCTTTTGACATGATTAATCGATTCAATTTATGGAAAAGGATGGGAT
CCTTATGTTGGATAAACTACCTTCCCAAAAGAGAACATCAGAGGTTTTTCATTGCTGAAAAGAA
AATCGTAAAAACAGAAAATGTCATAGGAATAAAAAAATTATCTTTTCATATCTGCAAGATTTT
TTTCATCAATAAAAAATTATCCTTGAAACAAGTGAGCTTTTGTTTTGGGGGGAGATGTTTACT
ACAAAATTAACATGAGTACATGAGTAAGAATTACATTATTTAACTTAAAGGATGAAAGGTATG
GATGATGTGACACTGAGACAAGATGTATAAATGAAATTTTAGGGTCTTGAATAGGAAGTTTAA
ATTTCTTCTAAGAGTAAGTGAAAAGTGCAGTTGTAACAACAAAGCTGTAACATCTTTTCTG
CCAATAACAGAAGTTTGGCATGCCGTGAAGGTGTTTGGAATATTATTGGATAAGAATAGCTC
AATTATCCCAAATAAATGGATGAAGCTATAATAGTTTGGGGAAAAGATTCTCAAATGTATAA
AGTCTTAGAACAAAAGAATTCTTTGAAATAAAAAATATTATATATAAAAGTAAAAA

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FIGURE 410

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGDGSGQPLFLTPYIEAGKIQKGRELSLV
GPFPGLNMKSYAGFLTIVNKTYSNLEFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEHGP
YVVTSNMTLRDRDFPWTTLTSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQFFQI
FPEYKNNDIFYVTGESYAGKYVPATAHLIHSNPNVREVKINLNGIAIGDGYSDPESIIGGYAEF
LYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGDLTSDPSYFQNVGTGCSNYY
NFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNOTFNDGTIVEKYLREDTVQSVKPWLTEIMNNY
KVLIYNGQLDIIVAAALTERSLMGMDWKGSQEYKKAEEKVWKIFKSDSEVAGYIRQAGDFHQV
IIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428**Tyrosine kinase phosphorylation site.**

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

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FIGURE 411

GCAAGCCAAGGCGCTGTTTGAGAAGGTGAAGAAGTTCCGGACCCATGTGGAGGAGGGGGACATTGTGTACCGCCT
CTACATGCGGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGTCTACTACGTGCACAA
CATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCACCC
CCTGGCCACACTCTTCAAGATCCTGGCGTCCTTCTACATCAGCCTAGTCATCTTCTACGGCCTCATCTGCATGTA
CACACTGTGGTGGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTTGAGTCGATCCGTGAGGAGAGCAGCTACAG
CGACATCCCCGACGTCAAGAACGACTTCGCCTTCATGCTGCACCTCATTGACCAATACGACCCGCTCTACTCCAA
GCGCTTCGCCGTCTTCTGTGCGGAGGTGAGTGAGAACAAGCTGCGGCAGCTGAACCTCAACAACGAGTGGACGCT
GGACAAGCTCCGGCAGCGCTCACCAAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTTTCATGCTCAGTGGCAT
CCCTGACACTGTGTTTGACCTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCCCGCC
CAGCATTGCCAGCTCACGGGCTCAAGGAGCTGTGGCTTACCACACAGCGGCCAAGATTGAAGCGCCTGCGCT
GGCCTTCTGCGCGAGAACCTGCGGGCGCTGCACATCAAGTTCACCGACATCAAGGAGATCCCGCTGTGGATCTA
TAGCCTGAAGACACTGGAGGAGCTGCACCTGACGGGCAACCTGAGCGCGGAGAACAACCGCTACATCGTCATCGA
CGGGCTGCGGGAGCTCAAACGCTCAAGGTGCTGCGGCTCAAGAGCAACCTAAGCAAGCTGCCACAGGTGGTCAC
AGATGTGGGCGTGCACCTGCAGAAGCTGTCCATCAACAATGAGGGCAGCAAGCTCATCGTCTCAACAGCCTCAA
GAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCACTCCATCTTCAGCCT
CCACAACCTGCAGGAGATTGACCTCAAGGACAACAACCTCAAGACCATCGAGGAGATCATCAGCTTCAGCACCT
GCACCGCCTCACCTGCCTTAAGCTGTGGTACAACCACATCGCCTACATCCCCATCCAGATCGGCAACCTCACCAA
CCTGGAGCGCTCTACCTGAACCGCAACAAGATCGAGAAGATCCCCACCCAGCTCTTCTACTGCCGAAGCTGCG
CTACCTGGACCTCAGCCACAACAACCTGACCTTCTCCTGCCGACATCGGCCTCCTGCAGAACCTCCAGAACCT
AGCCATCACGGCCAACCGGATCGAGACGCTCCCTCCGGAGCTCTTCCAGTGCCGGAAGCTGCGGGCCCTGCACCT
GGGCAACAACGTGCTGCAGTCACTGCCCTCCAGGGTGGGCGAGCTGACCAACCTGACGAGATCGAGCTGCGGGG
CAACCGGCTGGAGTGCTGCCCTGTGGAGCTGGGCGAGTGCCCACTGCTCAAGCGCAGCGGCTTGGTGGTGGAGGA
GGCGGCCCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCTCAGGCCCGGAGGGGAGGCTAGCTTCTCCCAG
AACTCCCGGACAGCCAGGACAGCCTCGCGGCTGGGCGAGGCTGGGCGCGCTTGTGAGTCAGGCCAGAGCGAGA
GGACAGTATCTGTGGGGCTGGCCCCCTTTCTCCTCTGAGACTCACGTCCCCAGGGCAAGTGCTTGTGGAGGAG
AGCAAGTCTCAAGAGCGCAGTATTTGGATAATCAGGGTCTCCTCCTGGAGGCCAGCTCTGCCCCAGGGGCTGAG
CTGCCACCAGAGGTCTGGGACCTCACTTTAGTTCTTGGTATTTATTTTCTCCATCTCCCACCTCCTTCATCC
AGATACTTATACATTTCCCAAGAAAGTTTCAGCCCAGATGGAAGGTGTTTCAGGGAAAGGTGGGCTGCCCTTTTCCCC
TTGTCTTATTTAGCGATGCCGCCGGGCATTTAACACCCACCTGGACTTCAGCAGAGTGGTCCGGGGCGAACCCAG
CCATGGGACGGTCACCCAGCAGTGCCGGCTGGGCTCTGCGGTGCGGTCCACGGGAGAGCAGGCCCTCCAGCTGGA
AAGGCCAGGCTGGAGCTTGCCCTCTCAGTTTTTGTGGCAGTTTTAGTTTTTGTTTTTTTTTTTTTTAAATCAA
AAACAATTTTTTTTTTAAAAAAGCTTTGAAATGGATGGTTTGGGTATTAAGGAAAAAAGCTTAAAAA
AAAAGACACTAACGGCCAGTGAGTTGGAGTCTCAGGGCAGGGTGGCAGTTTCCCTTGAGCAAAGCAGCCAGAGT
TGAAGTGTGTTTCCCTTTCCCTGGGCGCAGGGTGAGGGTGTCTTCCGATCTGGTGTGACCTTGGTCCAGGAGTT
CTATTTGTTTCTGGGGAGGGAGGTTTTTTGTTTGTGTTTTTGGGTTTTTTTGGTGTCTTGTGTTTTCTTCTCCTCC
ATGTGTCTTGGCAGGCACTCATTTCTGTGGCTGTGCGCCAGAGGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAG
ACTCGGGTTGGCTAATCCCCGGATGAACGGTGCTCCATTGCGACCTCCCCCTCCTCGTGCCTGCCCTGCCTCTCCA
CGCACAGTGTTAAGGAGCCAAGAGGAGCCACTTCGCCAGACTTTGTTTCCCCACCTCCTGCGGCATGGGTGTGT
CCAGTGCCACCGCTGGCCTCCGCTGCTTCCATCAGCCCTGTGCGCACCTGGTCTTTCATGAAGAGCAGACACTTA
GAGGCTGGTCGGGAATGGGGAGGTGCGCCCTGGGAGGGCAGGCGTTGGTTCCAAGCCGGTCCCGTCCCTGGCGC
CTGGAGTGCCACACAGCCAGTCGGCACCTGGTGGCTGGAAGCCAACCTGCTTTAGATCACTCGGGTCCCCACCTT
AGAAGGGTCCCCGCTTAGATCAATCAGTGGACACTAAGGCACGTTTTAGAGTCTTGTCTTAATGATTATGT
CCATCCGTCTGTCCGTCCATTTGTGTTTTCTGCGTGTGTCATTGGATATAATCCTCAGAAATAATGCACACTAG
CCTCTGACAACCATGAAGCAAAAATCCGTTACATGTGGGTCTGAAGTCTGAGACTCGGTACAGTATCAAATAAA
ATCTATAACAGAAAAA

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FIGURE 412

MRQTIKVIKFILIIICYTVYYVHNIKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYIS
LVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSKRF
AVFLSEVSENKLRQLNLNNEWTLDKLRQRLTKNAQDKLELHLFMLSGIPDTVFDLVELEVLKL
ELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLENLRLALHIKFTDIKEIPLWIYSLK
TLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSINNEG
KLIVNSLKKMANLTELELIRCDLERIPHSIFSLHNLQEIDLKDNNLKTIEEIIISFOHLHRLT
CLKLWYNHIAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLTFLPADIG
LLQNLQNLAITANRIETLPPELFQCRKLRLHLGNNVLQSLPSRVGELTNLTQIELRGNRLEC
LPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497**N-myristoylation site.**

amino acids 173-179, 261-267, 395-401, 441-447

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FIGURE 413

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGCAAGCCGTGGGGGTTTTGAGCTCATC
TTCATCATTTCATATGAGGAAATAAGTGGTAAATCCTTGGAAATACA**ATG**GAGACTCATCAGAA
ACATTTACATATTTTGTAGTATTGTTATGACAGCAGAGGGTGATGCTCCAGAGCTGCCAGAAG
AAAGGGAACCTGATGACCAACTGCTCCAACATGTCTCTAAGAAAGGTTCCCGCAGACTTGACCC
CAGCCACAACGACACTGGATTTATCCTATAACCTCCTTTTCAACTCCAGAGTTCAGATTTTC
ATTCTGTCTCCAACTGAGAGTTTTGATTCTATGCCATAACAGAATTCAACAGCTGGATCTCA
AAACCTTTGAATTCAACAAGGAGTTAAGATATTTAGATTTGTCTAATAACAGACTGAAGAGTG
TAACTTGGTATTTACTGGCAGGTCTCAGGTATTTAGATCTTTCTTTAATGACTTTGACACCA
TGCCTATCTGTGAGGAAGCTGGCAACATGTCACACCTGGAAATCCTAGGTTTGAGTGGGGCAA
AAATACAAAATCAGATTTCCAGAAAATTGCTCATCTGCATCTAAATACTGTCTTCTTAGGAT
TCAGAACTCTTCTCATTATGAAGAAGGTAGCTGCTGCCATCTTAAACACAACAAAACCTGCACA
TTGTTTTACCAATGGACACAAATTTCTGGGTCTTTTTGCGTGATGGAATCAAGACTTCAAAAA
TATTAGAAATGACAAATATAGATGGCAAAGCCAATTTGTAAGTTATGAAATGCAACGAAATC
TTAGTTTAGAAAATGCTAAGACATCGGTTCTATTGCTTAATAAAGTTGATTTACTCTGGGACG
ACCTTTTCTTATCTTACAATTTGTTTGGCATAACATCAGTGGAAACACTTTTCAGATCCGAAATG
TGACTTTTGGTGGTAAGGCTTATCTTGACCACAAATTCATTTGACTACTCAAATACTGTAATGA
GAACATAAAAATTTGGAGCATGTACATTTTCAGAGTGTTTTACATTCAACAGGATAAAATCTATT
TGCTTTTGACCAAAATGGACATAGAAAACCTGACAATATCAAATGCACAAATGCCACACATGC
TTTTCCCGAATTATCCTACGAAATTCCAATATTTAAATTTTGCCAATAATATCTTAACAGACG
AGTTGTTTAAAGAATATCCAACCTGCCTCACTTGAAAACCTCTCATTTTGAATGGCAATAAAC
TGGAGACACTTTCTTTAGTAAGTTGCTTTGCTAACAAACACACCCCTTGGAACTTGGATCTGA
GTCAAATCTATTACAACATAAAAATGATGAAAATTGCTCATGGCCAGAACTGTGGTCAATA
TGAATCTGTCATACAATAAATTGTCTGATTCTGTCTTCAGGTGCTTGCCCCAAAGTATTCAA
TACTTGACCTAAATAATAACCAATCCAACTGTACCTAAAGAGACTATTCATCTGATGGCCT
TACGAGAATAAATATTGCATTTAATTTTCTAACTGATCTCCCTGGATGCAGTCAATTCAGTA
GACTTTTCAGTTCTGAACATTGAAATGAACCTTCACTCTCAGCCATCTCTGGATTTTGTTCAGA
GCTGCCAGGAAGTTAAAACCTCTAAATGCGGGAAGAAATCCATTCCGGTGTACCTGTGAATTAA
AAAATTTTCATTTCAGCTTGAACATATTCAGAGGTTCATGATGGTTGGATGGTCAGATTCATACA
CCTGTGAATACCCTTTAAACCTAAGGGGAAGTGGTTAAAGACGTTTCATCTCCACGAATTAT
CTTGCAACACAGCTCTGTTGATTGTCAACATTTGTGGTTATTATGCTAGTTCTGGGGTTGGCTG
TGGCCTTCTGCTGTCTCCACTTTGATCTGCCCTGGTATCTCAGGATGCTAGGTCAATGCACAC
AAACATGGCACAGGGTTAGGAAAACAACCCAAGAACAACCTCAAGAGAAATGTCCGATTCCACG
CATTTATTTTCATACAGTGAACATGATTCTCTGTGGGTGAAGAATGAATTGATCCCCAATCTAG
AGAAGGAAGATGGTTCTATCTTGATTTGCCCTTTATGAAAGCTACTTTGACCCTGGCAAAAGCA
TTAGTGAAAATATTGTAAGCTTCATTGAGAAAAGCTATAAGTCCATCTTTGTTTGTCTCCCA
ACTTTGTCCAGAATGAGTGGTGCCATTATGAATTTCTACTTTGCCCACCACAATCTCTTCCATG
AAAATTTCTGATCATATAATTCTTATCTTACTGGAACCCATTCCATTCTATTGCATTCCCACCA
GGTATCATAACTGAAAGCTCTCCTGGAAAAAAGCATACTTGGAAATGGCCCAAGGATAGGC
GTAAATGTGGGCTTTTCTGGGCAACCTTCGAGCTGCTATTAATGTTAATGTATTAGCCACCA
GAGAAATGTATGAACCTGCAGACATTACAGAGTTAAATGAAGAGTCTCGAGGTTCTACAATCT
CTCTGATGAGAACAGATTGTCTA**TAA**AATCCCACAGTCCCTTGGGAAGTTGGGGACCACATACA
CTGTTGGGATGTACATTGATACAACTTTATGATGGCAATTTGACAATATTTATTAAATAAA
AAATGGTTATTCCCTTCATATCAGTTTCTAGAAGGATTTCTAAGAATGTATCCTATAGAAACA
CCTTCACAAGTTTATAAGGGCTTATGGAAAAGGTGTTTCATCCAGGATTGTTTATAATCATG
AAAAATGTGGCCAGGTGCAGTGGCTCACTCTTGTAATCCCAGCACTATGGGAGGCCAAGGTGG
GTGACCCACGAGGTCAAGAGATGGAGACCATCCTGGCCAACATGGTGAAACCCCTGTCTCTACT
AAAAATACAAAATTAGCTGGGCGTGATGGTGCACGCCTGTAGTCCCAGCTACTTGGGAGGCT
GAGGCAGGAGAATCGCTTGAACCCGGGAGGTGGCAGTTGCAGTGAGCTGAGATCGAGCCACTG
CACTCCAGCCTGGTGACAGAGCGAGACTCCATCTCAAAAAAAGAAAAAAGAAAAA
ATGGAAAACATCCTCATGGCCACAAAATAAGGTCTAATTCAATAAATTATAGTACATTAATGT
AATATAATATTACATGCCACTAAAAAGAATAAGGTAGCTGTATATTTCCCTGGTATGGAAAAA
CATATTAATATGTTATAAACTATTAGGTTGGTGCAAACTAATTGTGGTTTTTGGCATTGAAA
TGGCATTGAAATAAAAGTGTAAGAAATCTATACCAGATGTAGTAACAGTGGTTTTGGTCTGG
GAGGTTGATTACAGGGAGCATTGATTCTATGTTGTGTATTCTATAATGTTTGAATTGTT
TAGAATGAATCTGTATTTCTTTTATAAGTAGAAAAAATAAAGATAGTTTTTACAGCCT

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FIGURE 414

MRLIRNIYIFCSIIVMTAEGDAPELPEEREELMTNCSNMSLRKVPADLTPATTTLDLSYNLLFQL
QSSDFHSVSKLRVLIILCHNRIQQDLKTFFFNKELRYLDLSNNRLKSVTWYLLAGLRYLDLSF
NDFDTMPICEEAGNMSHLEILGLSGAKIQKSDFQKIAHLHLNTVFLGFRTLPHYEEGSLPILN
TTKLHIVLPMDTNFVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLLLNKV
DLLWDDLFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFRVFYIQ
QDKIYLLLTKMDIENLTISNAQMPHMLFPNYPTKFQYLNFANNILTDELFKRTIQLPHLKTLLI
LNGNKLETLSLVSCFANNTPLEHLDLSQNLQHKNDENC SWPETVVNMNLSYNKLSDSVFRCL
PKSIQILDNLNNQIQTVPKETIHLMALRELNIAFNFLTDLPGCSHF SRLSVLNIEMNFILSPS
LDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLETYSEVMMVGWSDSYTCEYPLNLRGTRLKDV
HLHELSCNTALLIVTIVVIMLVGLAVAFCCCLHFDLPWYLRMLGQCTQTWHRVRKTTQEQLKR
NVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENIVSFIEKSYKSI
FVLSPNFVQNEWCHYEFYFAHHNLFHENS DHIILILLEPIPFYCIPTRYHKLKALLEKKAYLE
WPKDRRKCGLFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLMRTDCL

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FIGURE 415

CGGACGCGTGGGCGGACGCGTGGGCCTGGGCAAGGGCCGGGGCGCCGGGCGGAGCCACCTCTTCCCCTCCCCCGC
TTCCCTGTCGCGCTCCGCTGGCTGGACGCGCTGGAGGAGTGGAGCAGCACCCGGCCGGCCCTGGGGGCTGACAGT
CGGCAAAGTTTGGCCCCGAAGAGGAAGTGGTCTCAAACCCCGGCAGGTGGCGACCAGGGCCAGACCAGGGGCGCTCG
CTGCCTGCGGGCGGGCTGTAGGCGAGGGCGCGCCCCAGTGCCGAGACCCGGGGCTTCAGGAGCCGGCCCCGGGAG
AGAAGAGTGGGGCGGCGGACGGAGAAAACAACTCCAAGTTGGCGAAAGGCACCGCCCCCTACTCCCAGGGCTGCCG
CCGCCCTCCCGCCCCCAGCCCTGGCATCCAGAGTACGGGTTCGAGCCCGGGCCATGGAGCCCCCTGGGGAGGCGG
CACCAGGGAGCCTGGGCGCCCGGGGCTCCGCCGCGACCCCATCGGGTAGACCACAGAAGCTCCGGGACCCCTTCCG
GCACCTCTGGACAGCCAGGATGCTGTTGGCCACCCTCCTCCTCCTCCTTGGAGGCGCTCTGGCCCATCCAG
ACCGGATTATTTTCCAAATCATGCTTGTGAGGACCCCCCAGCAGTGCTCTTAGAAGTGCAGGGCACCTTACAGA
GGCCCCCTGGTCCGGGACAGCCGCACCTCCCCTGCCAACTGCACCTGGCTCATCCTGGGCAGCAAGGAACAGACTG
TCACCATCAGGTTCCAGAAGCTACACCTGGCCTGTGGCTCAGAGCGCTTAACCCCTACGCTCCCCTCTCCAGCCAC
TGATCTCCCTGTGTGAGGCACCTCCCAGCCCTCTGCAGCTGCCCGGGGGCAACGTCACCATCACTTACAGCTATG
CTGGGGCCAGAGCACCCCATGGGCCAGGGCTTCTGCTCTCTACAGCCAAGATTGGCTGATGTGCCTGCAGGAAG
AGTTTCAGTGCCTGAACCACCGCTGTGTATCTGCTGTCCAGCGCTGTGATGGGGTTGATGCCGTGGCGATGGCT
CTGATGAAGCAGGTTGCAGCTCAGACCCCTTCCCTGGCCTGACCCCAAGACCCGTCCCCTCCCTGCCTTGCAATG
TCACCTTGGAGGACTTCTATGGGGTCTTCTCCTCTCCTGGATATACACACCTAGCCTCAGTCTCCACCCCCAGT
CCTGCCATTGGCTGCTGGACCCCCATGATGGCCGGCGGCTGGCCGTGCGCTTCACAGCCCTGGACTTGGGCTTTG
GAGATGCAGTGCATGTGTATGACGGCCCTGGGCCCTCTGAGAGCTCCCGACTACTGCGTAGTCTCACCCACTTCA
GCAATGGCAAGGCTGTCACTGTGGAGACACTGTCTGGCCAGGCTGTTGTGTCTACCACACAGTTGCTTGGAGCA
ATGGTCGTGGCTTCAATGCCACCTACCATGTGCGGGGCTATTGCTTGCTTGGGACAGACCCTGTGGCTTAGGCT
CTGGCCTGGGAGCTGGCGAAGGCCTAGGTGAGCGCTGTACAGTGAGGCACAGCGCTGTGACGGCTCATGGGACT
GTGCTGACGGCACAGATGAGGAGGACTGCCCAGGCTGCCACCTGGACACTTCCCCTGTGGGGCTGCTGGCACCT
CTGGTGCCACAGCCTGCTACCTGCCTGCTGACCGCTGCAACTACCAGACTTTCTGTGCTGATGGAGCAGATGAGA
GACGCTGTGCGCATTTGCCAGCCTGGCAATTTCCGATGCCGGGACGAGAAGTGCGTGTATGAGACGTGGGTGTGCG
ATGGGCAGCCAGACTGTGCGGACGGCAGTGATGAGTGGGACTGCTCCTATGTTCTGCCCCGCAAGGTCATTACAG
CTGCAGTCATTGGCAGCCTAGTGTGCGGCCTGCTCCTGGTCATCGCCCTGGGCTGCACCTGCAAGCTCTATGCCA
TTTCGACCCAGGAGTACAGCATCTTTGCCCCCTCTCCCGATGGAGGCTGAGATTGTGCAGCAGCAGGCACCCC
CTTCTACGGGCAGCTCATTTGCCAGGGTGCCATCCCACCTGTAGAAGACTTTCTACAGAGAATCCTAATGATA
ACTCAGTGCTGGGCAACCTGCGTTCTCTGCTACAGATCTTACGCCAGGATATGACTCCAGGAGGTGGCCAGGTG
CCCGCCGTGCTCAGCGGGGCGGCTTGATGCGACGCGCTGGTACGCCGTCTCCGCCGCTGGGGCTTGCTCCCTCGAA
CCAAACCCCCGGCTCGGGCCTCTGAGGCCAGATCCCAGGTACACCTTCTGCTGCTCCCCTTGAGGCCCTAGATG
GTGGCACAGGTCCAGCCCGTGAGGGCGGGGCGAGTGGGTGGGCAAGATGGGGAGCAGGCACCCCACTGCCCATCA
AGGCTCCCCTCCCATCTGCTAGCACGTCTCCAGCCCCACTACTGTCCCTGAAGCCCCAGGGCCACTGCCCTCAC
TGCCCCCTAGAGCCATCACTATTGTCTGGAGTGGTGCAGGCCCTGCGAGGCCGCTGTTGCCAGCCTGGGGCCCC
CAGGACCAACCCGGAGCCCCCTGGACCCACACAGCAGTCTGGCCCTGGAAGATGAGGACGATGTGCTACTGG
TGCCACTGGCTGAGCCGGGGGTGTGGTAGCTGAGGCAGAGGATGAGCCACTGCTTACCTGAGGGGACCTGGGGG
CTCTACTGAGGCCCTTCCCCTGGGGGCTCTACTCATAGTGGCACAACCTTTTAGAGGTGGGTGAGCCTCCCCTCC
ACCACTTCCCTCCCTGTCCCTGGATTTCAGGGACTTGGTGGGCCTCCCGTTGACCCTATGTAGCTGCTATAAAGT
TAAGTGTCCCTCAGGCAGGGAGAGGGCTCACAGAGTCTCCTCTGTACGTGGCCATGGCCAGACACCCCACTCCCT
TCACCACCACCTGCTCCCCACGCCACCACATTTGGGTGGCTGTTTTTAAAAAGTAAAGTTCTTAGAGGATCATA
GGTCTGGACACTCCATCCTTGCCAAACCTTACCCAAAAGTGGCCTTAAGCACCGGAATGCCAATTAAC TAGAGA
CCCTCCAGCCCCCAAGGGGAGGATTGGGCGAAGCTGAGGTTTTGCCATCCACAATCCCTCCTACAGGGCCTGG
CTCACAAAAGAGTGCAACAAATGCTTCTATTCCATAGCTACGGCATTGCTCAGTAAGTTGAGGTCAAAAATAAA
GGAATCATACATCTC

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FIGURE 416

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631

<subunit 1 of 1, 713 aa, 1 stop

<MW: 76193, pI: 5.42, NX(S/T): 4

MLLATLLLLLLGGALAHDPDRIIFPNHACEDPPAVLLEVQGTLQRPLVRDSRTSPANCTWLILG
SKEQTVTIRFQKLHLACGSERLTLRSPLQPLISLCEAPPSPLQLPGGNVTITYSYAGARAPMG
QGFLLSYSQDWLMCLQEEFQCLNHRCSVSAVQRCDGVDACGDGSDEAGCSSDPFPGLTPRPVPS
LPCNVTLEDFYGVFSSPGYTHLASVSHPQSCHWLLDPHDGRRRLAVRFTALDLGFGDAVHVYDG
PGPPESSRLRLSLTHFSNGKAVTVETLSGQAVVSYHTVAWSNGRGFNATYHVRGYCLPWDRPC
GLGSGLGAGEGLGERCYSEAQRCDGSWDCADGTDEEDCPGCPGHPGCGAAGTSGATACYLPA
DRCNYQTFCADGADERRCRHCQPGNFRCRDEKCVYETWVCDGQPD CADGSDEWDCSYVLPRKV
ITAAVIGSLVCGLLLVIALGCTCKLYAIRTQEYSIFAPLSRMEAEIVQQQAPPSYGQLIAQGA
IPPVEDFPTENPNDNSVLGNLRSLLQILRQDMTPGGGPGARRRQGRRLMRRLVRRRLRWGLLP
RTNTPARASEARSQVTPSAAPLEALDGGTGPAREGGAVGGQDGEQAPPLPIKAPLPSASTSPA
PTTVPEAPGPLPSLPLEPSLLSGVVQALRGRLPSLGP PGPTRSPPGPHTAVLALEDEDDVLL
VPLAEPGVWVAEAEDEPLLT

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 442-462

LDL-receptor class A (LDLRA) domain proteins

amino acids 411-431, 152-171, 331-350 and 374-393

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FIGURE 417

GTGTTTCCTTTGCTCTCTCGCGCCAGTCCTCCTCCCTGGTTCTCCTCAGCCGCTGTCGGAGGAGAGCACCCGGA
GACGCGGGCTGCAGTCGCGGGCGGCTTCTCCCGCCTGGGCGGCCTCGCCGCTGGGCAGGTGCTGAGCGCCCTAG
AGCCTCCCTTGCCGCCTCCTCCTCTGCCCCGCCGAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCG
GCCCCGGAGGCGGCGGTGGATGCGGCGCTGGGCAGAAGCAGCCGCGGATTCCAGCTGCCCGCGCGCCCCGGCG
CCCCCTGCGAGTCCCCGTTT CAGCCATGGGGACCTCTCCGAGCAGCAGCACC GCCCTCGCCTCCTGCAGCCGCATC
GCCGCGGAGCCACAGCCACGATGATCGCGGGCTCCCTTCTCCTGCTTGGATTCCCTTAGCACCACCACAGCTCAG
CCAGAACAGAAGGCCCTCGAATCTCATTGGCACATACCGCCATGTTGACCGTGCCACCGGCCAGGTGCTAACCTGT
GACAAGTGTCCAGCAGGAACCTATGTCTCTGAGCATTGTACCAACACAAGCCTGCGCGTCTGCAGCAGTTGCCCT
GTGGGGACCTTTACCAGGCATGAGAATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCCATGGCCAATG
ATTGAGAAATTACCTTGTGCTGCCTTGACTGACCGAGAATGCACTTGCCACCTGGCATGTTCCAGTCTAACGCT
ACCTGTGCCCCCATAACGGTGTGTCTGTGGGTGGGGTGTGCGGAAGAAAGGGACAGAGCTGAGGATGTGCGG
TGTAAGCAGTGTGCTCGGGGTACCTTCTCAGATGTGCTTCTAGTGTGATGAAATGCAAAGCATACACAGACTGT
CTGAGTCAGAACCTGGTGGTATCAAGCCGGGGACCAAGGAGACAGACAACGTCTGTGGCACACTCCCGTCTTTC
TCCAGCTCCACCTCACCTTCCCCTGCCACAGCCATCTTTCACGCCCTGAGCACATGGAAACCCATGAAGTCCCT
TCCTCCACTTATGTTCCCAAAGGCATGAACCTCAACAGAATCCAACTCTTCTGCCTCTGTTAGACCAAAGGTACTG
AGTAGCATCCAGGAAGGGACAGTCCCTGACAACACAAGCTCAGCAAGGGGGAAGGAAGACGTGAACAAGACCCTC
CCAAACCTTCAGGTAGTCAACCACCAGCAAGGCCCCACCACAGACACATCCTGAAGTGTGCTGCCGTCCATGGAG
GCCACTGGGGGCGAGAAGTCCAGCAGCGCCATCAAGGGCCCCAAGAGGGGACATCCTAGACAGAACCTACACAAG
CATTTTGACATCAATGAGCATTTGCCCTGGATGATTGTGCTTTTCTGCTGCTGGTGTGTTGGTGATTGTGGTG
TGCAGTATCCGAAAAGCTCGAGGACTCTGAAAAAGGGGCCCGGCAGGATCCAGTGCCATTGTGGAAGGCA
GGGCTGAAGAAATCCATGACTCCAACCCAGAACCGGGAGAAATGGATCTACTACTGCAATGGCCATGGTATCGAT
ATCCTGAAGCTTGTAGCAGCCCCAAGTGGGAAGCCAGTGGAAAGATATCTATCAGTTTCTTTGCAATGCCAGTGAG
AGGGAGGTTGCTGCTTTCTCCAATGGGTACACAGCCGACCAGAGCGGGCCTACGCAGCTCTGCAGCATGGACC
ATCCGGGGCCCCGAGGCCAGCCTCGCCAGCTAATTAGCGCCCTGCGCCAGCACC GGAGAAACGATGTTGTGGAG
AAGATTCTGTTGGCTGATGGAAGACACCCAGCTGGAAACTGACAACTAGCTCTCCCGATGAGCCCCAGCCCCG
CTTAGCCCCAGCCCCATCCCCAGCCCCAACGCGAAACTTGAGAATTCCGCTCTCCTGACGGTGGAGCCTTCCCCA
CAGGACAAGAACAAGGGCTTCTTCGTGGATGAGTCGGAGCCCTTCTCCGCTGTGACTCTACATCCAGCGGCTCC
TCCGCGCTGAGCAGGAACGGTTCCTTTATTACCAAAGAAAAGAAGGACACAGTGTGCGGCAGGTACGCTGGAC
CCCTGTGACTTGCAGCCTATCTTTGATGACATGCTCCACTTTCTAAATCCTGAGGAGCTGCGGGTGATTGAAGAG
ATCCCCAGGCTGAGGACAACTAGACCGGCTATTGCGAATTATTGGAGTCAAGAGCCAGGAAGCCAGCCAGACC
CTCCTGGACTCTGTTTATAGCCATCTTCTGACCTGCTGTAGAACATAGGGATACTGCATTCTGGAAATTACTCA
ATTTAGTGGCAGGGTGGTTTTTTAATTTTCTTCTGTTTCTGATTTTTGTTGTTTGGGGTGTGTGTGTGTGTGTGT
GT
TCTCTCTCTTTTTTTTTTTTAAATAACTCTTCTGGGAAGTTGGTTTATAAGCCTTTGCCAGGTGTAAGTGTGTGAA
ATACCCACCACTAAAGTTTTTTAAGTTCATATTTTCTCCATTTTGCCTTCTTATGTATTTTCAAGATTATCTG
TGCACTTTAAATTTACTTAACTTACCATAAATGCAGTGTGACTTTTCCACACACTGGATTGTGAGGCTCTTAAC
TTCTTAAAAGTATAATGGCATCTTGTGAATCCTATAAGCAGTCTTTATGTCTCTTAACATTACACCTACTTTTT
AAAAACAAATATTATTACTATTTTTATTATTGTTTGTCTTTATAAATTTTCTTAAAGATTAAGAAAATTTAAGA
CCCCATTGAGTTACTGTAATGCAATCAACTTTGAGTTATCTTTTAAATATGTCTTGTATAGTTCAATATTCATGG
CTGAAACTTGACCACACTATTGCTGATTGTATGGTTTTTCACCTGGACACCGTGTAGAATGCTTGATTACTTGTAC
TCTTCTTATGCTAATATGCTCTGGGCTGGAGAAATGAAATCCTCAAGCCATCAGGATTTGCTATTTAAGTGGCTT
GACAACCTGGGCCACCAAAGAACTTGAACCTTACCTTTTAGGATTTGAGCTGTTCTGGAACACATTGCTGCACCTT
GGAAAGTCAAATCAAGTGCCAGTGGCGCCCTTTCCATAGAGAATTTGCCAGCTTTGCTTTAAAAGATGTCTTG
TTTTTTATATACATAATCAATAGGTCCAATCTGCTCTCAAGGCCTTGGTCTGGTGGGATTCTTCCACCAATT
ACTTTAATTAATAATGGCTGCAACTGTAAAGACCCTTGTCTGATATATTGCAACTATGCTCCCATTTACAAATG
TACCTTCTAATGCTCAGTTGCCAGGTTCCATGCAAAGGTGGCGTGGACTCCCTTTGTGTGGGTGGGGTTTGTGG
GTAGTGGTGAAGGACCGATATCAGAAAAATGCCTTCAAGTGTACTAATTTATTAATAAACATTAGGTGTTTGTGA
AAAAA

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FIGURE 418

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594

><subunit 1 of 1, 655 aa, 1 stop

><MW: 71845, pI: 8.22, NX(S/T): 8

MGTSPSSSTALASCSRIARRATATMIAGSLLLLGFLSTTTAQPEQKASNLIQTYRHVDRATGQ
VLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTRHENGIEKCHDCSQPCPWPMEIKLPAAAL
TDRECTCPPGMFQSNATCAPHTVCPVGWGVRRKGTETEDVRCKQCARGTFSDVPSSVMKCKAY
TDCLSQNLVVIKPGTKETDNVCGTLPFSFSSSTSPSPGTAFPRPEHMETHEVPSSTYVPKGMN
STESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPNLQVVNHQQGPHHRHILKLLPS
MEATGGEKSSTPIKGPKRGHPRQNLHKHFDINEHLPWMIVLFLLLVLVIVVCSIRKSSRTLK
KGPRQDPSAIVEKAGLKKSMTPTQNREKWIYYCNGHGIDILKLVAQVGSQWKDIYQFLCNAS
EREVAAFSNGYTADHERAYAAALQHWITIRGPEASLAQLISALRQHRNDVVEKIRGLMEDTTQL
ETDKLALPMSPSPSPSPSPNAKLENSALLTVEPSPQDKNKGFFVDESEPLLRC DSTSSGS
SALSRNGSFITKEKKD TVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQAEDKLDRLFE
IIGVKSQEASQTLLDSVYSHLPDLL

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 350-370

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FIGURE 419

ATGGCTGGTGACGGCGGGGCCGGGCAGGGGACCGGGGCCGGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGA
ATCACC GCCTGGCCCCGACTCCACCATGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAG
AAGGGGACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTACTGCTGGCT
GCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCATCCCACAGCACCTGCCTTACA
GAGGCCTGCATTCGAGTGGCTGGAAAAATCCTGGAGTCCCTGGACCGAGGGGTGAGCCCCCTGTGAGGACTTTTAC
CAGTTCTCCTGTGGGGGCTGGATTTCGGAGGAACCCCTGCCGATGGGCGTTCTCGCTGGAAACACCTTCAACAGC
CTCTGGGACCAAAACCAGGCCATACTGAAGCACCTGCTTGAAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAG
CAGAAGACACAGCGCTTCTACCTATCTTGCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCAGCCACTGAGA
GACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAGGACAACCTTTATGGAGGTGTTGAAG
GCAGTAGCAGGGACCTACAGGGCCACCCATTCTTCACCGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGC
AATGTTATCCAGGTGGACCACTGCTGGGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAG
AAAGTGCTCACTGCCTATCTGGATTACATGGAGGAACCTGGGGATGCTGCTGGGTGGGCGGCCACCTCCACGAGG
GAGCAGATGCAGCAGGTGCTGGAGTTGGAGATACAGCTGGCCAAACATCACAGTGCCCCAGGACCAGCGCGCGAC
GAGGAGAAGATCTACCACAAGATGAGCATTTCGGAGCTGCAGGCTCTGGCGCCCTCCATGGACTGGCTTGAGTTC
CTGTCTTTCTTGTGTCAACATTGGAGTTGAGTGACTCTGAGCCTGTGGTGGTGTATGGGATGGATTATTTGCAG
CAGGTGTGAGAGCTCATCAACCGCACGGAACCAAGCATCCTGAACAATTACCTGATCTGGAACCTGGTGCAAAAG
ACAACCTCAAGCCTGGACCGACGCTTTGAGTCTGCACAAGAGAAGCTGCTGGAGACCCCTCTATGGCACTAAGAAG
TCCTGTGTGCCGAGGTGGCAGACCTGCATCTCCAACACGGATGACGCCCTTGGCTTTGCTTTGGGGTCACTCTTC
GTGAAGGCCACGTTTGACCGGCAAAGCAAAGAAATTGCAGAGGGGATGATCAGCGAAATCCGGACCGCATTGTAG
GAGGCCCTGGGACAGCTGGTTTGGATGGATGAGAAGACCCGCCAGGCAGCCAAGGAGAAAGCAGATGCCATCTAT
GATATGATTGGTTTCCCAGACTTTATCCTGGAGCCCAAAGAGCTGGATGATGTTTATGACGGGTACGAAATTTCT
GAAGATTCTTTCTCCAAAACATGTTGAATTTGTACAACTTCTCTGCCAAGGTTATGGCTGACCAGCTCCGCAAG
CCTCCCAGCCGAGACCAGTGGAGCATGACCCCCCAGACAGTGAATGCCTACTACCTTCCAACTAAGAAATGAGATC
GTCTTCCCCGCTGGCATCCTGCAGGCCCTTCTATGCCCGCAACCAACCCCAAGGCCCTGAACCTTCGGTGGCATC
GGTGTGGTCATGGGCCATGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTG
CGGCCCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACACACGGCCTGCATGGAGGAACAGTACAATCAA
TACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACATTACTGACAACGGGGGGCTGAAG
GCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATGGGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACC
AACCACCAGCTCTTCTTCGTGGGATTTGCCAGGTGTGGTGTCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGG
CTGGTGACCGACCCCAACAGCCCTGCCCGCTTCCGCGTGCTGGGCACTCTCTCCAACCTCCCGTGACTTCTGCGG
CACTTCGGCTGCCCTGTGCGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTTAGACCTGGATCAGGGGA
GAAATGGCCAGCTGTACACAGACCTGGGGCAGCTCTCCTGACAAAGCTGTTTGCTCTTGGGTGGGAGGAAGCAA
ATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCACAGGTGACATGAGTACAGACCCTCCTCAATCACCACATTG
TGCTCTGCTTTGGGGGTGCCCTGCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTCCGTGTACCCCT
GCCTGGAAGAGGTCTGGGTGGGGAGGCCAGT'TCCCATAGGAAGGAGTCTGCC

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FIGURE 420

MNVALQELGAGSNVGFQKGTROQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSHS
TCLTEACIRVAGKILES LDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQAIL
KHLENTTFNSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLIEKIGGWNITGPWDQDNFME
VLKAVAGTYRATPFFTVYISADSKSSNSNVIQVDQSGFLPSRDYYLNRTANEKVLTA YLDYM
EELGMLLGGRPTSTREQMQQVLELEIQ LANITVPQDQRRDEEKIYHKMSISELQALAPSMDWL
EFLSFLLSPLLESDSEPVVVYGMDYLQQVSELINRTEPSILNNYLIWNLVQKTTSSLD RRFES
AQEKLETTYGTTKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKEIAEGMISEIRTAF
EEALGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISEDSFFQNM LNL
NFSKVMADQLRKPPSRDQWSMTPQTVNAYYLP TKNEIVFPAGILQAPFYARNHPKALNFGGI
GVVMGHELTHAFDDQGREYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQYQVNGERLNGRQT
LGENITDNGGLKAAYNAYKAWLRKHGEEQQLP AVGLTNHQLFFVGFAQVWCSVRTPESSHEGL
VTDPHSPARFRVLGTLSNSRDFLRHFGCPVGSPMNP GQLCEVW

Type II Transmembrane domain:

amino acids 32-57

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FIGURE 421

GGCGCCGCGTAGGCCCGGGAGGCCGGGCGGCGGGCTGCGAGCGCCTGCCCCATGCGCCGCC
GCCTCTCCGCACG**ATG**TCCCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGCAG
GTCCGGGTTGCTCTCCGGCGGCCTCCCTCGGAAGTGTTCCGTCTTCCACCTGTTTCGTGGCCTG
CCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGGCCCCG
GGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGCCCTCCCCGTGCCTGCCCCCAGAGCCGCC
CCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCCACC GCCTGGCAGTGCTGGTGCCCTT
CCGCGAACGCTTCGAGGAGCTCCTGGTCTTCGTGCCCCACATGCGCCGCTTCCTGAGCAGGAA
GAAGATCCGGCACCATCTACGTGCTCAACCAGGTGGACCACTTCAGGTTCAACCGGGCAGC
GCTCATCAACGTGGGCTTCCTGGAGAGCAGCAACAGCACGGACTACATTGCCATGCACGACGT
TGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCTGAGGCTGGGGCCCTTCACGT
GGCCTCCCCGGAGCTCCACCCTCTCTACCACTACAAGACCTATGTCGGCGGCATCCTGCTGCT
CTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGGCTGGGGCCCGGA
GGACGACGAGTTCTACCGGCGCATTAAAGGGAGCTGGGCTCCAGCTTTTCCGCCCCCTCGGGAAT
CACAACCTGGGTACAAGACATTTGCCACCTGCATGACCCAGCCTGGCGGAAGAGGGACCAGAA
GCGCATCGCAGCTCAAAAACAGGAGCAGTTCAAGGTGGACAGGGAGGGAGGCCTGAACACTGT
GAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGGCGGGGCCCCCTGCACTGTCTCAA
CATCATGTTGGACTGTGACAAGACCGCCACACCCTGGTGCACATTCAGCT**TCAG**CTGGATGGAC
AGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGACAAGGCCTCAGGTCGTGG
GCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCAAGCTACGCAATTGCAGCCA
CCCGGCCGCCAAGGCAGGCTTGGGCTGGGCCAGGACACGTGGGGTGCCTGGGACGCTGCTTGC
CATGCACAGTGATCAGAGAGAGGCTGGGGTGTGTCTGTCCGGGACCCCCCTGCCTTCCTGC
TCACCCTACTCTGACCTCCTTCACGTGCCCAGGCCTGTGGGTAGTGGGGAGGGCTGAACAGGA
CAACCTCTCATCACCTACTCTGACCTCCTTCACGTGCCCAGGCCTGTGGGTAGTGGGGAGGG
CTGAACAGGACAACCTCTCATCACCCCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAA

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FIGURE 422

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531
><subunit 1 of 1, 327 aa, 1 stop
><MW: 37406, pI: 9.30, NX(S/T): 1
MFPSRRKAAQLPWEDGRSGLLSGGLPRKCSVFHLFVACLSLGGFFSLLWLQLSCSGDVARAVRG
QGQETSGPPRACPPPEPPPEHWEEDASWGPHRLAVLVPPFRERFEELLVFVPHMRRLSRKKIRH
HIYVLNQVDHFRFNRAALINVGFLSSNSTDYIAMHDVDLLPLNEELDYGFPEAGPFHVASPE
LHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDFYRRIKGAGLQLFRPSGITTGY
KTFRHLHDPAWRKRDKRIAAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVLNIMLD
CDKTATPWCTFS
```

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 29-49 (type II)

N-glycosylation site.

amino acids 154-158

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 27-31

Tyrosine kinase phosphorylation site.

amino acids 226-233

N-myristoylation site.

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

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FIGURE 423

CCATCCCTGAGATCTTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATAACCAGATC
TCACCAGAGAGTCGCAGACACT**ATG**CTGCCTCCCATGGCCCTGCCAGTGTGTCTGGATGCT
GCTTTCCTGCCTCATTCTCCTGTGTCAAGGTTCAAGGTGAAGAAACCCAGAAGGAAGTGCCTC
TCCACGGATCAGCTGTCCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGTTTTT
GTCACCAAAATCCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGGAAAAGTGGT
GTCTGTGCTCAGTGGGGCTGAGGGATCCTTCGTGTCCTCCCTGGTGAGGAGCATTAGTAACAG
CTACTCATACATCTGGATTGGGCTCCATGACCCACACAGGGCTCTGAGCCTGATGGAGATGG
ATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAAATCCCTCCACCAT
CTTAAACCTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTGAAAGATTA
TAACTGTGATGCAAAGTTACCCTATGTCTGCAAGTTCAAGGACT**TAG**GGCAGGTGGGAAGTCAG
CAGCCTCAGCTTGGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGACTCACCTGGAA
GAGAATATTCTCCCCAAACTGCCCTACCTGACTACCTTGTCATGATCCTCCTTCTTTTTCCTT
TTTCTTCACCTTCATTTCAAGGCTTTTCTCTGTCTTCCATGTCTTGAGATCTCAGAGAATAATA
ATAAAAATGTTACTTTATAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 424

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965

<subunit 1 of 1, 175 aa, 1 stop

<MW: 19330, pI: 7.25, NX(S/T): 1

MLPPMALPSVSWMLLSCLILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWMD

ADLACQKRPSGKLVSVLSGAEGSFVSSLVRSISNSYSYIWIGLHDPTQGSEPDGDGWEWSSTD

VMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPYVCKFKD

Important features:**Signal peptide:**

amino acids 1-26

C-type lectin domain signature.

amino acids 146-171

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FIGURE 425

CGGACGCGTGGGCGCCACCTCCGGAACAAGCC**ATG**GTGGCGGCGACGGTGGCAGCGGCGTG
CTGCTCCTGTGGGCTGCGGCCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGGTC
AACATCCGGGGCAAACCTGGTGTGCTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTGAAT
GTGGCCAGCGAGTGC GGCTT CACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCGAGAC
CTGGGCCCCCACCACCTTTAACGTGCTCGCCTTCCCTGCAACCAGTTTGGCCAACAGGAGCCT
GACAGCAACAAGGAGATTGAGAGCTTTGCCCCGCCGACCTACAGTGTCTCATTCCCCATGTTT
AGCAAGATTGCAGTCACCGGTACTGGTGCCCATCCTGCCTTCAAGTACCTGGCCCAGACTTCT
GGGAAGGAGCCCACCTGGAACCTTCTGGAAGTACCTAGTAGCCCCAGATGGAAAGGTGGTAGGG
GCTTGGGACCCAACTGTGTCAGTGGAGGAGGTCAGACCCAGATCACAGCGCTCGTGAGGAAG
CTCATCCTACTGAAGCGAGAAGACTT**TAA**CCACCGCGTCTCCTCCTCCACCACCTCATCCCG
CCCACCTGTGTGGGGCTGACCAATGCAAACCTCAAATGGTGCTTCAAAGGGAGAGACCCACTGA
CTCTCCTTCCTTTACTCTTATGCCATTGGTCCCATCATTCCTTGTGGGGGAAAAATTCTAGTAT
TTTGATTATTTGAATCTTACAGCAACAAATAGGAACCTCCTGGCCAATGAGAGCTCTTGACCAG
TGAATCACCAGCCGATACGAACGTCTTGCCAACAAAAATGTGTGGCAAATAGAAGTATATCAA
GCAATAATCTCCCACCCAAGGCTTCTGTAAACTGGGACCAATGATTACCTCATAGGGCTGTTG
TGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGCCAAATAGGAGGCATTC
AATGAACATTTTTTGCATATAAACCAAAAAATAACTTGTTATCAATAAAAACTTGCATCCAAC
ATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTTGTTATTTCTCTGTATTA
TTTTCTTCATTACAAAAGAAATGCAAGTTCATTGTAACAATCCAAACAATACCTCACGATATA
AAATAAAAATGAAAGTATCCTCCTCAAAAA

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FIGURE 426

MVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLEKYRGSVSLVVNVASECGFTDQH
YRALQQQLQORDLGPHHFENVLAFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTGAH
PAFKYLAQTSGKEPTWNFWKYL VAPDGKVVGAWDPTVSVEEVRPQITALVRKLILLKREDL

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FIGURE 427

CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCC**ATG**GGGGTGGAGATTGCC
TTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCCAGGTTGTTCTT
CTCCAGCCAGTTCCAACCTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGCTTT
GCCGGCCACTCA**TG**AGAGTGTTTTTGTGTAAAGTATTTTTTAGAATACTGTTGACTTCTTCAT
GATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCTCAAATTT
TTGTTATACTAGATGGCTTCCATTTACCCACCACTATTTTAAGGTCCCTTTATTTTTAGGTTT
AAGGTTCAATTTGACTTGAGAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTTTATCTTCACTA
TTAATTGTAACGATTAAAAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATTTTATCCCTG
GGTGCCCTGACACATTTATGTAGTGATCCCACAAATGTGATTGTTAATTTAAATGTTATTCT
AATATTAGTACATTCAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTTAAAGTTTTG
AGTATATTTTTCACTAGATATTTGTATAGAAAGACTGAATAGTGATG

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FIGURE 428

MGVEIAFASVILTCLSLAAGVSQVLLQPVPTQETGPKAMGDLSCGFAGHS

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FIGURE 429

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCTG
CACAGGGCAGCTTTACTTACTCCAGCACCTTCCTCTCCCAGGCAA**ATGG**TGCTGACCATCTTT
GGGATACAATCTCATGGATACGAGGTTTTTAAACATCATCAGCCCAAGCAACAATGGTGGCAAT
G TTCAGGAGACAGTGACAATTGATAATGAAAAAATAACGCCATCGTTAACATCCATGCAGGA
TCATGCTCTTCTACCACAATTTTTGACTATAAACATGGCTACATTGCATCCAGGGTGCTCTCC
CGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAATCTCCAA
TGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTGGGTCAAG
TACAACCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTTGGGTCACCCATTGAG
AAACTCTGCAAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACATAATGTCGGT
GCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTGTGCAGACATT
CATGTT**TAG**GATGATTAGCCCTCTTGTTTTATCTTTTCAAAGAAATACATCCTTGGTTTACAC
TCAAAAGTCAAATTAAATTCTTTCCAATGCCCCAACTAATTTTGAGATTCACTCAGAAAATA
TAAATGCTGTATTTATA

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FIGURE 430

><ss.DNA57834
><subunit 1 of 1, 176 aa, 1 stop
><MW: 19616, pI: 7.11, NX(S/T): 0
MVLTIIFGIQSHGYEVFNIIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTTIFDYKH
GYIASRVLSRRACFILKMDHQNIPPLNNLQWYIYEKQALDNMFSNKYTWVKYNPLESLIK
DVDWFLLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

Important features:**Signal peptide:**

Amino acids 1-26

N-myristoylation sites:

Amino acids 48-54;153-159;156-162;167-173

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FIGURE 431

GCGTGGGGATGTCTAGGAGCTCGAAGGTGGTGGCTGGGCCTCTCGGTGCTGCTGACGGCGGCCA
CAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTATCA
GAGACATTGAGAGGCAAATTCGGAAAAAAGAAAACATTCGTCTTTGGGAGAACAGATTATTT
TGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAAGGATCTCAAAAATCAT
GACTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTTGATGGAGA
GTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTTAAACTTGATCAAATAAA
GGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGAGTGTGGG
CAGACACTTTTTGGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGGTCACTGTC
CAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGATGGATAGTA
GCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACATCGACCTCAG
AAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC

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FIGURE 432

MSRSSKVVVLGLSVLLTAATVAGVHVKKQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILTE
QLEAEREKMLLAKGSQKS

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FIGURE 433

GAATTCGTGTCTCGGCACTCACTCCCGGCCGCCGGACAGGGAGCTTTCGCTGGCGCGCTTGGCCGGCGACAGGA
CAGGTTCCGGGACGTCCATCTGTCCATCCGTCCGGAGAGAAATTACAGATCCGCAGCCCCGGGATGGGGCCGGCCCC
CGCTGCCGCTGCTGCTGGGCCTCTTCTCCCGCGCTCTGGCGTAGAGCTATCACTGAGGCAAGGGAAGCCCA
AGCCTTACCCGCTATTCCCGGGACCTTTTCCAGGGAGCCTGCAAACAGACCACACACCGCTGTTATCCCTTCTC
ACGCCAGTGGGTACCAGCCTGCCTTGATGTTTTACCAACCCAGCCTGGAAGACCACATACAGGAAACGTAGCCATT
CCCCAGGTGACCTCTGTGAATCAAAGCCCCCTACCGCCTCTTGCCCTTCAAACACACAGTTGGACACATAATACTT
TCTGAACATAAAGGTGTCAAATTTAATTGCTCAATCAATGTACCTAATATATACCAGGACACCACAATTTCTTGG
TGGAAAGATGGGAAGGAATTGCTTGGGGGACATCATCGAATTACACAGTTTTATCCAGATGATGAAGTTACAGCA
ATAATCGCTTCTTTCAGCATAACCAAGTGTGCAGCGTTTACAGCAATGGTTCGTATATCTGTAAGATGAAATAAAC
AATGAAGAGATCGTGTCTGATCCCATCTACATCGAAGTACAAGGACTTCTCACTTTACTAAGCAGCCTGAGAGC
ATGAATGTCACCAGAAACACAGCCTTCAACCTCACCTGTCAGGCTGTGGGCCCGCCTGAGCCCGTCAACATTTTC
TGGGTTCAAACAGTAGCCGTGTTAACGAACAGCCTGAAAAATCCCCCGCGCTGCTAACTGTTCCAGGCCCTGACG
GAGATGGCGGTCTTCAGTTGTGAGGCCACAAATGACAAAGGGCTGACCGTGTCCAGGGAGTGACAGATCAACATC
AAAGCAATTTCCCTCCCCACCAACTGAAGTCAGCATCCGTAACAGCACTGCACACAGCATTCTGATCTCCTGGGTT
CCTGGTTTTGATGGATACTCCCCGTTCAAGGAATTGCAGCATTCAAGTCAAGGAAGCTGATCCGCTGGGTAATGGC
TCAGTCATGATTTTACACCTCTGCCTTACCACATCTGTACCAAATCAAGCAGCTGCAAGCCCTGGCTAATTAC
AGCATTGGTGTCTTCCATGAATGAAATAGGCTGGTCTGCAGTGAGCCCTTGGATTCTAGCAAGCAGACTGAA
GGAGCCCCATCAGTAGCACCTTAAATGTCACTGTGTTTCTGAATGAATCTAGTGATAATGTGGACATCAGATGG
ATGAAGCCTCCGACTAAGCAGCAGGATGGAGAAGTGGTGGGCTACCGGATATCCACGCTGTGGCAGAGTGACAGG
ATTTCCAAAGAGCTCTTGGAGGAAGTTGGCCAGAATGGCAGCCGAGCTCGGATCTCTGTTCAAGTCCACAATGCT
ACGTGCACAGTGAGGATTGCAGCCGTCAACAGAGGGGAGTTGGGCCCTTCACTGATCCAGTGAATAATTTATC
CCTGCACACGTTTGGTAGATTATGCCCCCTCTTCAACTCCGGCGCCTGGCAACGCAGATCCTGTGCTCATCATC
TTTGGCTGCTTTTTGTGGATTATTTTGTATTGGGTTGATTTTATACATCTCCTTGGCCATCAGAAAAAGAGTCCAG
GAGACAAAGTTTGGGAATGCATTACAGAGGAGGATTCTGAATTAGTGGTGAATTATATAGCAAAGAAATCCTTC
TGTCGGCGAGCCATTGAACCTTACCTTACATAGCTTGGGAGTCAGTGAGGAACTACAAAATAAAGTAGAAGATGTT
GTGATTGACAGGAATCTCTAATTTCTTGGAAAAATTTCTGGGTGAAGGAGAGTTTGGGTCTGTAATGGAAGGAAAT
CTTAAGCAGGAAGATGGGACCTCTCTGAAAGTGGCAGTGAAGACCATGAAGTTGGACAACCTTTCACATCGGGAG
ATCGAGGAGTTTCTCAGTGAGGCAGCGTGCATGAAGACTTCAGCCACCCAAATGTCATTGCACTTCTAGGTGTG
TGATAGAAATGAGCTCTCAAGGCATCCCAAAGCCCATGGTAATTTTACCCTTCATGAAATACGGGGACCTGCAT
ACTTACTTACTTTATTCCCATTGGAGACAGGACCAAAGCATATTCCTCTGCAGACACTATTGAAGTTCATGGTG
GATATTGCCCTGGGAATGGAGTATCTGAGCAACAGGAATTTTCTTCATCGAGATTTAGCTGCTCGAAACTGCATG
TTGCGAGATGACATGACTGTCTGTGTTGCGGACTTCGGCCTCTCTAAGAAGATTTACAGTGGCGATTATTACCGC
CAAGGCCGCATTGCTAAGATGCCTGTTAAATGGATCGCCATAGAAAGTCTTGCAGACCGAGTCTACACAAGTAA
AGTGATGTGTGGGCATTGGCGTGACCATGTGGGAAATACGTACGCGGGGAATGACTCCCTATCTTGGGGTCCAG
AACCATGAGATGTATGACTATCTTCTCCATGGCCACAGGTTGAAGCAGCCCCGAAGACTGCCTGGATGAAGTGTAT
GAAATAATGTAATCTTGTGGAGAACCGATCCCTTAGACCGCCCCACCTTTTCACTATTGAGGCTGCAGCTAGAA
AACTCTTAGAAAGTTTGCCTGACGTTCCGAACCAAGCAGACGTTATTTACGTCAATACACAGTTGCTGGAGAGC
TCTGAGGGCCTGGCCCAGGGCCCCACCTTGCTCCACTGGACTTGAACATCGACCCCTGACTCTATAATTGCCTCC
TGCACTCCCCGCGCTGCCATCAGTGTGGTCACAGCAGAAGTTCATGACAGCAAACCTCATGAAGGACGGTACATC
CTGAATGGGGGAGTGAGGAATGGGAAGATCTGACTTCTGCCCTCTGCTGCAGTCACAGCTGAAAAGAACAGT
GTTTTACCGGGGAGAGACTTGTTAGGAATGGGGTCTCCTGGTCCCATTGAGCATGCTGCCCTTGGGAAGCTCA
TTGCCCGATGAACTTTGTGTTGCTGACGACTCCTCAGAAGGCTCAGAAGTCTGATGTGAGGAGAGGTGCGGGGA
GACATTCCAAAAATCAAGCCAATTCTTCTGCTGTAGGAGAATCCAATTGTACCTGATGTTTTTGGTATTTGTCTT
CCTTACCAAGTGAACCTCATGGCCCCAAAGCACCAGATGAATGTTGTTAAGGAAGCTGTCATTAATAATACATAA
TATATATTTATTTAAAGAGAAAAATATGTGTATATCATGAAAAAGACAAGGATATTTTAATAAAACATTACTTA
TTTCATTTCACTTATCTTGCATATCTTAAATTAAGCTTCAGCTGCTCCTTGATATTAACCTTTGTACAGAGTTG
AAGTTGTTTTTCAACTTCTTTTCTTTTCACTATTAATAATGTAATAATATTTGTAATAATGAAATGCCATATT
TGACTTGGCTTCTGGTCTTGATGTATTTGATAAGAATGATTAATTTTCTGATATGGCTTCCATAATAAATTGAA
ATAGGA

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FIGURE 434

MGPAPLPLLLGLFLPALWRRRAITEAREEAKPYPLFPGPFPGLQTDHTPLLSLPHASGYQPALMFSPTQPGRPHT
GNVAIPQVTSVESKPLPPLAFKHTVGHIILSEHKGVKFNC SINVPNIYQD TTISWWKDGKELLGGHHRITQFY PD
DEVTAI IASF SITSVQRSDNGSYICKMKINNEEIVSDPIYIEVQGLPHFTKQPESMNVT RNTAFNLTCQAVGPPE
PVNIFWVQNSSRVNEQPEKSPGVLTVPGLTEMAVFSC EAHNDKGLTVSQGVQINIKAI P SP PTEVSIRNSTAHSI
LISWVPGFDGYSPFRNC SIQVKEADPLNGSVMIFNTSALPHLYQIKQLQALANYSIGVSCMNEIGWSAVSPWIL
ASTTEGAPSVAPLNVTVFLNESSDNVDIRWMKPPTKQQDGELVGYRISHVWQSAGISKELLEEVQNGSRARISV
QVHNATCTVRIAAVTRGGVGPFS DPVKIFIPAHGWVDYAPSSTPAPGNADPVLIIFGCF CGFILIGLILYISLAI
RKRVQETKFGNAFTEEDSELVVNYIAKKSFCRR AIELTLHSLGVSEELQNKLEDVVIDRNLLILGKILGEGEFGS
VMEGNLKQEDGTS LKVAVKTMKLDNSSHREIEEFLSEAACMKDFSHPNVIRLLGVCIEMSSQGIPKPMVILPFMK
YGD LHTYLLYSRLETGPKHIPLQTL LKFMVDIALGMEYLSNRNFLHRDLAARNCMLRDDMTVCVADFGLSKKIYS
GDYYRQGRIAKMPVKWIAIESLADR VYTSKSDVWAFGVTMWEIRTRGMT PYPGVQNH EMYDYLLHGHRLKQPEDC
LD ELYEIMYSCWR TDPLDRPTFSVLR LQLEKLL ESLPDVRNQADV IYVNTQLLESSEGLAQGP TLAPLDL NIDPD
SIIASCTPRAAISVVTAEVHDSKPH EGRYILNGGSEEWEDLTSAPSAAVTA EKNSVLPGERLVRNGVSWSHS SML
PLGSSLPDELLFADDSSEGSEVLM

Signal sequence:	Amino acids 1-18
Transmembrane domain:	Amino acids 501-520
N-glycosylation sites:	Amino acids 114-118;170-174;207-211; 215-219;234-238;294-298;316-320;329-333; 336-340;354-358;389-393;395-399;442-446; 454-458;625-629
Tyrosine kinase phosphorylation sites:	Amino acids 675-683;865-873;923-930
N-myristoylation sites:	Amino acids 41-47;110-116;171-177; 269-275;275-281;440-446;507-513;535-541; 966-972
Prokaryotic membrane lipoprotein lipid attachment site:	Amino acids 351-362
Tyrosine protein kinases specific active-site signature:	Amino acids 719-732

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FIGURE 435

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTTAGCACCACTACTGGATG
TGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTCAGTGTCCGATTCTGATTCCGGCAAGGAT
CCAAGCATGGAAATGCTGCCGTCGGGCAACTCCTGGCACACTGCTCCTCTTTCTGGCTTTCCTG
CTCCTGAGTTCCAGGACCGCACGCTCCGAGGAGGACCGGGACGGCCTATGGGATGCCTGGGGC
CCATGGAGTGAATGCTCACGCACCTGCGGGGGAGGGGCCTCCTACTCTCTGAGGCGCTGCCTG
AGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGACTGCCCA
CCAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCACCATGGC
CAGTTTTATGAATGGCTTCCTGTGTCTAATGACCCTGACAACCCATGTTCACTCAAGTGCCAA
GCCAAAGGAACAACCCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTACGCGTTGCTAT
ACAGAATCTTTGGATATGTGCATCAGTGGTTTATGCCAAATTGTTGGCTGCGATCACCAGCTG
GGAAGCACCGTCAAGGAAGATAACTGTGGGGTCTGCAACGGAGATGGGTCCACCTGCCGGCTG
GTCCGAGGGCAGTATAAATCCCAGCTCTCCGCAACCAAATCGGATGATACTGTGGTTGCACTT
CCCTATGGAAGTAGACATATTGCGCTTGTCTTAAAGGTCTGATCACTTATATCTGGAAACC
AAAACCTCCAGGGGACTAAAGGTGAAAACAGTCTCAGCTCCACAGGAACTTTCCTTGTGGAC
AATTCTAGTGTGGACTTCCAGAAATTTCCAGACAAAGAGATACTGAGAATGGCTGGACCACTC
ACAGCAGATTTTCATTGTCAAGATTCGTAACCTCGGGCTCCGCTGACAGTACAGTCCAGTTCATC
TTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCTTTCCTTGCTCAGCAACCTGT
GGAGGAGGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGGAGCAACCGTGTGGTTGCT
GACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACCCAAGCTTCAGGAGTGCAAC
TTGGATCCTTGTCCAGCCAGTGACGGATAACAAGCAGATCATGCCTTATGACCTCTACCATCCC
CTTCCTCGGTGGGAGGCCACCCCATGGACCGCGTGCTCCTCCTCGTGTGGGGGGGGCATCCAG
AGCCGGGCAGTTTCCTGTGTGGAGGAGGACATCCAGGGGCATGTCACTTCAGTGGAAGAGTGG
AAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCTGCAACATTTTTGACTGCCCTAAA
TGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGTGGCCAGGGCCTCAGATACCGTGTG
GTCCTCTGCATCGACCATCGAGGAATGCACACAGGAGGCTGTAGCCCAAAAACAAAGCCCCAC
ATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATAAAACCAAAGAGAACTTCCAGTCGAG
GCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTAGAAGAAGGAGCTGCTGTGTGTCAGAGGAG
CCCTCGTTAAGTTGTAAAAGCACAGACTGTTCTATATTTGAAACTGTTTTGTTTAAAGAAAGCA
GTGTCTCACTGGTTGTAGCTTTCATGGGTTCTGAACTAAGTGTAATCATCTCACCAAAGCTTT
TTGGCTCTCAAATTAAAGATTGATTAGTTTCAAAAAAAAAA

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FIGURE 436

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847

<subunit 1 of 1, 525 aa, 1 stop

<MW: 58416, pI: 6.62, NX(S/T): 1

MECCRRATPGTLLLFIAFLLLSSRTARSEEDRDGLWDAWGPWSECSRTC GGGASYSLRRCLSS
KSCEGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNDPDNPCSLKCQAK
GTTLVVELAPKVLDTGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCRLVR
GQYKSQLSATKSDDTVVALPYGSRHIRLVKGPDLHYLETCTLQGTKGENSLSSSTGTFLVDNS
SVDFQKFDPKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFFP SATCGG
GYQLTSAECYDLRSNRVADQYCHYYPENIKPKPKLQECNLDPCPASDGYKQIMPYDLYHPLP
RWEATPWTACSSSSCGGGIQSRAVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNIFDCPKWL
AQEWSPCTVTCGQLRYRVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPKEKLPVEAK
LPWFKQAQELEEGAAVSEEPS

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 251-254

Thrombospondin 1

amino acids 385-399

von Willebrand factor type C domain proteins

amino acids 385-399, 445-459 and 42-56

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FIGURE 437

AACTGGAAGGAAAGAAAGAAAGGTCAGCTTTGGCCCAGATGTGGTTACCCCTTGGTCTCCTGT
CTTTATGTCTTTCTCCTCTTCCTATTCTGTTCATCTCCCTCACTTAAGTCTCAGGCCTGTCAGC
AGCTCCTGTGGACATTGCCATCCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATGTTA
TGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGTGATC
TCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTTGAAATCTGGCATGAGATG
GCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCTGCCCCTATTCCTCCTCCCAAGTCTGT
TCTCTTATTGTCAACCTCAGCACAAACAGGCTGGCGCCAATGGCATTACAGAGAAAGCAATCTG
TGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGTAGCCACCT
CCCTGTCAGCCAGTATTAACATGTCCCCTTCCCCCTGCCCCGCCGTAGATTACAGGACATTCGC
CCCTGTGTGCCACCAAACCAGGACTTTCCCCTTGGCTTGGCATCCCTGGCTCTCTCCTGGTAC
CCAGCAAGACGTCTGTTCCAGGGCAGTGTAGCATCTTTCAAGCTCCGTTACTATGGCGATGGC
CATGATGTTACAATCCCACCTTGCTGAATAATCAAGTGGGAAGGGGAAGCAGAGGGAAATGGG
GCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCCTGAGGAAAAACCAAAGGGAAGCAACAGG
AACTTCTGCAACTGGTTTTTATCGGAAAGATCATCCTGCCTGCAGATGCTGTTGAAGGGGCAC
AAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGTAAGGAAATAGAACAGTCTGCT
GGGAGTCAGACCTGGAATTCTGATTCCAAACTCTTTATTACTTTGGGAAGTCACTCAGCCTCC
CCGTAGCCATCTCCAGGGTGACGGAACCCAGTGTATTACCTGCTGGAACCAAGGAAACTAACA
ATGTAGGTTACTAGTGAATACCCAATGGTTTCTCCAATTATGCCCATGCCACCAAAACAATA
AAACAAAATTCTCTAACACTGAAA

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FIGURE 438

MWLPLGLLSLCLSPILSSPSLKSQACQQLWTLPSPLVAFRANRTTYVMDVSTNQSGMEH
RNHLCFCDLYDRATSPPLKCSLL

FIGURE 439

TTTCTCATAGTTTGGCGTCTTCTAAAGGAAAAAACTAAAATGAGGAACCTCAGCGGACCGGGAGCGACGCAGCTT
GAGGGAAGCATCCCTAGCTGTTGGCGCAGAGGGGCGAGGCTGAAGCCGAGTGGCCCCAGGTTGCTGATGGGGCTGG
GCGAAAGGTGAAAGAGTTTCAGAAACAAGCTTCTTGGAAACCCATGAGCTCTTGCGACATTTATACCGT
CTGAGGGTAGCAGCTCGAAACTAGAAGAAGTGGAGTGTGCCAGGAGCGGCAGTATCTCTTTGTGTGACCTGGC
GGCCTATAGGGACGTTGGCTTCAGACCTTTGTGATACACCATGCTGCGTGGGACGATGACGGCGTGGAGAGGAATG
AGGCCTGAGGTACACTGGCTTGCTCTCTAGCCACAGCAGGCTGCTTTGCTGACTTGAACGAGGTCCCTCAG
GTCAACCGTCCAGCTGCGTCCACCGTCCAGAAGCCCGGAGGCATGTGATCTTGGGCTGCGTGGTGAACCTCCA
AGGATGAATGTAACTTGGCGCTGAATGGAAGAGGAGCTGAATGGCTCGGATGATGCTCTGGGTGCTCTCATCACC
CAGGGGACCCCTCGTCATCACTGCCCTTAACAACCACACTGTGGGACGGTACCAGTGTGTGGCCCGGATGCCGCC
GGGGCTGTGGCCAGCGTGCCAGCCACTGTGACATAAGCCAATCTCCAGGACCTCAAGTTAGATGTGCAGCACGT
ATTGAAGTGGATGAGGGAAACACAGCAGTCTATTGCTGCCACCTGCCTGAGAGCCACCCCCAAGCCCCAGGTCCGG
TACAGCGTCAAACAAGAGTGGCTGGAGGCTCCAGAGGTAACCTACCTGATCATGCCCTCAGGGAACCTCCAGATT
TGAATGCCAGCCAGGAGGACGAGGGCATGTACAAGTGTGCAGCCTACAACCAGTGAACCCAGGAAGTGA
TCCGGCTCCAGGACAGGCTACGTGTGCGCGCTCCACCGCTGAGGCTGCCCGCATCATCTACCCCCAGAGGCC
CAAACCATCATCGTCACCAAGCCAGAGTGTCTATTGAGTGTGTGGCCAGTGAATCCCCACCCCGGCT
ACCTGGGCCAAGGATGGGTCCAGTGTACCGGTACACAAGAGCGCTTCTGCTGAGCAACCTCTCATCGAC
ACCAACGAGCAGGAGGACTCAGGCACCTACCGCTGCATGGCCGACAATGGGGTTGGGCAGCCCCGGGCGAGCGGT
ATCCTCTACAATGTCCAGGTGTTTGAACCCCTGAGGTACCATGGAGCTATCCAGCTGGTATCCCCCTGGGG
CAGAGTGCCAAAGCTTACCTGTGAGGTGCGTGGGAACCCCCCGCCCTCCGCTGTGGCTGAGGAATGCTGTGCC
CTCATCTCCAGGACCGCTCCGGCTCTCCGCAAGGCCCCGCGCTGCTCAGCATGGGGCTGAGGACGAAGGC
TCTACCAAGTGCATGGCCGAGAACGAGGTTGGGAGCGCCCATGCCGTAGTCCAGCTGCGGACCTCCAGGCCAAGC
ATAACCCCAAGGCTATGGCAGGATGCTGAGCTGGCTACTGGCACACCTCTGTATCACCTCCAAACTCGGCAAC
CCTGAGCAGATGCTGAGGGGGCAACCGGCGCTCCCCAGACCCCCACCTCAGTGGGCGCTGTCTCCCCGAGTGT
CCAGAGAGAAGGGGCGAGGGGCTCCGCGAGGCTCCCATCATCTCAGCTGCCCCGCACCTCCAGACGAGAC
TCATATGAAGTGGTGTGGCGGCTCGGCATGAGGGCAGTGGCCGGGCGCCAATCTCTACTATGTGGTGAACAC
CGCAAGCAGGTCACAAATTCCTCTGACGATTGACCATCTCTGGCATCCAGCCCAACGACCGCCCTGACCCCT
ACGAGCTTGACCCCGGGAGCTTGTATGAAGTGGAGATGGCAGCTTACAAGTGTGCGGAGAGGGCCAGACGCC
ATGTTCACTTCCGAACTGGACGGCGGCCAAACCGAGATCATGGCACAAGAGCAGCAGATCCAGAGAGAC
GACCTTGAGCCAGTCCCCAGAGCAGCAGCCAGCCAGACCACGGCCGCTCTCCCCCCAGAAGCTCCCGACAGG
CCCACCATCTCCACGGCTCCGAGACCTCAGTGTACGTGACCTGGAATCCCCGTGGGAATGGTGGGTTCCCAATC
CAGTCTCTCCGTGGAGTACAAGAAGCTAAGAAGTGGGAGACTGGATTCTGGCCACACGCGCATCCCCCA
TCGCGGCTCTCGTGGAGATCAGGGGCTTAGAGAAGGCACTCTACAAGTTTCAGTCCGGGCTCTGAACATG
CTGGGGGAGAGCGAGCCAGCGCCCCCTCTCGGCCCTACGTGGTGTGCGGCTACAGCGGTGCGGTGTACGAGAGG
CCCGTGGCAGGTCTTATATCACTTTCACGATGCGGTCAATGAGACCACCTCATGCTCAAGTGGATGTACATC
CCAGCAAGTAAACAACAACACCCCAATCCATGGCTTTTATATCTATTATCGACCCACAGACAGTACATATGAT
GACTACAAGAAGGATATGGTGAAGGGGACAAGTACTGGCACTCTATCAGCCACCTGCAGCCAGAGACCTCTAC
GACATTAAGATGCAGTGCTTCAATGAAGGAGGGGAGAGCGAGTTCAGCAACGTGATGATCTGTGAGACCAAAGCT
CGGAAGTCTTCTGGCCAGCCTGGTGCAGTGCACCCCCAACTCTGGCCCCACACAGCGCCCCCTTCTGAAACC
ATAGAGCGGCGCGTGGGCACTGGGGCCATGGTGGCTCGCTCCAGCGACCTGCCCTATCTGATTGTGCGGCTGT
CTGGGCTCCATGTTCTCATCATCGTCACTTCTATCCCCCTCTGCTGTGGAGGGCCTGGTCTAAGCAAAAACAT
ACAACAGACCTGGGTTTTCTCGAAGTGCCTTCCACCTCTCTGCCGTATACTATGGTGCCATTGGGAGGACTC
CCAGGCCACCAGGCCAGTGGACAGCCCTACTCAGTGGCATCAGTGGACGGGCTGTGCTAATGGGATCCACATG
AATAGGGGCTGCCCCCTCGGCTGCAGTGGGCTACCCGGGCATGAAGCCCCAGCAGCATGCCAGGCGAGCTTCAG
CAGCAGATTGACACACAGCAGCCTGCTGAGGCAGACCATCTTGGAATGGATGATGACCCCCAAGTCACCATG
ACGAGGGGTCCCAAGTCTAGCCCGGACGAGGGCTCTTTCTTATACACACTGCCCGACGACTCCTCACCAGCTG
CTGCAGCCCATCAGCATGCTGCTGCAACGCCAGGAGCAGCTGCTGCTGTGGGCGAGTCAGGGGTGAGGAGAGCC
CCGACAGTCTCTGCTGGAAGCAGTGTGGGACCTTCATTCTCACTCAGGCCCCCATGCTGCTTGGGCTTGTG
CCAGTTGAAGAGGTGGACAGTCTGACTCTGCAAGTGAAGTGGAGGAGACTGGTGTCCCCAGCACCCCGTAGGG
GCCTACGTAGGACAGGAACCTGGAATGCAGCTCTCCCCGGGGCCACTGGTGGTGTGTCTTTTGAACACCACCT
CTCACAATTTAGGCAGAAGCTGATATCCAGAAAGACTATATTTGTTTTTTTTTAAAAAAGAAAGAA
AGAGACAGAGAAAATTGGTATTTATTTTCTATTATAGCATATTTATATTTATGCACTTGTAAATAATGTA
TATGTTTTATAATTCTGGAGAGATAAGGAGTCTACCCGTTGAGTTGGAGAGGAAAAAAGAAAGCTGCCA
CTTAACAGGAGTCAACCAGGAAAGCACCGCACAGGCTGGCGCGGGACAGACTCTAACCTGGGGCCTCTGCAGTG
GCAGGCGAGGCTGCAGGAGGCCACAGATAAGCTGGCAAGAGGAAGGATCCAGGCACATGGTTCATCAGGACA
TGAGGGAACAGAAAGGGCAGGTTACACAGCCTGGAGACACCCACACAGATGGCTGGATCCGTTGCTACGGGAA
ACATTTTCTAAGATGCCCATGAGAACACACAGCAAGATGTGTACAGCACTATGAGCATTAATAAACCTCCAGAA
CAATAATCCGTGGCAACATATCTCTGTAAAAACAACACTGTAACTCTAATAAATGTTTAGTCTTCCCTGTAAAA

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FIGURE 440

MLRGTM TAWRGMRPEVTLACL LLLATAGCFADLNEVPQVTVQPASTVQKPGGT VILGCVVEPPR
MNV TWR LNKELNGSDDALGV LITHGTLVIT ALNNHTVGRYQCVARMPAGAVASVPATVTLAN
LQDFKLDVQH VIEVDEGNTAVIACHLPESH PKAQVRYSVKQEWLEASRGNYLIMPSGNLQIVN
ASQEDEGMYKCAAYNPVTQE VKTSGSSDRLRVRRSTAEAA RIIYPPEAQTIIVTKGQSLILEC
VASGIPPPRV TWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGQPGAAVILY
NVQVFEPPEVTMELS QLVIPWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLSRRALRV
LSMGPEDEGVYQCMAENEV GSAHAVVQLRTSRPSITPRLWQDAELATGTPPVSPSKLGNPEQM
LRGQPALPRPPTSVGPASPKCPGEGKGQGA PAEAPIILSSPRTSKTDSYELVWRPRHEGSGRAP
ILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLTRLDPGSLYEVE MAAYNCAGEGQTAMVTFR
TGRRPKPEIMASKEQQIQRDDPGAS PQSSSQPDHGR LSPPEAPDRPTISTASETSVYVTWIPR
GNGGFP IQSFRVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGT SYKFRVRALNMLGESEP
SAPSRPYVVS GYSGRVYERP VAGPYITFTDAVN ETTIMLKWMIYPASNNTPIHGFYIYYRPT
DSDNDS DYKKDMVEGD KYWHSISHLQ PETS YDIKMQC FNEGGESEFSNVMICETKARKSSGQP
GRLPPPTLAPPQPPLPETIERPVGTGAMVARSSDLPYLIVGVVLG SIVLIIVTFIPFCLWRAW
SKQKHTTDLGFPRSALPPSCP YTMVPLGGLPGHQASGQPYLSGISGRACANGIHMNRGCPSAA
VGYPGMKPQQHCPGELQQQSDTSSLLRQTHLGNGYDPQSHQITRGPKSSPDEGSFLYTL PDDS
THQLLQPHHDCCQRQE QPAAVGQSGVRRAPDSPVLEAVWD PPFHSGPPCCLGLVPVEEVDSPD
SCQVSGGDWCPQH PVGAYVGQEPGMQLSPG PLVRVSFETPPLTI

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 16-30 (type II), 854-879

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FIGURE 441

GAGAGAATAGCTACAGATTCTCCATCCTCAGTCTTTGCAAGGCGACAGCTGTGCCAGCCGGGC
TCTGGCAGGCTCCTGGCAGCATGGCAGTGAAGCTTGGGACCCTCCTGCTGGCCCTTGCCCTGG
GCCTGGCCCAGCCAGCCTCTGCCCGCCGGAAGCTGCTGGTGTTTCTGCTGGATGGTTTTCGCT
CAGACTACATCAGTGATGAGGCGCTGGAGTCATTGCCTGGTTTCAAAGAGATTGTGAGCAGGG
GAGTAAAAGTGGATTACTTGACTCCAGACTTCCCTAGTCTCTCGTATCCCAATTATTATACCC
TAATGACTGGCCGCCATTGTGAAGTCCATCAGATGATCGGGAACCTACATGTGGGACCCACCA
CCAACAAGTCCTTTGACATTGGCGTCAACAAAGACAGCCTAATGCCTCTCTGGTGGAATGGAT
CAGAACCTCTGTGGGTCACTCTGACCAAGGCCAAAAGGAAGGTCTACATGTACTACTGGCCAG
GCTGTGAGGTTGAGATTCTGGGTGTGAGACCCACCTACTGCCTAGAATATAAAAATGTCCCAA
CGGATATCAATTTTGCCAATGCAGTCAGCGATGCTCTTGACTCCTTCAAGAGTGGCCGGGCCG
ACCTGGCAGCCATATACCATGAGCGCATTGACGTGGAAGGCCACCACTACGGGCCTGCATCTC
CGCAGAGGAAAGATGCCCTCAAGGCTGTAGACACTGTCCTGAAGTACATGACCAAGTGGATCC
AGGAGCGGGGCCTGCAGGACCGCCTGAACGTCATTATTTTCTCGGATCACGGAATGACCGACA
TTTTCTGGATGGACAAAGTGATTGAGCTGAATAAGTACATCAGCCTGAATGACCTGCAGCAAG
TGAAGGACCGCGGGCCTGTTGTGAGCCTTTGGCCGGCCCCTGGGAAACACTCTGAGATATATA
ACAAACTGAGCACAGTGGAACACATGACTGTCTACGAGAAAGAAGCCATCCCAAGCAGGTTCT
ATTACAAGAAAGGAAAGTTTGTCTCTCCTTTGACTTTAGTGCGTGATGAAGGCTGGTTCATAA
CTGAGAATCGAGAGATGCTTCCGTTTTGGATGAACAGCACCGGCAGGCGGGAAGGTTGGCAGC
GTGGATGGCACGGCTACGACAACGAGCTCATGGACATGCGGGGCATCTTCCTGGCCTTCGGAC
CTGATTTCAAATCCAACCTTCAGAGCTGCTCCTATCAGGTCGGTGACGTCTACAATGTCATGT
GCAATGTGGTGGGCATCACCCCGCTGCCCCAACAACGGATCCTGGTCCAGGGTGATGTGCATGC
TGAAGGGCCGCGCCGCACTGCCCCGCCTGTCTGGCCAGCCACTGTGCCCTGGCACTGATTC
TTCTCTTCCTGCTTGCATAACTGATCATATTGCTTGTCTCAGAAAAAACACCATCAGCAAAG
TGGGCCTCCAAAGCCAGATGATTTTCATTTTATGTGTGAATAATAGCTTCATTAACACAATCA
AGACCATGCACATTGTAAATACATTATTCTTGGATAATTCTATACATAAAAGTTCCTACTTGT
TAAA

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FIGURE 442

MAVKLGTLILLALALGLAQPASARRKLLVFLLDGFERSDYISDEALES LPGFKEIVSRGVKVDYL
TPDFPSLSYPNYYTLM TGRHCEVHQMIGNYMWDPTTNKSF DIGVNKDSL MPLWWNGSEPLWVT
LTKAKRKVYMYYPGCEVEILGVRPTYCLEYKNVPTDINFANAVSDALDSEFKSGRADLA AIYH
ERIDVEGHYGPASPQRKDALKAVDTVLKYMTKWIQERGLQDRLNVIIFSDHGMTDIFWMDKV
IELNKYISLNDLQQVKDRGPVVS LWPAPGKHSEIYNKLSTVEHMTVYEKEAIPSRFYKKGKF
VSPLTLVADEGWFITENREMLPFWMNSTGRREGWQRGWHGYDNELMDMRGIFLAFGPDFKSNE
RAAPIRSVDVYNVMCNVVGITPLPNNGSWSRVMCMLKGRAGTAPPVWPSHCALALILLFLLA

Important features of the protein:**Signal peptide:**

amino acids 1-22

N-glycosylation sites.

amino acids 100-104, 118-122, 341-345, 404-408

N-myristoylation sites.

amino acids 148-154, 365-371

Amidation site.

amino acids 343-347

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FIGURE 443

AGTGACTGCAGCCTTCCTAGATCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAGC
ACCA GTGTGTGAGGGGAGCAGGCAGCGGTCTAGCCAGTTCCTTGATCCTGCCAGACCACCCA
GCCCCCGGCACAGAGCTGCTCCACAGGCACCA**ATG**AGGATCATGCTGCTATTCACAGCCATCCT
GGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGGTTCC
TGGCGGGGGCCGCAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTCAAAG
CCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAAGGAATC
AACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGAGGAGCGT
CCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCCTCGGCCCTTCATCC
CAATCAGCTTGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACCTTTA**TAAGA**
CTCTCCTACGGATGTGAATCAAGAGAACGTCCCCAGCTTTGGCATCCTCAAGTATCCCCCGAG
AGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTCTTTCCCTGTCC
CAATCCCCAGGTGCGCACGCTCCTGTTACCTTTCTCTTCCCTGTTCTTGTAACATTCTTG
CTTTGACTCCTTCTCCATCTTTTCTACCTGACCCTGGTGTGGAACTGCATAGTGAATATCCC
CAACCCCAATGGGCATTGACTGTAGAATACCCTAGAGTTCCTGTAGTGTCTACATTAAAAAT
ATAATGTCTCTCTCTATTCCTCAACAATAAAGGATTTTGCATATGAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 444

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLKA
LSQASTDPKESTSPEKRDMDHDFVGLMGKRSVQPEGKTGPFLPSVRVPRPLHPNQLGSTGKSS
LGTEEQRPL

Important features:**Signal peptide:**

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

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FIGURE 445

TGGACTTCTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCAGTCCACCATGATCCATCTGGGTCACAT
CCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAGAGATCATCACTCCCTGCCTTTTA
CCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCCCTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGA
TGCGGTGGCATCGCTGCTCATCGTGGGGGCGGTGTTCTGTGCGCACGCCCACGCCGCAGCCCCGCCCAAGATGG
CAAAGTCTACATCAACATGCCAGGCAGGGGCTGACCCCTCCTGCAGCTTGGACCTTTGACTTCTGACCCTCTCATC
CTGGATGGTGTGTGGTGGCACAGGAACCCCGCCCCAACTTTGGATTGTAATAAAACAATTGAAACACCA

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FIGURE 446

MIHLGHILFLLLLPVAAAQTTPGERSSSLPAFYPTSGSCSGCSLSLPLLAGLVAADAVASLLIVGAVFLCARPR
RSPAQDGKVYINMPGRG

Signal peptide:	Amino acids 1-18
transmembrane domain:	Amino acids 51-70
Glycosaminoglycan attachment site:	Amino acids 40-44
N-myristoylation sites:	Amino acids 34-40;37-43;52-58
Prokaryotic membrane lipoprotein lipid attachment site:	Amino acids 29-40

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FIGURE 447

GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCTCCC
CGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCACCATGACCCCTCCCTCAGGGG
GCACCCCCACAGTCACGGTACCCACACTGCTACTCGGCTGAGGAAGTGGCCCTCGGCCAGGC
CCCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGTAGCCCTGGTGTC
CAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAGTGCCC
GGTGCTGCCGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCGCTCCATCTCACCCCTGGAG
ATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGCCTGTG
CAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCT
CCAGAGCCTGCTGGTGCTGCGCCGCCGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACC
TGGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTGGGCTGCACCTGCGTGCTGCC
CCGTTCAGTGTGACCGCCGAGGCCGTGGGGCCCCCTAGACTGGACACGTGTGCTCCCCAGAGGG
CACCCCTATTTATGTGTATTTATTGTTATTTATATGCCTCCCCAACACTACCCTTGGGGTC
TGGGCATTCCCCGTGTCTGGAGGACAGCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGT
TGGGGGTAGAAGGAGCTCAGCACCTCTTCCAGCCCTTAAAGCTGCAGAAAAGGTGTCACACGG
CTGCCTGTACCTTGGCTCCCTGTCCTGCTCCCGGCTTCCCTTACCCTATCACTGGCCTCAGGC
CCCGCAGGCTGCCTCTTCCCAACCTCCTTGGAAGTACCCCTGTTTCTTAAACAATTATTTAAG
TGTACGTGTATTATTAAACTGATGAACACATCCCCAAA

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FIGURE 448

MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHLLARGAKWGQALP
VALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDYPQKLAF
AECLCRGCIDARTGRETAALNSVRLQSLVLRRRPCSRDGSGGLPTPGAFAFHTEFIHVPVGC
TCVLPRSV

Important features:

Signal peptide:

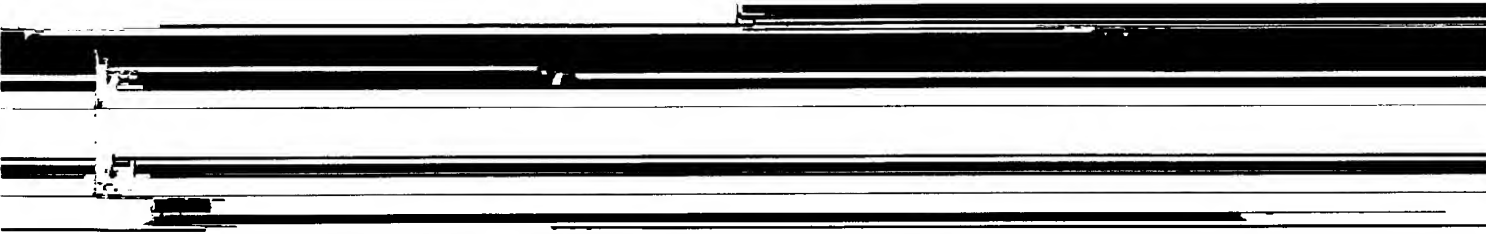
amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 112-121

N-myristoylation sites.

amino acids 32-38, 55-61, 133-139



amino acids 3-25

Homologous region to IL-17.

amino acids 99-195

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FIGURE 449

TGCAGAGCTTGTGGAGGCC**ATG**GGGCGCGTCGTCGCGGAGCTCGTCTCCTCGCTGCTGGGGTT
GTGGCTGTTGCTGTGCAGCTGCGGATGCCCCGAGGGCGCCGAGCTGCGTGCTCCGCCAGATAA
AATCGCGATTATTGGAGCCGGAATTGGTGGCACTTCAGCAGCCTATTACCTGCGGCAGAAATT
TGGGAAAGATGTGAAGATAGACCTGTTTGAAAGAGAAGAGGTCGGGGGCCGCTGGCTACCAT
GATGGTGCAGGGGCAAGAATACGAGGCAGGAGGTTCTGTCTCATCCATCCTTTAAATCTGCACAT
GAAACGTTTTGTCAAAGACCTGGGTCTCTCTGCTGTTTCAGGCCTCTGGTGGCCTACTGGGGAT
ATATAATGGAGAGACTCTGGTATTTGAGGAGAGCAACTGGTTCATAATTAACGTGATTAAATT
AGTTTGGCGCTATGGATTTCAATCCCTCCGTATGCACATGTGGGTAGAGGACGTGTTAGACAA
GTTTCATGAGGATCTACCGCTACCACTCTCATGACTATGCCTTCAGTAGTGTCGAAAAATTACT
TCATGCTCTAGGAGGAGATGACTTCCTTGGAATGCTTAATCGAACACTTCTTGAAACCTTGCA
AAAGGCCGGCTTTTCTGAGAAGTTCCTCAATGAAATGATTGCTCCTGTTATGAGGGTCAATTA
TGGCCAAAGCACGGACATCAATGCCTTTGTGGGGCGGTGTCACTGTCCTGTTCTGATTCTGG
CCTTTGGGCAGTAGAAGGTGGCAATAAACTTGTTTGCTCAGGGCTTCTGCAGGCATCCAAAAG
CAATCTTATATCTGGCTCAGTAATGTACATCGAGGAGAAAACAAAGACCAAGTACACAGGAAA
TCCAACAAAGATGTATGAAGTGGTCTACCAAATTGGAAGTGAAGTTCGTTTCAGACTTCTATGA
CATCGTCTTGGTGGCCACTCCGTTGAATCGAAAAATGTCGAATATTACTTTTCTCAACTTTGA
TCCTCCAATTGAGGAATTCCATCAATATTATCAACATATAGTGACAACCTTTAGTTAAGGGGA
ATTGAATACATCTATCTTTAGCTCTAGACCCATAGATAAATTTGGCCTTAATACAGTTTTAAC
CACTGATAATTCAGATTTGTTTCATTAAACAGTATTGGGATTGTGCCCTCTGTGAGAGAAAAGGA
AGATCCTGAGCCATCAACAGATGGAACATATGTTTGGAAGATCTTTTCCCAAGAACTCTTAC
TAAAGCACAAATTTTAAAGCTCTTTCTGTCTATGATTATGCTGTGAAGAAGCCATGGCTTGC
ATATCCTCACTATAAGCCCCGGAGAAATGCCCTCTATCATTCTCCATGATCGACTTTATTA
CCTCAATGGCATAGAGTGTGCAGCAAGTGCCATGGAGATGAGTGCCATTGCAGCCACAACGC
TGCACTCCTTGCCATCACCGCTGGAACGGGCACACAGACATGATTGATCAGGATGGCTTATA
TGAGAACTTAAACTGAAGT**TGA**AGTGACACACTCCTTTTTCCCTCCTAGTTCCAAATGA
CTATCAGTGGCAAAAAAGAACAAAATCTGAGCAGAGATGATTTTGAACCAGATATTTTGCCAT
TATCATTGTTTAATAAAAGTAATCCCTGCTGGTCATAGGAAAAAAAAAAAAA

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FIGURE 450

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62880
<subunit 1 of 1, 505 aa, 1 stop
<MW: 56640, pI: 6.10, NX(S/T): 4
MGRVVAELVSSLLGLWLLLCSCGCPEGAELRAPDPKIAIIGAGIGGTSAAYYLRQKFGKDVKI
DLFEREEVGGRLATMMVQGQYEAGGSVIHPLNLHMKRFVKDLGLSAVQASGGLLGIYNGETL
VFEESNWFIIINVIKLVWRYGFQSLRMHMMWVEDVLDKFMRIYRYQSHDYAFSSVEKLLHALGGD
DFLGMLNRTLLETLOKAGFSEKFLNEMIAFVMRVNYGQSTDINAFVGAVSLSCSDSGLWAVEG
GNKLVCSEGLLQASKSNLISGSVMYIEEKTCTKYTGNP TKMYEVVYQIGTETRSDFYDIVLVAT
PLNRKMSNITFLNFDPPIEEFHQYYQHIVTTLVKGELNTSIFSSRPIDKFG LNTVLT TDNSDL
FINSIGIVPSVREKEDPEPSTDGTYVWKIFSQETLTKAQILKLFLSYDYAVKKPWLAYPHYKP
PEKCPSIILHDLRYLLNGIECAASAMEMSAIAAHNAALLAYHRWNGHTDMIDQDGLYEKLKTEL
```

Important features:**Signal peptide:**

amino acids 1-23

N-glycosylation sites.

amino acids 196-200, 323-327, 353-357

Tyrosine kinase phosphorylation site.

amino acids 291-298

N-myristoylation sites.amino acids 23-29, 41-47, 43-49, 45-51, 46-52, 72-78, 115-121,
119-125, 260-266, 384-390, 459-465**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 12-23, 232-243

FIGURE 451

[illegible]

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FIGURE 452

MASYLYGVLEFAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDEAFRLYRRLVLET
PSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIHQGFQHLVHSLTVPSK
DLTLKMGSALFVKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQGVVD
IIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAFGVDT
ELNCFVLQMDYKGDVAFFVLPSKGMROLEQALSARTLIKWSHSLQKRWIEVFIPRFSISAS
YNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTTKFIVRS
KDGPSYFTVSFNRTFLMMITNKATDGILFLGKVENPTKS

Signal peptide:
amino acids 1-20

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FIGURE 453

CTCCGGGTCCCCAGGGGCTGCGCCGGGCCGGCCTGGCAAGGGGGACGAGTCAGTGGACACTCCAGGAAGAGCGGC
CCCCGGGGGGGCGATGACCGTGCGCTGACCCTGACTCACTCCAGGTCCGGAGGCGGGGGCCCCGGGGCGACTCG
GGGGCGGACCGCGGGGGCGGAGCTGCCGCCCGTGAGTCCGGCCGAGCCACCTGAGCCCCGAGCCGCGGGACACCGTC
GCTCCTGCTCTCCGAATGCTGCGCACCGCGATGGGCCTGAGGAGCTGGCTCGCCGCCCATGGGGCGCGCTGCCG
CCTCGGCCACCGCTGCTGCTGCTCCTGCTGCTGCTGCTCCTGCTGCAGCCGCCGCTCCGACCTGGGCGCTCAGC
CCCCGGATCAGCCTGCCCTCTGGGCTCTGAAGAGCGGCCATTCCTCAGATTGGAAGCTGAACACATCTCCAACCTAC
ACAGCCCTTCTGCTGAGCAGGGATGGCAGGACCCTGTACGTGGGTGCTCGAGAGGCCCTCTTTGCACTCAGTAGC
AACCTCAGCTTCTGCCAGGCGGGGAGTACCAGGAGCTGCTTTGGGGTGCAGACGCAGAGAAGAAACAGCAGTGC
AGCTTCAAGGGCAAGGACCCACAGCGGAGCTGTCAAACCTACATCAAGATCCTCCTGCCGCTCAGCGGCAGTCAC
CTGTTACCTGTGGCACAGCAGCCTTCAGCCCCATGTGTACCTACATCAACATGGAGAATTCACCTTGGCAAGG
GACGAGAAGGGGAATGTCTCCTGGAAGATGGCAAGGGCCGTTGTCCCTTCGACCCGAATTTCAAGTCCACTGCC
CTGGTGGTTGATGGCGAGCTCTACACTGGAACAGTCAGCAGCTTCCAAGGGAATGACCCGGCCATCTCGCGGAGC
CAAAGCCTTCGCCCCACCAAGACCGAGAGCTCCCTCAACTGGCTGCAAGACCCAGCTTTTGTGGCCTCAGCCTAC
ATTCTGAGAGCCTGGGCGAGCTGCAAGGCGATGATGACAAGATCTACTTTTCTTCAGCGAGACTGGCCAGGAA
TTTGAGTTCTTTGAGAACACCATTGTGTCCCGCATTGCCCGCATCTGCAAGGGCGATGAGGGTGGAGAGCGGGTG
CTACAGCAGCGCTGGACCTCCTTCCCTCAAGGCCAGCTGCTGTGCTCACGGCCGACGATGGCTTCCCCTTCAAC
GTGCTGCAGGATGTCTTACGCTGAGCCCCAGCCCCAGGACTGGCGTGACACCCTTTTCTATGGGGTCTTCACT
TCCCAGTGGCACAGGGGAACCTACAGAAGGCTCTGCGCTCTGTGCTTCAATGAAGGATGTGCAGAGAGTCTTC
AGCGGCTCTACAAGGAGGTGAACCGTGAGACACAGCAGTGGTACACCGTGACCCACCCGGTGCCACACCCCGG
CCTGGAGCGTGATCACCACAGTGCCCCGGAAAGGAAGATCAACTCATCCCTGCAGCTCCAGACCCGCTGCTG
AACTTCTCAAGGACCACTTCTGATGGACGGGCGAGTCCGAAGCCGATGCTGCTGCTGCAGCCCCAGGCTCGC
TACCAGCGCGTGGCTGTACACCGCTCCCTGGCCTGCACCACACCTACGATGTCTCTTCTTGGGCACTGGTGAC
GGCCGGCTCCACAAGGCAGTGAGCGTGGGCCCCCGGGTGACATCATTTGAGGAGCTGCAGATCTTCTCATCGGGA
CAGCCCGTGAGAACTCTGCTCCTGGACCCACAGGGGGCTGCTGTATGCGGCCCTCACACTCGGGCGTAGTCCAG
GTGCCATGGCCAACCTGCAGCCTGTACCGGAGCTGTGGGGACTGCCTCCTCGCCCCGGGACCCCTACTGTGCTTGG
AGCGGCTCCAGCTGCAAGCAGCTCAGCCTCTACCAGCCTCAGCTGGCCACCAGGCGGTGGATCCAGGACATCGAG
GGAGCCAGCGCAAGGACCTTTCAGCGCGTCTTCGGTTGTGTCCCCGTCTTTTGTACCAACAGGGGAGAAGCCA
TGTGAGCAAGTCCAGTTCAGCCCCACACAGTGAACACTTTGGCCTGCCCGCTCCTCTCCAACCTGGCGACCCGA
CTCTGGCTACGCAACGGGGCCCCCGTCAATGCCTCGGCCTCCTGCCACGTGCTACCCACTGGGGACCTGCTGCTG
TGCGGACACCAACAGCTGGGGGAGTTCCAGTGCTGGTCACTAGAGGAGGGCTTCCAGCAGTGGTAGCCAGCTAC
TGCCCCAGAGGTGGTGGAGACGGGGTGGCAGACCAACAGATGAGGGTGGCAGTGTACCCGTCAATTATCAGCACA
TCGCGTGTGAGTGACACAGCTGGTGGCAAGGCCAGCTGGGGTGCAGACAGGTCTACTGGAAGGAGTTCTGGTG
ATGTGCACGCTCTTTGTGCTGGCCGTGCTGCTCCAGTTTTATTTCTGCTCTACCGGCACCGGAACAGCATGAAA
GTCTTCTGAAGCAGGGGGAATGTGCCAGCGTGACCCCAAGACCTGCCCTGTGGTGCTGCCCCCTGAGACCCGC
CCACTCAACGGCCTAGGGCCCCCTAGCACCCCGCTCGATCACCGAGGGTACCAGTCCCTGTGAGACAGCCCCCG
GGGGCCCCGAGTCTTCACTGAGTCAGAGAAGAGGCCACTCAGCATCCAAGACAGCTTCGTGGAGGTATCCCCAGTG
TGCCCCCGGGCCCCGGTCCGCCTTGGCTCGGAGATCCGTGACTCTGTGGTGAGAGCTGACTTCCAGAGGACGC
TGCCCTGGCTTCAGGGGCTGTGAATGCTCGGAGAGGGTCAACTGGACCTCCCTCCGCTCTGCTCTTCTGGAAC
ACGACCGTGGTGCCCGGCCCTTGGGAGCCTTGGAGCCAGCTGGCCTGCTGCTCTCCAGTCAAGTAGCGAAGCTCC
TACCACCCAGACACCCAAACAGCCGTGGCCCCAGAGGTCTGGCCAAATATGGGGGCTGCCTAGGTGGTGGA
CAGTGCTCCTTATGTAACTGAGCCCTTTGTTTAAAAACAATTCCAAATGTGAACTAGAAATGAGAGGGAAGAG
ATAGCATGGCATGCAGCACACAGGCTGCTCCAGTTTATGGCCTCCAGGGGTGCTGGGGATGCATCCAAAGTGG
TTGTCTGAGACAGAGTTGGAAACCTCACCAACTGGCCTCTTACCTTCCACATTATCCCGTGCCACCGGCTGC
CCTGTCTCACTGCAGATTACAGGACAGCTTGGGCTGCGTGCGTTCTGCCTTGCCAGTCAGCCGAGGATGTAGTTG
TTGCTGCCGTGCTCCACCACCTCAGGGACAGAGGGCTAGGTTGGCACTGCGGCCCTCACCAGTCTTGGGCTC
GGACCCAACTCCTGGACCTTTCAGCCTGTATCAGGCTGTGGCCACACGAGAGGACAGCGCGAGCTCAGGAGAGA
TTTCGTGACAATGTACGCCTTTCCCTCAGAATTCAGGGAAGAGACTGTGCGCTGCCTTCTCCTCGTTGTTGCGTGA
GAACCCGTGTGCCCTTCCACCATATCCACCTCGCTCCATCTTTGAACTCAAACACGAGGAACCTAAGTGCACC
CTGGCTCTCCCGAGTCCCGAGTTCACCTCCATCCCTCAGCTTCCCTCCACTTAAGGGATATCAACACTGCCC
AGCACAGGGGCCCTGAATTTATGTGGTTTTTATACATTTTTTAATAAGATGCACCTTATGTCAATTTTTTAATAAA
GTCTGAAGAATTACTGTTTAAAAA

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FIGURE 454

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLLLLLQPPPPTWALSPRISLPLGSEERPFLRFE
AEHISNYTALLLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEKKQQCSFKGKD
PQRDCQNYIKILLPLSGSHLFTCGTAAFSMCTYINMENFTLARDEKGNVLLEDGKGRCPFDP
NEKSTALVVDGELYTGTVSSFQGNPAISRSQSLRPTKTESSLNWLQDPAFVASAYIPESLGS
LQGDDDKIYFFFSETGQEFEEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLCSPDD
GFPFNVLQDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTEGSAVCVFTMKDVQRVFSGLYKEVN
RETQQWYTVTHPVPTPRPGACITNSARERKINSSLQLPDRVLNFKDHFLMDGQVRSRMLLLQ
PQARYQRVAVHRVPGLHHTYDVLFLGTGDGRLHKAVSVGPRVHIIIEELQIFSSGQPVQNLLLD
THRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSLYQPQLATRPWIQ
DIEGASAKDLCASASSVSPSFVPTGEKPCQVQFQPNVTNLTACPLLSNLATRLWLRNGAPVN
ASASCHVLPTGDLLLVTQQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQTDEGGSPVPII
STSRVSAPAGGKASWGADRSYKFEFLVMCTLFVLAVLLPVLFLLYRHRNSMKVFLKQGECAV
HPKTCPVVLPPEPTRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTSEKRPLSIQDSFVEVSP
VCPRPRVRLGSEIRDSV
```

Transmembrane domains:

amino acids 23-46 (type II), 718-738

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FIGURE 455

TAAGATGAGGGCATCCCTCACGTTACACCCCCTGGTGGCATCTGCCAGCCCTGTTCTGGGGAC
AAGGCGGGCTTTTCGTGGGAGCCATGCTCAGCCTGCCAGGAAGCCAAGCCCTACAGTGCAGAGG
AAACAGAATTTCAACGGGAAGCTGGTTTGCTTCATACCATTGGGATCTGCTGGTAAAGCTGTT
ATTTGGGTTTAGGGACTGATCCCTTGACGTTTACTTCTGGATCACCATGAATGGCCAAGATGG
TGGCAGAACACGCTGTGGACCCCTGAGTTAGAGACAATGCAAATGTTGGATTGGGTGTAATTCT
TTTTGAATCCCAGATCCAGTCTGTACTTGAATATGAGCAGAAGATCTACAAGAATGCTGACAG
GGAACCGTGTTAAGACCCAGCACCCCTATTCCCAGGAGCTTCTGGCCTGACCATCTGCAGCCA
AAGCACTAACAGGGACAGATATGGGAATGTCCACCTTTGATCCGCATCCTGCACAATAGTGGT
CCCACCATGGCTGCCACTTTTTTATACTATTTGGAGAAAAGACCTTGTATAAATTCGAGGCCC
GAGTGAATAACGTCTCTGTACACCGGAAATGGGTACTTGGTGGCATAGAGAAACACAATTAGC
CACTTTTTTCAGCTACACTTCTCACTCAGCTGCACCCCTACACTTCTCACTCAGGTGCACCCCT
TCTGCTGTCTTTTCCCAACGTACTGGGTCCCAGCGTGGTGGGTATTTGCCACACTGGGTGC
CAGCTCAGCAGCCCCCCTCTCTTTATTCTCTCCAAAGCTGGTCTTTCTGACTATCATTGT
GGTAGGGGGAGGACAGATGCTAAAGGTGGAAGCTGACCTGGAGAAAGAGACACACGGGGTGAC
TGTGGCAAAGGACAGCTGGAAAAGAACTCTATCACTTCTTCATTGGCAACCACAAGGCACCC
GAGGCCATGGCACTCCCAGAGGCTGTGCGCAGAGCCAAGCCTCTCAACCTCTTCTGGCCCTGC
GTCCTGCAGCGAAGTCTCTGCTGTAAGACAGTAGACTCCTTCGATGAGGTGCTCAAAAATGCT
ACCCGGGGTGGTGGTGTCTGGCTTGCAGTCTGGCCAGTTCAGAGAAAGTTGCAGAGATCAGGG
GCCAAGGATGTCATAGCCCCAGGTTGTCTCAGGGTCCAATCCTAGGGCAGGGTGTGCATGG
AAGCAAGAACTATGGAAACCTAGCTCCAGTCTGCAGGCTCTGAGCCCCCTAGTTCTCTCACTCCA
GCGGGGCTCCCTCACTGCACAGAACCCACCCCTTCTGTGTGGGCACTGCTGACCACACAGATG
ACCCAGACCCAAAGAGCCTGGCAGAAGCTCTGTGGTTGGAGCTGGGCTCCGTCTCCAGGTCTG
GTTCAGGGGGATCAGGAAGGCTCTTTTCCACCTGTGGCTTCACTGGCCCTTTGAGATTTCTTA
TCTCACCGTTACTTCAGTTACCCTTGCAGGGGGCCAGGGAGTCAAGAATATACCGTGTTCCTC
CAGGGTTTAAGCCGGCCATGCCTTCCCCGAGAGCATAACCAACTTGACAGGGGTGCCAGTTAC
CCCACAACTGAAGGAAGGAGATCCTTCCCCCGTCCCAGGAGTGCTCTCAACCAGCCTCAGA
AAGCTTGAGAAGATGGACCCTTTGCCCACCAGGGTTAATTCTTGGTGGGGCAGCTCGGCTGTG
ATCAGGGCAACCAAACCTATAGGAAGCCTTCCAGTGTGAGCTGGAATTAGACTGAACATGTGC
TTGGGCCTGCCTCTCCCTAGACGCAGTTGCGGGGCACTCCAGGGAATGAACCAGCTCAAGTGT
GTCCCTAACAGCAGCCTGGAGCTACCCCCAATCCCTCACAGCCTGACCCTCTCATTCCATCA
GATCTCGTGCCG

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FIGURE 456

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA69555
><subunit 1 of 1, 148 aa, 1 stop
><MW: 16214, pI: 10.22, NX(S/T): 0

MGTWWHRETQLATFSATLLTQLHPTLLTQVHPLLLSFPQRTGSRAWVVFATLGASSAAPH
LSLFSPKLVFLTIIVVGGQMLKVEADLEKETHGVTVAKDSWKRNSITSSLATTRHPRPW
HSQRLCAEPSLSTSSGPASCSEVSAVRQ

Important features of the protein:**Signal peptide:**

Amino acids 1-28

Transmembrane domain:

Amino acids 64-78

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 103-107

N-myristoylation sites:

Amino acids 53-59;94-100

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FIGURE 457

CCCGCGCGCCCCTGGCACTCAATCCCCGCC**ATG**TGGGGGCTCCTGCTCGCCCTGGCCGCCTTC
GCGCCGCGCGTCCGCCCCGGCTCTGGGGGCGCCCAGGAACTCGGTGCTGGGCCTCGCGCAGCCC
GGGACCACCAAGGTCCCAGGCTCGACCCCGGCCCTGCATAGCAGCCCGGCACAGCCGCCGGCG
GAGACAGCTAACGGGACCTCAGAACAGCATGTCCGGATTTCGAGTCATCAAGAAGAAAAAGGTC
ATTATGAAGAAGCGGAAGAAGCTAACTCTAACTCGCCCCACCCACTGGTGACTGCCGGGCCC
CTTGTGACCCCCACTCCAGCAGGGACCCCTCGACCCCGCTGAGAAACAAGAAACAGGCTGTCTT
CCTTTGGGTCTGGAGTCCCTGCGAGTTTCAGATAGCCGGCTTGAGGCATCCAGCAGCCAGTCC
TTTGGTCTTGAGCACACCGAGGACGGCTCAACATTCATTTCAGGCCTGGAGGACGGCGATCTA
TATGATGGAGCCTGGTGTGCTGAGGAGCAGGACGCCGATCCATGGTTTCAGGTGGACGCTGGG
CACCCACCCGCTTCTCGGGTGTTATCACACAGGGCAGGAACTCTGTCTGGAGGTATGACTGG
GTCACATCATAACAAGGTCCAGTTCAGCAATGACAGTCGGACCTGGTGGGGAAGTAGGAACCAC
AGCAGTGGGATGGACGCAGTATTTCTGCCAATTCAGACCCAGAACTCCAGTGCTGAACCTC
CTGCCGGAGCCCCAGGTGGCCCGCTTCATTCGCCTGCTGCCCCAGACCTGGCTCCAGGGAGGC
GCGCCTTGCTCCGGGCAGAGATCCTGGCCTGCCAGTCTCAGACCCCAATGACCTATTCTCTT
GAGGCCCTGCGTCGGGATCCTCTGACCCTCTAGACTTTTCAGCATCACAATTACAAGGCCATG
AGGAAGCTGATGAAGCAGGTACAAGAGCAATGCCCCAACATCACCCGCATCTACAGCATTGGG
AAGAGCTACCAGGGCCTGAAGCTGTATGTGATGGAAATGTGCGACAAGCCTGGGGAGCATGAG
CTGGGGGAGCCTGAGGTGCGCTACGTGGCTGGCATGCATGGGAACGAGGCCCTGGGGCGGGAG
TTGCTTCTGCTCCTGATGCAGTTCCTGTGCCATGAGTTCCTGCGAGGGAACCCACGGGTGACC
CGGCTGCTCTCTGAGATGCGCATTACCTGCTGCCCTCCATGAACCCTGATGGCTATGAGATC
GCCTACCACCGGGGTTTCAGAGCTGGTGGGCTGGGCCGAGGGCCGCTGGAACAACCAGAGCATC
GATCTTAACCATAATTTTGCTGACCTCAACACACCACTGTGGGAAGCACAGGACGATGGGAAG
GTGCCCCACATCGTCCCCAACCATCACCTGCCATTGCCCACTTACTACACCCTGCCCAATGCC
ACCGTGGCTCCTGAAACGCGGGCAGTAATCAAGTGGATGAAGCGGATCCCCCTTTGTGCTAAGT
GCCAACCTCCACGGGGGTGAGCTCGTGGTGTCTTACCCATTTCGACATGACTCGCACCCCGTGG
GCTGCCCCGCGAGCTCACGCCCCACACAGATGATGCTGTGTTTCGCTGGCTCAGCACTGTCTAT
GCTGGCAGTAATCTGGCCATGCAGGACACCAGCCGCCGACCCTGCCACAGCCAGGACTTCTCC
GTGCACGGCAACATCATCAACGGGGCTGACTGGCACACGGTCCCCGGGAGCATGAATGACTTC
AGCTACCTACACACCAACTGCTTTGAGGTCAGTGTGGAGCTGTCTGTGACAAGTTCCCTCAC
GAGAATGAATTGCCCCAGGAGTGGGAGAACAACAAAGACGCCCTCCTCACCTACCTGGAGCAG
GTGCGCATGGGCATTGCAGGAGTGGTGGGGACAAGGACACGGAGCTTGGGATTGCTGACGCT
GTCATTGCCGTGGATGGGATTAACCATGACGTGACCACGGCGTGGGGCGGGGATTATTGGCGT
CTGCTGACCCCAGGGGACTACATGGTGAAGTGGCAGTGGCGAGGGCTACCATTTCAGTGACACGG
AACTGTGCGGGTCACCTTTGAAGAGGGCCCCCTTCCCCCTGCAATTTTCGTGCTCACCAAGACTCCC
AAACAGAGGCTGCGCGAGCTGCTGGCAGCTGGGGCCAAGGTGCCCCCGGACCTTCGCAGGCGC
CTGGAGCGGCTAAGGGGACAGAAGGAT**TGA**TACCTGCGGTTTAAGAGCCCTAGGGCAGGCTGG
ACCTGTCAAGACGGGAAGGGGAAGAGTAGAGAGGGAGGGACAAAGTGAGGAAAAGGTGCTCAT
TAAAGCTACCGGGCACCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 458

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71162
><subunit 1 of 1, 734 aa, 1 stop
><MW: 81677, pI: 6.60; 'NX(S/T)': 6
MWGLLLALAAFAVGPALGAPRNSVLGLAQPGETTKVPGSTPALHSSPAQPPAETANGTS
EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL
ESLRVSDSRLEASSSSQSFGLGPHRGRLNIHSGLEDGDLYDGAWCAEEQDADPWFQVDAGH
PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL
NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH
NYKAMRKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH
GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAYHRGSELVG
WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYTLPNATVAPETR
AVIKWMKRIPFVLSANLHGGELVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSN
LAMQDTSRRPCHSQDFSVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE
NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTELGIADAVIAVDGINHDVTTAWGGDY
WRLLTTPGDYMTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPP
DLRRRLERLRGQKD
```

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FIGURE 459

TAAAACAGCTACAATATTCCAGGGCCAGTCACTTGCCATTTCTCATAACAGCGTCAGAGAGAA
AGAACTGACTGAAACGTTTGAGATGAAAGAAAGTTCTCCTCCTGATCACAGCCATCTTGGCAGT
GGCTGTTGGTTTCCCAGTCTCTCAAGACCAGGAACGAGAAAAAAGAAGTATCAGTGACAGCGA
TGAATTAGCTTCAGGGTTTTTTGTGTTCCCTTACCCATATCCATTTGCCCCACTTCCACCAAT
TCCATTTCCAAGATTTCCATGGTTTAGACGTAATTTTCCCTATTCCAATACCTGAATCTGCCCC
TACAACTCCCCTTCCTAGCGAAAAGTAAACAAGAAGGATAAGTCACGATAAACCTGGTCACCT
GAAATTGAAATTGAGCCACTTCCTTGAAGAATCAAAATTCCTGTTAATAAAAGAAAAACAAAT
GTAATTGAAATAGCACACAGCATTCTCTAGTCAATATCTTTAGTGATCTTCTTTAATAAACAT
GAAAGCAAAGATTTTGGTTTCTTAATTTCCACA

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FIGURE 460

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71290
><subunit 1 of 1, 85 aa, 1 stop
><MW: 9700, pI: 9.55, NX(S/T): 0
MKKVLLLLITAILAVAVGFPVSQDQEREKRSISDSDELASGFFVFPYPYPFRPLPPIPFPRFPW
FRRNFPIPIPIESAPTTPLPSEK
```

Important features of the protein:**Signal peptide:**

amino acids 1-17

Homologous region to B3-hordein:

amino acids 47-85

Important features of the protein:**Signal peptide:**

Amino acids 1-20

N-glycosylation sites:

Amino acids 57-61;210-214;220-224;318-322;428-432;472-476

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 80-84

N-myristoylation sites:Amino acids 3-9;20-29;39-48;152-161;161-170;262-271;358-364;
538-544;560-566;637-643**Zinc carboxypeptidases, zinc-binding region 2 signature:**

Amino acids 498-509

Zinc carboxypeptidases:

Amino acids 391-411

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FIGURE 461

AGCAGGAGCAGGAGAGGGACAA**ATG**GAAAGCTGCCCCGTCCAGGTTTCATGTTCTCTTATTTCTC
CTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCCTGGT
GCTGCCCAGGAACCCACGTGGCTCACAGATGTCCAGCTGCCATGGAATTCATTGCTGCCACT
GAGGTGGCTGTCATAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCCATACTCCATAGC
ATGGTGCAAAAATTCCCAGGCGTGTCATTTGGGATCAGCACTGATTCTGAGGTTCTGACACAC
TACAACATCACTGGGAACACCATCTGCCTCTTTCGCCTGGTAGACAATGAACAACCTGAATTTA
GAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCATTGAGATCAACAGC
CTCCACATGGTGACAGAGTACAACCCCTGTGACTGTGATTGGGTTATTCAACAGCGTAATTCAG
ATTCATCTCCTCCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATGCACAGATAC
CAGAAGGCAGCCAAGCTCTTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAGTGGTATGAAA
GAAAATGGGAAGGTGATATCATTTTTCAAACCTAAAGGAGTCTCAACTGCCAGCTTTGGCAATT
TACCAGACTCTAGATGACGAGTGGGATACACTGCCCACAGCAGAAGTTTCCGTAGAGCATGTG
CAAACTTTTGTGATGGATTCCCTAAGTGGAAAATTGTTGAAAGAAAATCGTGAATCAGAAGGA
AAGACTCCAAAGGTGGAAC**CTGA**CTTCTCCTTGGAACCTACATATGGCCAAGTATCTACTTTA
TGCAAAGTAAAAAGGCACAACCTCAAATCTCAGAGACACTAAACAACAGGATCACTAGGCCTGC
CAACCACACACACACGCACGTGCACACACGCACGCACGCGTGCACACACACACGCGCACACAC
ACACACACACAGAGCTTCATTTCTGTCTTAAATCTCGTTTTCTCTTCTTCTTCTTTTAA
TTTCATATCCTCACTCCCTATCCAATTTCTTCTTATCGTGCATTCATACTCTGTAAGCCCAT
CTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATGCCTCTATGAAAGAGAGGCA
TTCCTAGAGAAAGATTGTTCCAATTTGTCAATTTAATATCAAGTTTGTATACTGCACATGACTT
ACACACAACATAGTTCCTGCTCTTTAAGGTTACCTAAGGGTTGAAACTCTACCTTCTTTCAT
AAGCACATGTCCGTCTCTGACTCAGGATCAAAAACCAAAGGATGGTTTTAAACACCTTTGTGA
AATTGTCTTTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTCCCTGAACTCAGCAGAAATAGACC
ATGTGAAAACCTCATGCTTGGTTAGCATCTCCAACCTCCCTATGTAAATCAACAACCTGCATAA
TAAATAAAAGGCAATCATGTTATA

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FIGURE 462

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401
><subunit 1 of 1, 273 aa, 1 stop
><MW: 30480, pI: 4.60, NX(S/T): 1
MEAAPSRFMFLFLLTCELAEEVAAEVEKSSDGPAAQEPTWLTDVPAAMEFIAATEVAVIGF
FQDLEIPAVPILHSMVQKFPGVSEFGISTDSEVLTHYNITGNTICLFRLLVDNEQLNLEDEDIES
IDATKLSRFIEINSLHMTYNPVTVIGLFNSVIQIHLLIMNKASPEYEENMHRYQKAAKLF
QGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDWDTLPTAEVSVEHVQNFCDGF
LSGKLLKENRESEGKTPKVEL
```

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 143-162

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FIGURE 463

CTCGCTTCTTCCTTCTGGATGGGGGGCCAGGGGGCCAGGAGAGTATAAAGGCGATGTGGAGG
GTGCCCCGGCACAACCAGACGCCCAGTCACAGGCGAGAGCCCTGGG**ATG**CACCGGCCAGAGGCC
ATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTATGGC
CCTGGAGGAGGCAAGTATTTTCAGCACCACTGAAGACTACGACCATGAAATCACAGGGCTGCGG
GTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCCAGGTGAACTTGGAGACTCCTGGGACGTG
AAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCCTGCAGCCAGGCGAATACATCACA
AAAGTCTTTGTCGCCTTCCAAGCTTTCCCTCCGGGGTATGGTCATGTACACCAGCAAGGACCGC
TATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCAGCCAAGAGGGGCAG
GTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGCTTTGAATGG
AATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTCAGCAAACCTCA
CCCGTGGGTGCGT**TAG**GGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGTGTGGTGGTGGC
TGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATAAATAAAGCTTCT
GCAGAAAA

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FIGURE 464

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSQVVKL
GDSWDVKLGALGGNTQEVTLQPGYITKVVFVAFQAFLRGMVMTSKDRYFYFGKLDGQISSAY
PSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR
```

Signal peptide:
amino acids 1-22

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FIGURE 465

CGGACGCGTGGGTCCGGCGGCCTGAGGCTGCACCGGGACGCGGTGGCCGCAATCCAGCCTGGGCGGAGCCGGAG
TTGCGAGCCGCTGCCTAGAGCCGAGGAGCTCACAGCTATGGGCTGGAGCCCCGGAGAGCTCGGGGGACCCCGT
TGCTGCTGCTGCTACTACTGCTGCTGCTCTGGCCAGTGCCAGGCGCCGGGGTGCTTCAAGGACATATCCCTGGGC
AGCCAGTCACCCCGCACTGGGTCTGGATGGACAACCCTGGCGCACCGTCAGCCTGGAGGAGCCGGTCTCGAAGC
CAGACATGGGGCTGGTGGCCCTGGAGGCTGAAGGCCAGGAGCTCTGCTTGAGCTGGAGAAGAACCACAGGCTGC
TGGCCCCAGGATACATAGAAAACCCACTACGGCCCCAGATGGGCAGCCAGTGGTGCTGGCCCCAACCACACGGATC
ATTGCCACTACCAAGGGCGAGTAAGGGGCTTCCCCGACTCCTGGGTAGTCTCTGCACCTGCTCTGGGATGAGTG
GCCTGATCACCCCTCAGCAGGAATGCCAGCTATTATCTGCGTCCCTGGCCACCCCGGGGCTCCAAGGACTTCTCAA
CCCACGAGATCTTTTCGGATGGAGCAGCTGCTCACCTGGAAGGAACCTGTGGCCACAGGGATCCTGGGAACAAAG
CGGGCATGACCAGCCTTCTTGGTGGTCCCCAGAGCAGGGGCGAGGCGAGAAGCGCGCAGGACCCGGAAGTACCTGG
AACTGTACATTGTGGCAGACCACACCCTGTCTTGAATCGGCACCGAACTTGAACCACACCAACAGCGTCTCC
TGGAAAGTCGCCAACTACGTGGACAGCTTCTCAGGACTCTGGACATTCAAGTGCGGCTGACCGGCCCTGGAGGTGT
GGACCGAGCGGGACCGCAGCCGCGTCACGCAGGACGCCAACGCCACGCTCTGGGCTTCTGTCAGTGGCGCCGGG
GGCTGTGGGCGCAGCGGCCCCACGACTCCGCGCAGCTGCTCACGGGCGCGCCTTCCAGGGCGCCACAGTGGGCC
TGGCGCCCGTCGAGGGCATGTGCCGCGCCGAGAGCTCGGGAGGCGTGAGCACGGACCACTCGGAGCTCCCATCG
GCGCCGACGCCACCATGGCCCATGAGATCGGCCACAGCCTCGGCCTCAGCCACGACCCCGACGGCTGCTGCGTGG
AGGCTGCGGCGGAGTCCGGAGGCTGCGTCATGGCTGCGGCCACCGGGCACCCGTTTCCGCGCGTGTTCAGCGCCT
GCAGCCGCGCCAGCTGCGCGCCTTCTTCCGCAAGGGGGGCGGCGCTTGCCCTCTCCAATGCCCGGACCCCGGAC
TCCCGGTGCCGCGCGCGCTCTGCGGGAACGGCTTCGTGGAAGCGGGCGAGGAGTGTGACTGCGGCCCTGGCCAGG
AGTGCCGCGACCTCTGCTGCTTGTCTCACAAGTCTGCTGCGCCCGGGGGCCAGTGCGCCACGGGGACTGCT
GCGTGCGCTGCTGCTGAAGCCGGCTGGAGCGCTGTGCCGCCAGGCCATGGGTGACTGTGACCTCCCTGAGTTTT
GCACGGGCACCTCCTCCCACTGTCCCCAGACGTTTACCTACTGGACGGCTCACCCCTGTGCCAGGGGCGAGTGGCT
ACTGCTGGGATGGCGCATGTCCACGCTGGAGCAGCAGTGCCAGCAGCTCTGGGGGCTGGCTCCCACCCAGCTC
CCGAGGCTGTGTTCCAGGTGGTGAACCTCTGCGGAGATGCTCATGGAACTGCGGCCAGGACAGCGAGGGCCACT
TCCTGCCCTGTGTCAGGGAGGGATGCCCTGTGTGGGAAGCTGCAGTGCCAGGGTGGAAAGCCAGCCTGCTCGCAC
CGCACATGGTGCCAGTGGACTCTACCGTTACCTAGATGGCCAGGAAGTGAATGTGCGGGGAGCCTTGGCACTCC
CCAGTGCCAGCTGGACCTGCTTGGCCTGGGCTGGTAGAGCCAGGCACCCAGTGTGGACCTAGAATGGTGTGCC
AGAGCAGGCGCTGCAGGAAGATGCCCTTCCAGGAGCTTCAGCGCTGCCTGACTGCCTGCCACAGCCACGGGGTTT
GCAATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGGCTCCACCCTTCTGTGACAAGCCAGGCTTTGGTGGCA
GCATGGACAGTGGCCCTGTGACGGCTGAAAACCATGACACCTTCTGCTGGCCATGCTCCTCAGCGTCTGCTGCTGC
CTCTGCTCCAGGGGCGCGCCTGGCCTGGTGTGCTACCGACTCCAGGAGCCCATCTGCAGCGATGCAGTGGG
GCTGCAGAAGGGACCCTGCGTGCAGTGGCCCCAAAGATGGCCACACAGGGACCAACCCCTGGGCGGCGTTCACC
CCATGGAGTTGGGCCCCACAGCCACTGGACAGCCCTGGCCCTGGACCTGAGAACTCTCATGAGCCAGCAGCC
ACCCTGAGAAGCCTCTGCCAGCAGTCTGCGCTGACCCCCAAGCAGATCAAGTCCAGATGCCAAGATCCTGCCTCT
GGTGAAGGTAGCTCCTAAAATGAACAGATTTAAAGACAGGTGGCCACTGACAGCCACTCCAGGAAGTTGAAGTG
CAGGGGCAGAGCCAGTGAATCACCGGACCTCCAGCACCTGCAGGCAGCTTGAAGTTTCTTCCCGAGTGGAGCT
TCGACCCACCCACTCCAGGAACCCAGAGCCACATTAGAAGTTCTGAGGGCTGGAGAACACTGCTTGGGCACACT
CTCCAGCTCAATAAACCATCAGTCCCAGAAGCAAAGGTACACAGCCCTGACCTCCCTCACCAGTGGAGGCTGG
GTAGTGTGGCCATCCAAAAGGGCTCTGTCTGGGAGTCTGGTGTGTCTCTACATGCAATTTCCACGGACCCA
GCTCTGTGGAGGGCATGACTGCTGGCCAGAAGCTAGTGGTCTGGGGCCCTATGGTTCGACTGAGTCCACACTCC
CCTGCAGCCTGGCTGGCCTCTGCAACAAACATAATTTTGGGGACCTTCCTTCTGTTTCTTCCACCCCTGTCTT
CTCCCTAGGTGGTTCCTGAGCCCCACCCCCAATCCAGTGTACACCTGAGGTTCTGGAGCTCAGAATCTGAC
AGCCTCTCCCCATTCTGTGTGTGTCCGGGGGACAGAGGGAACCATTTAAGAAAAGATACCAAAGTAGAAGTCAA
AAGAAAGACATGTTGGCTATAGGCGTGGTGGCTCATGCCTATAATCCCAGCACTTTGGGAAGCCGGGTAGGAGG
ATCACAGAGGCCAGCAGGTCCACACCAGCCTGGGCAACACAGCAAGACACCGCATCTACAGAAAAATTTAAAA
TTAGCTGGGCGTGGTGGTGTACCTGTAGGCCTAGTGTCTCAGGAGGCTGAAGCAGGAGGATCACTTGAGCCTG
AGTTCAACACTGCAGTGAAGTATGGTGGCACCACTGCACTCCAGCCTGGGTGACAGAGCAAGACCCCTGTCTCTAA
AATAAATTTTAAAGGACTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGAAAA

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FIGURE 466

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76788
><subunit 1 of 1, 813 aa, 1 stop
><MW: 87739, pI: 6.94, NX(S/T): 5

MGWRPRRARGTFLLLLLLLLLLLLLWFPVPGAGVLQGHIPGQPVTPHWVLDGQPWRTVSLEEPVSKPDMGLVALEAEGQ
ELLLELEKHNHRLAPGYIETHYGPDGQPVVLAPNHTDHCHYQGRVRFPSWVVLCTCSGMSGSLITLSRNASYLL
RPWPPRGSKDFSTHEIFRMEQLLTWKGTGCHRDPGNKAGMTSLPGGPQSRGRREARRTRKYLELYIVADHTLFLT
RHRNLNHTKQRLLEVANYVDQLRLTDIQVALTGLEVWTERDRSRVTQDANATLWAFLOWRRGLWAQRPHDSAQL
LTGRAFGQATVGLAPVEGMCRAESSGGVSTDHSELPIGAAATMAHEIGHSLGLSHDPDGCCVEAAAESGGCVMAA
ATGHPFPRVFSACSRRLRAFFRKGGGACLSNAPDPGLPVPPALCGNGFVEAGEECDGPGQECDLCCFAHNCS
LRPGAQCAHGDCCVRCLLKPAGALCRQAMGDCDLPEFCTGTSSHCPPDVYLLDGSPCARGSGYCWDGACPTLEQQ
CQQLWGPGSHPAPEACFQVVSAGDAHGNCQDSEGHFLPCAGRDALCGKLQCQGGKPSLLAPHMVPVDSTVHLD
GQEVTCRGALALPSAQLDLLGLGLVEPGTQCGPRMVCQSRRCRKNFQELQRCLTACHSHGVCNSNHNCHCAPGW
APPFCDKPGFGGSMDSGPVQAEHDTFLLAMLLSVLLPLLPGAGLAWCCYRLPGAHLQRCSWGCRDRPACSGPKD
GPHRDHPLGGVHPMELGPTATGQPWPLDPENSHEPSSHPEKPLPAVSPDPQADQVQMPRSLIW

Important features of the protein:**Signal peptide:**

Amino acids 1-27

Transmembrane domain:

Amino acids 702-720

N-glycosylation sites:

Amino acids 109-113;145-149;231-235;276-280;448-452

Tyrosine kinase phosphorylation site:

Amino acids 236-244

N-myristoylation sites:

Amino acids 29-35;185-191;195-201;308-314;318-324;326-332;338-344;370-376;
400-406;402-408;454-460;504-510;510-516;517-523;580-586;
601-607;661-667;687-693;717-723;719-725

Amidation site:

Amino acids 200-204

Neutral zinc metallopeptidases, zinc-binding region signature:

Amino acids 342-352

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FIGURE 467

[illegible]

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FIGURE 468

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77623
><subunit 1 of 1, 97 aa, 1 stop
><MW: 10160, pI: 6.56, NX(S/T): 0
MQLGTGLLLAAVLSLQLAAAEAIWCHQCTGFGGCSHGSRCLRDSTHCVTTATRVLSNTEDLPL
VTKMCHIGCPDIPSLGLGPYYSIACCQTSLCNHD

Important features of the protein:**Signal peptide:**

amino acids 1-20

N-myristoylation sites.

amino acids 6-11 and 33-38

Prokaryotic membrane lipoprotein lipid attachment sites.

amino acids 24-34 and 78-88

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FIGURE 469

CATGGAGCCTCTTGCAGCTTACCCGCTAAAATGTTCCGGGCCCCAGAGCAAAGGTATTTGCAGT
TTTGCTGTCTATAGTTCTATGCACAGTAACGCTATTTCTTCTACAACATAAAATTCCTCAAACC
TAAAATCAACAGCTTTTATGCCTTTGAAGTGAAGGATGCAAAAGGAAGAAGTGTCTCTGGA
AAAGTATAAAGGCAAAGTTTCACTAGTTGTAAACGTGGCCAGTGACTGCCAACTCACAGACAG
AAATTACTTAGGGCTGAAGGAAGTGCACAAAGAGTTTGGACCATCCCACTTCAGCGTGTGGC
TTTTCCCTGCAATCAGTTTGGAGAATCGGAGCCCCGCCCAAGCAAGGAAGTAGAATCTTTTGC
AAGAAAAAAGTACGGAGTAACTTTCCCATCTTCCACAAGATTAAGATTCTAGGATCTGAAGG
AGAACCTGCATTTAGATTTCTTGTGATTCTTCAAAGAAGGAACCAAGGTGGAATTTTGGAA
GTATCTTGTCAACCCCTGAGGGTCAAGTTGTGAAGTTCTGGAGGCCAGAGGAGCCCATTGAAGT
CATCAGGCCTGACATAGCAGCTCTGGTTAGACAAGTGATCATAAAAAAGAAAGAGGATCTAT**GA**
GAATGCCATTGCGTTTCTAATAGAACAGAGAAATGTCTCCATGAGGGTTGGTCTCATTTTA
AACATTTTTTTTTTGGAGACAGTGTCTCACTCTGTCACCCAGGCTGGAGTGCAGTAGTGCCTT
CTCAGCTCATTTGCAACCTCTGCCTTTTTTAAACATGCTATTAAATGTGGCAATGAAGGATTTTT
TTTTAATGTTATCTTGCTATTAAAGTGGTAATGAATGTTCCCAGGATGAGGATGTTACCCAAAG
CAAAAATCAAGAGTAGCCAAAGAATCAACATGAAATATATTAAGTACTTCCCTCTGACCATACT
AAAGAATTCAGAATACACAGTGACCAATGTGCCTCAATATCTTATTGTTCAACTTGACATTTT
CTAGGACTGTACTTGATGAAAATGCCAACACACTAGACCACTCTTTGGATTCAAGAGCACTGT
GTATGACTGAAATTTCTGGAATAACTGTAAATGGTTATGTTAATGGAATAAAACACAAATGTT
GAAAATGTAAATATATATACATAGATTCAAATCCTTATATATGTATGCTTGTTTTGTGTAC
AGGATTTTGTTTTTTCTTTTTAAGTACAGGTTCCCTAGTGTTTTACTATAACTGTCACTATGTA
TGTAAGTACATATATAAATAGTCATTTATAAATGACCGTATTATAACATTTGAAAAAGTCTT
CATCAAAAAAAAAAAAAA

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FIGURE 470

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA80136
><subunit 1 of 1, 209 aa, 1 stop
><MW: 23909, pI: 9.68, NX(S/T): 0
MEPLAAYPLKCSGPRAKVFAVLLSIVLCTVTLFLLQLKFLKPKINSFYAFEVKDAKGRTVSLE
KYKGKVSLLVNVASDCQLTDRNYLGLKELHKEFGPSHFVLAFFPCNQFGESEPRPSKEVESFA
RKNYGVTFPIFHKIKILGSEGEPAFRFLVDSSKKEPRWNFWKYLVNPEGQVVKFWRPEEPIEV
IRPDIAALVRQVIIKKKEDL
```

Important features of the protein:**Signal peptide:**

amino acids 1-31

Glutathione peroxidases signature 2.

amino acids 104-112

Glutathione peroxidases.

amino acids 57-82

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FIGURE 471

GCCCTAACCTTCCAGGGCTCAGCTCTTTGGAGCTGCCATTCTCCGGCTGCGAGAAAGGACGCGCGCCCTGCG
TCGGGCGAAGAAAAGAAGCAAACTTGTCTGGGAGGGTTTCGTCATCAACCTCCTTCCCGCAAACCTAAACCTCCT
GCCGGGGCCATCCCTAGACAGAGGAAAGTTCTGTCAGAGCCGACCAGCCCTAGTGGATCTGGGGCAGGCAGCGGC
GCTGGCTGTGGAATTAGATCTGTTTTGAACCCAGTGGAGCGCATCGCTGGGGCTCGGAAGTCACCGTCCGCGGGC
ACCGGGTTGGCGCTGCCCGAGTGAACCGACAGTTTGGCAGCCTCGGCTGCAAGTGGCCTCTCCTCCCGCGGTT
GTTGTTCACTGTCTGGGTGAGGGCTGCGAGTGTGGCAAGTTGCAAAAGAGAGCCTCAGAGGTCCGAAGAGCGCTGCG
CTCCTACTCGCGTTGCTTCTTCTCTTCTCGGTTCCCTACTGTGAAATCGCAGCGACATTTACAAAGGCCTCCG
GGTCTACCGAGACCGATCCGAGCGTTTGGCCCGGTGCTGCCTATTGCATCGGGAGCCCCGAGCACCGGCGGAA
GGACTGGCGGGTGGGGTAGGGAGGTGGCGGCGGCGGCATGGCGAGGTTCCCGAAGGCCGACCTGGCCGCTGCAGG
AGTTATGTTACTTTGCCACTTCTTCACGGACCAAGTTTTCAGTTTCGCCGATGGGAAACCCGGAGACCAAATCCTTGA
TTGGCAGTATGGAGTTACTCAGGCCTTCCCTCACACAGAGGAGGAGGTGGAAGTTGATTACACGCGTACAGCCA
CAGGTGGAAAAGAACTTGGACTTCTCAAGGCGGTAGACACGAACCGAGCAAGCGTCGGCCAAGACTCTCCTGA
GCCAGAAGCTTACAGACCTGCTGCTGGATGATGGGCAGGACAATAACACTCAGATCGAGGAGGATACAGACCA
CAATTACTATATATCTCGAATATATGGTCCATCTGATTCTGCCAGCCGGGATTTATGGGTGAACATAGACCAAAT
GGAAAAAGATAAAGTGAAGATTTCATGGAATATTGTCCAATACTCATCGCAAGCTGCAAGAGTGAATCTGTCTT
CGATTTTCCATTTTATGGCCACTTCCCTACGTGAAATCACTGTGGCAACCGGGGTTTCATATACACTGGAGAAGT
CGTACATCGAATGCTAACAGCCACACAGTACATAGCACCTTTAATGGCAAATTTTCGATCCCAGTGTATCCAGAAA
TTCAACTGTCTAGATATTTGATAATGGCACAGCACTTGTGGTCCAGTGGGACCATGTACATCTCCAGGATAATTA
TAACCTGGGAAGCTTACATTCCAGGCAACCTGCTCATGGATGGACGAATCATCTTTGGATACAAAGAAATTC
TGTCTTGGTCACACAGATAAGTTCAACCAATCATCCAGTGAAGTTCGGACTGTCCGATGCATTTGTCTGTGCCA
CAGGATCCAACAAATTTCCCAATGTTGGAAGAAGAACAATTTATGAATACCACCGAGTAGAGCTACAAATGTCAAA
AATTACCAACATTTCCGGCTGTGGAGATGACCCCATACCCACATGCCTCCAGTTTAAACAGATGTGGCCCCCTGTGT
ATCTTCTCAGATTGGCTTCAACTGCAGTTGGTGTAGTAACTTCAAAGATGTTCCAGTGGATTTGATCGTCATCG
GCAGGACTGGGTGGACAGTGGATGCCCTGAAGAGTCAAAAGAGAAGATGTGTGAGAATACAGAACCAGTGGAAAC
TTCTTCTCGAACCACCACAACCGTAGGAGCGACAACCACCCAGTTTCAGGGTCCTAACTACCACCAGAAGAGCAGT
GACTTCTCAGTTTCCACCAGCCTCCCTACAGAAGATGATACCAAGATAGCACTACATCTAAAAGATAATGGAGC
TTCTACAGATGACAGTGCAGCTGAGAAGAAAGGGGAACCCCTCCACGCTGGCCTCATCATTGGAATCCTCATCCT
GGTCTCTATTGTAGCCACAGCCATTCTTGTGACAGTCTATATGTATCACCACCCAACATCAGCAGCCAGCATCTT
CTTTATTGAGAGACGCCCCAAGCAGATGGCCTGCGATGAAGTTTAGAAGAGGCTCTGGACATCCTGCCTATGCTGA
AGTTGAACCACTTGGAGAGAAAGAAGGCTTTATTGTATCAGAGCAGTGCTTAAATTTCTAGGACAGAACAAACACC
AGTACTGGTTTACAGGTGTTAAGACTAAAATTTTGCCTATACCTTTAAGACAAACAAACAAACACACACAAAAC
AAGCTCTAAGCTGCTGTAGCCTGAAGAAGACAAGATTTCTGGACAAGCTCAGCCCAGGAAACAAAGGGTAAACAA
AAAACATAAACTTATACAAGATACCATTTACACTGAACATAGAATTCCTAGTGGAAATGTCATCTATAGTTCACT
CGGAACATCTCCCGTGGACTTATCTGAAGTATGACAAGATTATAATGCTTTTGGCTTAGGTGCAGGTTGCAAG
GGATCAGAAAAAAAATCATAATAAAGCTTTAGTTTCATGAGGG

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FIGURE 472

MARFPKADLAAAGVMLLCHFFTDQFQFADGKPGDQILDWQYGVTAQAFPHTEEEVEVD SHAYSH
RWKRNLDFLKAVDTNRASVGQDSPEPRSFTDLLLDDGQDNNTQIEEDTDHNYIISRIYGPSDS
ASRDLWVNIDQMEKDKVKIHGILSNTHRQAARVNLSFDFPFYGHFLREITVATGGFIYTGEVV
HRMLTATQYIAPLMANFDPSVSRNSTVRYFDNGTALVVQWDHVLQDNYNLGSFTFQATLLMD
GRIIFGYKEIPVLVTQISSTNHPVKVGLSDAFVVVHRIQQIPNVRRTIYEHYRVELQMSKIT
NISAVEMTPLPTCLQFNRCGPCVSSQIGFNCSCWSKLQRCSSGFDRHRQDWVDSGCPEESKEK
MCENTEPVETSSRTTTTVGATTTQFRVLTTRRAVTSQFPTSLPTEDDTKIALHLKDNGASTD
DSAAEKKGGTLHAGLIIGILILVLIVATAILVTVMYHHPTSAASIFFIERRPSRWPAMKFRR
GSGHPAYAEVEPVGEKEGFIVSEQC

Important features of the protein:**Transmembrane domain:**

amino acids 454-478

N-glycosylation sites.

amino acids 103-107, 160-164, 213-217, 221-225, 316-320, 345-349

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 297-301, 492-496, 503-507

N-myristoylation sites.amino acids 42-48, 100-106, 147-153, 279-285, 397-403, 450-456,
455-461

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FIGURE 473

CGCGGAGCCCTGCGCTGGGAGGTGCACGGTGTGCACGCTGGACTGGACCCCCATGCAACCCCG
CGCCCTGCGCCTTAACCAGGACTGCTCCGCGCGCCCTGAGCCTCGGGCTCCGGCCCGGACCT
GCAGCCTCCCAGGTGGCTGGGAAGAACTCTCCAACAATAAATACATTTGATAAGAAAG**ATGGC**
TTTAAAAGTGCTACTAGAACAAAGAGAAAACGTTTTTCACTCTTTTAGTATTACTAGGCTATTT
GTCATGTAAAGTGACTTGTGAATCAGGAGACTGTAGACAGCAAGAATTCAGGGATCGGTCTGG
AACTGTGTTCCCTGCAACCAGTGTGGGCCAGGCATGGAGTTGTCTAAGGAATGTGGCTTCGGC
TATGGGGAGGATGCACAGTGTGTGACGTGCCGGCTGCACAGGTTCAAGGAGGACTGGGGCTTC
CAGAAATGCAAGCCCTGTCTGGACTGCGCAGTGGTGAACCGCTTTCAGAAGGCAAATTTGTTCA
GCCACCAGTGATGCCATCTGCGGGGACTGCTTGCCAGGATTTTATAGGAAGACGAACTTGTC
GGCTTTCAAGACATGGAGTGTGTGCCTTGTGGAGACCCTCCTCCTTACGAACCGCACTGT
GCCAGCAAGGTCAACCTCGTGAAGATCGCGTCCACGGCCTCCAGCCACGGGACACGGCGCTG
GCTGCCGTTATCTGCAGCGCTCTGGCCACCGTCTGCTGGCCCTGCTCATCCTCTGTGTCTC
TATTGTAAGAGACAGTTTATGGAGAAGAAACCCAGCTGGTCTCTGCGGTCGCAGGACATTCAG
TACAACGGCTCTGAGCTGTCTGTTTTTGACAGACCTCAGCTCCACGAATATGCCACAGAGCC
TGCTGCCAGTGCCGCCGTGACTCAGTGCAGACCTGCGGGCCGGTGCGCTTGCTCCCATCCATG
TGCTGTGAGGAGGCCTGCAGCCCCAACCCGGCGACTCTTGGTTGTGGGGTGCAATTCTGCAGCC
AGTCTTCAGGCAAGAAACGCAGGCCAGCCGGGAGATGGTGCCGACTTTCTTCGGATCCCTC
ACGCAGTCCATCTGTGGCGAGTTTTTCAGATGCCTGGCCTCTGATGCAGAATCCCATGGGTGGT
GACAACATCTCTTTTTGTGACTCTTATCCTGAACTCACTGGAGAAGACATTCATTCTCTCAAT
CCAGAACTTGAAAGCTCAACGCTCTTGGATTCAAATAGCAGTCAAGATTTGGTTGGTGGGGCT
GTTCCAGTCCAGTCTCATTCTGAAAACCTTACAGCAGCTACTGATTTATCTAGATATAACAAC
ACACTGGTAGAATCAGCATCAACTCAGGATGCACTAACTATGAGAAGCCAGCTAGATCAGGAG
AGTGGCGCTGTCTATCCACCCAGCCACTCAGACGTCCCTCCAGGAAGCT**TAA**AGAACCTGCTTC
TTTCTGCAGTAGAAGCGTGTGCTGGAACCCAAAGAGTACTCCTTTGTTAGGCTTATGGACTGA
GCAGTCTGGACCTTGCATGGCTTCTGGGGCAAATAAATCTGAACCAAACCTGACGGCATTG
AAGCCTTTCAGCCAGTTGCTTCTGAGCCAGACCAGCTGTAAGCTGAAACCTCAATGAATAACA
AGAAAAGACTCCAGGCCGACTCATGATACTCTGCATCTTTCCTACATGAGAAGCTTCTCTGCCAC
AAAAGTGACTTCAAAGACTGATGGGTTGAGCTGGCAGCCTATGAGATTGTGGACATATAACAA
GAAACAGAAATGCCCTCATGCTTATTTTCATGGTGATTGTGGTTTACAAGACTGAAGACCCA
GAGTATACTTTTTCTTTCCAGAAATAATTTACATACCGCCTATGAAATATCAGATAAATTACCT
TAGCTTTTATGTAGAATGGGTTCAAAGTGAGTGTCTTCTATTTGAGAAGGACACTTTTTCATC
ATCTAAACTGATTTCGCATAGGTGGTTAGAATGGCCCTCATATTGCCTGCCTAAATCTTGGGTT
TATTAGATGAAGTTTACTGAATCAGAGGAATCAGACAGAGGAGGATAGCTCTTTCAGAAATCC
ACACTTCTGACCTCAGCCTCGGTCTCATGAACACCCGCTGATCTCAGGAGAACACCTGGGCTA
GGGAATGTGGTCGAGAAAGGGCAGCCCATTGCCAGAAATTAACACATATTGTAGAGACTTGTA
TGCAAAGGTTGGCATATTTATATGAAAATTAGTTGCTATAGAAACATTTGTTGCATCTGTCCC
TCTGCCTGAGCTTAGAAGGTTATAGAAAAAGGGTATTTATAAACATAAATGACCTTTTACTTG
CATTGTATCTTATACTAAAGGCTTTAGAAATTACAACATATCAGGTTCCCTACTACTGAAGT
AGCCTTCCGTGAGAACACACCACATGTTAGGACTAGAAGAAAATGCACAATTTGTAGGGGTTT
GGATGAAGCAGCTGTAACCTGCCCTAGTGTAGTTTGACCAGGACATTGTCGTGCTCCTTCCAAT
TGTGTAAGATTAGTTAGCACATCATCTCCTACTTTAGCCATCCGGTGTGGATTAAAGAGGAC
GGTGCTTCTTCTATTAAAGTGCTCCATCCCCTACCATCTACACATTAGCATTGTCTCTAGAG
CTAAGACAGAAATTAACCCCGTTCAGTCACAAAGCAGGGAATGGTTCATTTACTCTTAATCTT
TATGCCCTGGAGAAGACCTACTTGAACAGGGCATATTTTTTAGACTTCTGAACATCAGTATGT
TCGAGGGTACTATGATATTTTGGTTTGGAAATTGCCCTGCCCAAGTCACTGTCTTTAACTTTT
AACTGAATATTAAATGTATCTGTCTTCTCT

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FIGURE 474

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84210
><subunit 1 of 1, 417 aa, 1 stop
><MW: 45305, pI: 5.12, NX(S/T): 6
MALKVLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFRDRSGNCVPCNQCGPGMELSK
ECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNRFAQKNCSDAICGDCLPG
FYRKTKLVGFQDMECVPCGDPPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSLAT
VLLALLILCVIYCKRQFMEEKPSWSLRSQDIQYNGSELSCFDRPQLHEYAHRACCQCRD
SVQTCGPVRLLPSCCEEACSPNPATLGCQVHSAASLQARNAGPAGEMVPTFFGSLTQSI
CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV
PVQSHSENFATAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA
```

Important features of the protein:**Signal peptide:**

Amino acids 1-25

Transmembrane domain:

Amino acids 169-192

N-glycosylation sites:

Amino acids 105-109;214-218;319-323;350-354;368-372;379-383

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 200-204;238-242

Tyrosine kinase phosphorylation site:

Amino acids 207-214

N-myristoylation sites:

Amino acids 55-61;215-221;270-276

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 259-270

TNFR/NGFR family cysteine-rich region proteins:

Amino acids 89-96

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FIGURE 475

AGCCAGGCAGCACATCACAGCGGGAGGAGCTGTCCCAGGTGGCCCAGCTCAGCAATGGCAATG
GGGGTCCCCAGAGTCATTCTGCTCTGCCTCTTTGGGGCTGCGCTCTGCCTGACAGGGTCCCAA
GCCCTGCAGTGCTACAGCTTTGAGCACACCTACTTTGGCCCCTTTGACCTCAGGGCCATGAAG
CTGCCCAGCATCTCCTGTCTCATGAGTGCTTTGAGGCTATCCTGTCTCTGGACACCGGGTAT
CGCGCGCCGGTGACCCTGGTGCGGAAGGGCTGCTGGACCGGGCCTCCTGCGGGCCAGACGCAA
TCGAACCCGGACGCGCTGCCGCCAGACTACTCGGTGGTGCGCGGCTGCACAAGTACAAATGC
AACGCCCACCTCATGACTCATGACGCCCTCCCCAACCTGAGCCAAGCACCCGACCCGCCGACG
CTCAGCGGCGCCGAGTGCTACGCCTGTATCGGGGTCCACCAGGATGACTGCGCTATCGGCAGG
TCCCGACGAGTCCAGTGTACCAGGACCAGACCGCCTGCTTCCAGGGCAGTGGCAGAATGACA
GTTGGCAATTTCTCAGTCCCTGTGTACATCAGAACCTGCCACCGGCCCTCCTGCACCACCGAG
GGCACCACCAGCCCCCTGGACAGCCATCGACCTCCAGGGCTCCTGCTGTGAGGGGTACCTCTGC
AACAGGAAATCCATGACCCAGCCCTTCACCAGTGCTTCAGCCACCACCCCTCCCCGAGCACTA
CAGGTCCTGGCCCTGCTCCTCCAGTCCTCCTGCTGGTGGGGCTCTCAGCATAGACCGCCCT
CCAGGATGCTGGGGACAGGGCTCACACACCTCATTCTTGCTGCTTCAGCCCCTATCACATAGC
TCACTGGAAAATGATGTTAAAGTAAGAATTGCAAAA

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FIGURE 476

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA86576

><subunit 1 of 1, 251 aa, 1 stop

><MW: 26935, pI: 7.42, NX(S/T): 2

MAMGVPRVILLCLFGAALCLTGSQALQCYSFEHTYFGPFDLRAMKLPSISCPHECFEAILSLD
TGYRAPVTLVRKGCWTGPPAGQTQSNPDALPPDYSVVRGCTTDKCNAHLMTHDALPNLSQAPD
PPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQSGRMTVGNFSVPVYIIRTCHRPSC
TTEGTTSPWTAIDLQGSCEGYLCNRKSMTQPFTSASATTPPRALQVLALLLPVLLLVGLSA

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 233-251

N-glycosylation sites.

amino acids 120-124, 174-178

N-myristoylation sites.

amino acids 15-21, 84-90

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FIGURE 477

CCCACGCGTCCGGGACAGATGAACTTAAAGAGAAGCTTTAGCTGCCAAAGATTGGGAAAGGGAAAGGACAAAA
AGACCCCTGGGCTACACGGCGTAGGTGCAGGGTTTCCTACTGCTGTTCTTTTATGCTGGGAGCTGTGGCTGTAAC
CAACTAGGAAATAACGTATGCAGCAGCTATGGCTGTCTAGAGAGTTGTGCTTCCCAAGACAAAGGCAAGTCCTGTT
TCTTTTTCTTTTTGGGGAGTGTCTTGGCAGGTTCTGGGTTTGGACGTTATTTCGGTGACTGAGGAAACAGAGAA
AGGATCCTTTGTGGTCAATCTGGCAAAGGATCTGGGACTAGCAGAGGGGGAGCTGGCTGCAAGGGGAACCAGGGT
GGTTTCCGATGATAACAAACAATACCTGCTCCTGGATTACATACCGGGAATTTGCTCACAAATGAGAACTGGA
CCGAGAGAAGCTGTGTGGCCCTAAAGAGCCCTGTATGCTGTATTTCCAAATTTAATGGATGATCCCTTTCAGAT
TTACCGGGCTGAGCTGAGAGTCAGGGATATAAATGATCACGCGCCAGTATTTTCAGGACAAAGAAACAGTCTTAAA
AATATCAGAAAATACAGCTGAAGGGACAGCATTTAGACTAGAAAGAGCACAGGATCCAGATGGAGGACTTAACGG
TATCCAAAATACACGATCAGCCCCAATCTTTTTTCCATATTAACATTAGTGGCGGTGATGAAGGCATGATATA
TCCAGAGCTAGTGTGGACAAAGCACTGGATCGGGAGGAGCAGGGAGAGCTCAGCTTAACCCCTCACAGCGCTGGA
TGGTGGGTCTCCATCCAGGTCTGGGACCTCTACTGTACGCATCGTTGTCTTGGACGTCAATGACAATGCCCCACA
GTTTGGCCAGGCTCTGTATGAGACCCAGGCTCCAGAAAACAGCCCCATTGGGTTCTTATTGTTAAGGTATGGGC
AGAAGATGTAGACTCTGGAGTCAACGCGGAAGTATCCTATTCATTTTTGTATGCCTCAGAAAATATTGCAACGAC
CTTTCAAATCAATCCTTTTTCTGGGAAATCTTCTCAGAGAATTGCTTGATTATGAGTTAGTAAATTCTTACAA
AATAAATATACAGGCAATGGACGGTGGAGGCCCTTCTGCAAGATGTAGGGTTTATGTTGAAGTATTGGACACCAA
TGACAATCCCCCTGAATGATCGTATCATCATTTTTCCAATCTGTTGCTGAGAATTCTCCTGAGACGCCGCTGGC
TGTTTTTAAGATTAATGACAGAGACTCTGGAGAAAATGGAAAGATGGTTTGCTACATTCAAGAGAATCTGCCATT
CCTACTAAAACCTTCTGTGGAGAATTTTTACATCCTAATTACAGAAGGCGCGCTGGACAGAGAGATCAGAGCCGA
GTACAACATCACTATCACCGTCACTGACTTGGGGACACCCAGGCTGAAAACCGAGCACAAACATAACGGTCCCTGGT
CTCCGACGTCAATGACAACGCCCCCGCTTCACCCAAACCTCCTACACCCTGTTGCTCCGCGAGAACAACAGCCC
CGCCCTGCACATCGGCAGCGTCAGCGCCACAGACAGAGACTCGGGCACCAACGCCCAGGTACCTACTCGCTGCT
GCCGCCCAAGACCCGCACCTGCCCCCTCGCCTCCCTGGTCTCCATCAACGCGGACAACGGCCACCTGTTCCGCCCT
CAGGTCGCTGGACTACGAGGCCCTGCAGGCTTTTCAGTTCCGCGTGGGCGCCACAGACCGCGGCTCCCCGCGCT
GAGCAGAGAGGCGCTGGTGCGCTGCTGGTGGACGCCAACGACAACCTCGCCCTTCGTGCTGTACCCGCTGCA
GAACGGCTCCGCGCCCTGCACCGAGCTGGTGCCCCGGGCGGCGAGCCGGGCTACCTGGTGACCAAGGTGGTGGC
GGTGGACGGCGACTCGGGCCAGAACGCCTGGCTGTGCTACCAGCTGCTCAAGGCCACGGAGCCCGGGCTGTTCCG
TGTGTGGGCGCACAATGGGGAGGTGCGCACCGCCAGGCTGCTGAGCGAGCGCGACGCAAGCACAGGCTCGT
GGTGTGTTGTCAAGGACAATGGCGAGCCTCCTCGCTCGGCCACCGCCACGCTGCACTTGCTCCTGGTGGACGGCTT
CTCCCAGCCCTACCTGCCTCTCCCGAGGCGGCCCCGGCCAGGCCAGGCCAGGCCGAGGCCGACTTGCTCACCGTCTA
CCTGGTGGTGGCGTTGGCCTCGGTGCTTTCGCTCTTCTCCTCCTCCTCGGTGCTCCTGTTGCTGGCGGTGCGGCTGTG
CAGGAGGAGCAGGGCGGCTCGGTGGGTGCTGCTCGGTGCCCGAGGGTCTTTTCCAGGGCATCTGGTGGACGT
GAGGGGCGCTGAGACCCTGTCCAGAGCTACAGTATGAGGTGTGCTGACGGGAGGCCCCGGGACCAGTGAGTT
CAAGTTCTTGAAACAGTTATTTTCGGATATTCAGGCACAGGGCCCTGGGAGGAAGGGTGAAGAAAATTCACCTT
CCGAAATAGCTTTGGATTTAATATTAGTAAAGTCTGTTTTTAGTTTCATATACTTTTGGTGTGTTACATAGCCA
TGTTTTCTATTAGTTTACTTTTAAATCTCAAATTTAAGTTATTATGCAACTTCAAGCATTATTTTCAAGTAGTATA
CCCCGTGGTTTTTACAATGTTTCATCATTTTTTGCATTAATAACAACCTGGGTTTAATTTAATGAGTATTTTTTT
CTAAATGATAGTGTTAAGGTTTTAATTCTTTCCAATGCCCAAGGAATTAATTACTATTATATCTCATTACAGAA
ATCTGAGTTTTGATTCATTTAGAGCTTGCATCTCATGATTCTAATCACTTCTGTCTATAGTGTACTTGCTCTA
TTTAAGAAGGCATATCTACATTTCCAAACTCATTCTAACATTCTATATATTCTGTGTTTGAACCATGTCATTTA
TTTCTACATCATGTATTTAAAAAGAAATATTTCTCTACTACTATGCTCATGACAAAATGAAACAAAGCATATTGT
GAGCAATACTGAACATCAATAATACCCTTAGTTTATATACTTATTATTTTATCTTTAAGCATGCTACTTTTACTT
GGCCAATATTTTCTATGTAACTTTTGTGATGTATAAAACAGACTATGCCTTATAATTGAATAAAATATATAA
TCTGCCTGAAAATGAATAAAATAAAACATTTTGAAATGTGAAAAAAAAAAAAAAAAAAAAA

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FIGURE 478

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA87976
><subunit 1 of 1, 800 aa, 1 stop
><MW: 87621, pI: 4.77, NX(S/T): 7
MAVRELCFPRQRQVLFLEFLFWGVSLAGSGFGRYSVTEETKGSFVVNLAKDLGLAEGELAARG
TRVVSDDNKQYLLLDSTGNLLTNEKLDREKLCGPKEPCMLYFQILMDDPFQIYRAELRVRDI
NDHAPVFQDKETVLKISENTAEGTAFRLERAQDPDGGLNGIQNYTISPNSFFHINISGGDEGM
IYPELVLDKALDREEQGEISLTALTALDGGSPSRSGTSTVRIVVLDVNDNAPQFAQALYETQAP
ENSPIGFLIVKVWAEVDVDSGVNAEVSYSFFDASENIRTTTFQINPFSGEIFLRELLDYELVNSY
KINIQAAMDGGGLSARCRVLVEVLDTNDNPPELIVSSFSNSVAENSPETPLAVFKINDRDSGEN
GKMVCYIQENLPFLKPSVENFYILITEGALDREIRAENITITVTDLGTPLKTEHNITVLV
SDVNDNAPAFQTQTSYTLFVRENNSPALHIGSVSATDRDSGTNAQVTYSLPPQDPHLPASLV
SINADNGHLFALRSLDYEALQAFEFVRGATDRGSPALSREALVRVLVLDANDNSPFVLYPLQN
GSAPCTELVPRAAEPGYLVTKVAVDGDGQNAWLSYQLLKATEPGLFGVWAHNGEVRTARLL
SERDAAKHRLVVLVKDNGEPPRSATATLHLLLVDFGFSQPYLPPLPEAAPAQAEADLLTVYLV
VALASVSSLFLLSVLLFVAVRLCRRSRAASVGRCSVPEGPFPGLVDVVRGAETLSQSYQYEV
LTGGPGTSEFKFLKPVISDIQAQGPGRKGEENSTFRNSFGFNIQ

```

Important features of the protein:**Signal peptide:**

amino acids 1-26

Transmembrane domain:

amino acids 687-711

N-glycosylation sites.

amino acids 169-173, 181-185, 418-422, 436-440, 567-571, 788-792

Glycosaminoglycan attachment site.

amino acids 28-32

Tyrosine kinase phosphorylation sites.

amino acids 394-402, 578-585

N-myristoylation sites.amino acids 22-28, 27-33, 53-59, 82-88, 162-168, 184-190,
217-223, 324-330, 325-331, 471-477, 568-574, 759-765**Amidation site.**

amino acids 781-785

Aminoacyl-transfer RNA synthetases class-II signature 1.

amino acids 117-138

Cadherins extracellular repeated domain signature.

amino acids 121-132, 230-241, 335-346, 439-450, 549-560

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FIGURE 479

CTCGGCTGGATTTAAGGTTGCCGCTAGCCGCCTGGGAATTTAAGGGACCCACACTACCTTCCC
GAAGTTGAAGGCAAGCGGTGATTGTTTGTAGACGGCGCTTTGTC**ATG**GGACCTGTGCGGTGG
GAATATTGCTTTTCCTTTTTTTTGGCCGTGCACGAGGCTTGGGCTGGGATGTTGAAGGAGGAGG
ACGATGACACAGAACGCTTGCCCAGCAAATGCGAAGTGTAAGCTGCTGAGCACAGAGCTAC
AGGCGGAAGTGAAGTCGCACCGGTGATCTCGAGAGGTGCTGGAGCTGGGGCAGGTGCTGGATA
CAGGCAAGAGGAAGAGACACGTGCCTTACAGCGTTTCAGAGACAAGGCTGGAAGAGGCCCTTAG
AGAATTTATGTGAGCGGATCCTGGACTATAGTGTTACGCTGAGCGCAAGGGCTCACTGAGAT
ATGCCAAGGGTCAGAGTCAGACCATGGCAACACTGAAAGGCCTAGTGCAGAAGGGGGTGAAGG
TGGATCTGGGGATCCCTCTGGAGCTTTGGGATGAGCCCAGCGTGGAGGTACATACCTCAAGA
AGCAGTGTGAGACCATGTTGGAGGAGTTTGAAGACATTGTGGGAGACTGGTACTTCCACCATC
AGGAGCAGCCCCCTACAAAATTTTCTCTGTGAAGGTCATGTGCTCCCAGCTGCTGAAACTGCAT
GTCTACAGGAACTTGGACTGGAAAGGAGATCACAGATGGGGAAGAGAAAACAGAAGGGGAGG
AAGAGCAGGAGGAGGAGGAGGAAGAGGAGGAAGAGGAAGGGGGAGACAAGATGACCAAGACAG
GAAGCCACCCCAAACCTTGACCGAGAAGATCTT**TGA**CCCTTGCCTTTGAGCCCCCAGGAGGGGA
AGGGATCATGGAGAGCCCTCTAAAGCCTGCACTCTCCCTGCTCCACAGCTTTCAGGGTGTGTT
TATGAGTGACTCCACCCAAGCTTGTAGCTGTTCTCTCCCATCTAACCTCAGGCAAGATCCTGG
TGAAACAGCATGACATGGCTTCTGGGGTGGAGGGTGGGGGTGGAGGTCCTGCTCCTAGAGATG
AACTCTATCCAGCCCCCTAATTGGCAGGTGTATGTGCTGACAGTACTGAAAGCTTTCCTCTTT
AACTGATCCCACCCCCACCCAAAAGTCAGCAGTGGCACTGGAGCTGTGGGCTTTGGGGGAAGTC
ACTTAGCTCCTTAAGGTCTGTTTTTAGACCCTTCCAAGGAAGAGGCCAGAACGGACATTCTCT
GCGATCTATATACATTGCCTGTATCCAGGAGGCTACACACCAGCAAACCGTGAAGGAGAATGG
GACACTGGGTCATGGCCTGGAGTTGCTGATAATTTAGGTGGGATAGATACTTGGTCTACTTAA
GCTCAATGTAACCCAGAGCCCACCATATAGTTTTATAGGTGCTCAACTTTCATATATCGCTATT
AAACTTTTTTCTTTTTTTCTA

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FIGURE 480

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92256
><subunit 1 of 1, 248 aa, 1 stop
><MW: 28310, pI: 4.63, NX(S/T): 0
MGPVRLGILLFLFLAVHEAWAGMLKEEDDDTERLPSKCEVCKLLSTELQAELSRTGRSREVL
LGQVLDTGKRKRHPYPSVSETRLEEALENLCERILDYSVHAERKGSRLRYAKQSQTMATLKGL
VQKGVKVDLGIPLELWDEPSVEVTYLKKQCETMLEEFEDIVGDWYFHHQEQPLQNFLCEGHVL
PAAETACLQETWTGKEITDGEEKTEGEEEEEQEEEEEEEEEGGDKMTKTGSHPKLDREDL
```

Important features of the protein:**Signal peptide:**

amino acids 1-21

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 106-110

N-myristoylation site.

amino acids 115-121

Amidation site.

amino acids 70-74

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FIGURE 481

GGCGTGTGCAAGGCGGGGTCCGGCCCGCGCAGGTCGGGTAAGCGCGTCTAGGGCGCTGCGCGG
CGCAGCGAAA**ATG**GCGGCTTCCAGGTGGGCGCGCAAGGCCGTGGTCCTGCTTTGTGCCTCTGA
CCTGCTGCTGCTGCTGCTACTGCTACCACCGCCTGGGTCCTGCGCGGCCGAAGGCTCGCCCGG
GACGCCCCGACGAGTCTACCCACCTCCCCGGAAGAAGAAGGATATTGCGGATTACAATGA
TGCAGACATGGCGCGTCTTCTGGAGCAATGGGAGAAAGATGATGACATTGAAGAAGGAGATCT
TCCAGAGCACAAAGAGACCTTCAGCACCTGTCGACTTCTCAAAGATAGACCCAAGCAAGCCTGA
AAGCATATTGAAAATGACGAAAAAAGGGAAGACTCTCATGATGTTTGTCACTGTATCAGGAAG
CCCTACTGAGAAGGAGACAGAGGAAATTACGAGCCTCTGGCAGGGCAGCCTTTTCAATGCCAA
CTATGACGTCCAGAGGTTCAATTGTGGGATCAGACCGTGCTATCTTCATGCTTCGCGATGGGAG
CTACGCCTGGGAGATCAAGGACTTTTTGGTGGTCAAGACAGGTGTGCTGATGTAACCTCTGGA
GGGCCAGGTGTACCCCGGCAAAGGAGGAGGAAGCAAAGAGAAAAATAAAACAAAGCAAGACAA
GGGCAAAAAAAGAAGGAAGGAGATCTGAAATCTCGGTCTTCCAAGGAAGAAAATCGAGCTGG
GAATAAAGAGAAGACCT**GTGA**TGGGGCAGCAGTGACGCGCTGTGGGGGGACAGGTGGACGTG
GAGAGCTCTTTGCCAGCTCCTGGGGTGGGAGTGGTCTCAGGCAACTGCACACCGGATGACAT
TCTAGTGTCTTCTAGAAAGGGTCTGCCACATGACCAGTTTGTGGTCAAAGAATTACTGCTTAA
TAGGCTTCAAGTAAGAAGACAGATGTTTTCTAATTAATACTGGACACTGACAAATTCATGTTT
ACTATAAAATCTCCTTACATGGAAATGTGACTGTGTTGCTTTTTCCCATTTACACTTGGTGAG
TCATCAACTCTACTGAGATTCCACTCCCCCTCCAAGCACCTGCTGTGATTGGGTGGCCTGCTCT
GATCAGATAGCAAATTCTGATCAGAGAAGACTTTAAACTCTTGACTTAATTGAGTAAACTCT
TCATGCCATATACATCATTTTCATTATGTTAAAGGTAAAATATGCTTTGTGAACCTCAGATGTC
TGTAGCCAGGAAGCCAGGGTGTGTAATCCAAATCTATGCAGGAAATGCGGAGAATAGAAAA
TATGTCACTTGAAATCCTAAGTAGTTTTGAATTTCTTTGACTTGAATCTTACTCATCAGTAAG
AGAACTCTTGGTGTCTGTGAGGTTTTATGTGGTCTGTAAAGTTAGGGGTTCTGTTTTGTTTCC
TTATTTAGGAAAGAGTACTGCTGGTGTGAGGGGTTATATGTTCCATTTAATGTGACAGTTTT
AAAGGATTTAAGTAGGGAATCAGAGTCCTTTGCAGAGTGTGACAGACGACTCAATAACCTCAT
TTGTTTCTAAACATTTTCTTTGATAAAGTGCCTAAATCTGTGCTTTTCGTATAGAGTAACATG
ATGTGCTACTGTTGATGTCTGATTTTGCCGTTTCATGTTAGAGCCTACTGTGAATAAGAGTTAG
AACATTTATATACAGATGTCATTTCTAAGAACTAAAATTCTTTGGGAAAAACCCTCAAAAAA
AAAAAAAAAAAAAAAAAAAAA

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FIGURE 482

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92289
><subunit 1 of 1, 234 aa, 1 stop
><MW: 26077, pI: 8.13, NX(S/T): 1
MAASRWARKAVVLLCASDLLLLLLLLLPPPGSCAAEGSPGTPDESTPPPRKKKKDIRDYND
ADMARLLEQWEKDDDDIEEGDLPEHKRPSAPVDFSKIDPSKPESILKMTKKGKTLMMFVTV
SGSPTEKETEEITSLWQGSLEFNANYDVQRFIVGSDRAIFMLRDGSYAWWEIKDFLVGQDRC
ADVTLEGQVYPGKGGGSKEKNKTKQDKGKKKKEGDLKSRSSKEENRAGNKREDL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-32

N-glycosylation site:

Amino acids 201-205

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 85-89

Tyrosine kinase phosphorylation site:

Amino acids 50-59

N-myristoylation sites:

Amino acids 30-36;138-144;153-159;176-182

Amidation site:

Amino acids 207-211

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FIGURE 484

MALPPGPAALRHTLLLLPALLSSGWGELEPQIDGQTWAERALRENERHAFTCRVAGGPGTPRL
AWYLDGQLQEASTSRLLSVGGEAFSGGTSTFTVTAHRAQHELNCSLQDPRSGRSANASVILNV
QFKPEIAQVGAKYQEAQGPGLLVVLFALVRANPPANVTWIDQDGPVTVNTSDFLVLDAQNYPW
LTNHTVQLQLRSLAHNLSVVATNDVGVTASLPPAGPSRHPSLISSDSNNLKLNNVRLPRENM
SLPSNLQLNDLTPDSRAVKPADRQMAQNNSRPELLDPEPGGLLTSQGFIRLPVLGYIYRVSSV
SSDEIWL

N-glycosylation sites:

amino acids 106-110, 119-123, 162-166, 175-179, 192-196, 205-209,
251-255, 280-284

Glycosaminoglycan attachment site:

amino acids 23-27

Casein kinase II phosphorylation sites:

amino acids 36-40, 108-112, 164-168, 282-286, 316-320

N-myristoylation sites:

amino acids 34-40, 89-95, 215-221, 292-298, 293-299

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FIGURE 485

AGAGTTCCTTTTTCTAGGTCGATTAGGTTATACATTGTTGAAGTATAGTTTCGAGTTAGAATT
GGTCATTTTATTTTCAGTGTTTTCACAGAAATCGAAGAAGACAGAA**ATG**GCGCTTCTGTGGTGG
ATATCTACAGTAGCAATACTGTTGTTTACTTCGACGATTTTGGGAACATACGTTGAAGCTGGT
GCCGCTAAGTCTAACGAAGAAGAGATTGTGAACAAAAGCGAATTTGGAAGATTTCCACGAGGG
TCGAGAAAGGATGCATCGGGGTGCCACAAGCCGGGCTACCCTGTACCCCTCATTCTCGCTGC
CCTCCACCTCCCCATGTGCAGCGTCCTCGTCCTATTCTGCATGCT**TAG**TCTAACACCATCAGG
CTCGTTTATCTTTTCTGTCATTGATCTCACCAGGAGCAAATCACTAGTGCGTGCTTCTGATTTC
ACGTAACGTAGTATGTAAATAAATGTCAGTGATATTATGAATTGGTAAAACATTTCTGTTATC
TAAATAAACAGTGAAGTTTGTTTGACTAAAAAAA

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FIGURE 486

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96855
><subunit 1 of 1, 84 aa, 1 stop
><MW: 9274, pI: 9.70, NX(S/T): 1
MALLWWISTVAILLFTSTILGTYVEAGAAKSNEEEIVNKSEFGRFFPRGSRKDASGCHKPG
YPVPPHSRCPPPPHVQRPRPILHA
```

Signal peptide:

Amino acids 1-21

N-glycosylation site:

Amino acids 38-42

N-myristoylation site:

Amino acids 27-33

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FIGURE 487

CGGGGACGGAAGCGGCCCCCTGGGCCCCGAGGGGCTGGAGCCGGGCCGGGGCG**ATG**TGGAGCGCG
GGCCGCGGCGGGGCTGCCTGGCCGGTGCTGTTGGGGCTGCTGCTGGCGCTGTTAGTGCCGGGC
GGTGGTGCCGCCAAGACCGGTGCGGAGCTCGTGACCTGCGGGTCGGTGCTGAAGCTGCTCAAT
ACGCACCACCGCGTGCGGCTGCACTCGCACGACATCAAATACGGATCCGGCAGCGGCCAGCAA
TCGGTGACCGGCGTAGAGGCGTCGGACGACGCCAATAGCTACTGGCGGATCCGCGGCGGCTCG
GAGGGCGGGTGCCCGCGCGGGTCCCCGGTGCGCTGCGGGCAGGCGGTGAGGCTCACGCATGTG
CTTACGGGCAAGAACCTGCACACGCACCACTTCCCGTCGCCGCTGTCCAACAACCAGGAGGTG
AGTGCCTTTGGGGAAGACGGCGAGGGCGACGACCTGGACCTATGGACAGTGCGCTGCTCTGGA
CAGCACTGGGAGCGTGAGGCTGCTGTGCGCTTCCAGCATGTGGGCACCTCTGTGTTCCCTGTCA
GTCACGGGTGAGCAGTATGGAAGCCCCATCCGTGGGCAGCATGAGGTCCACGGCATGCCCAGT
GCCAACACGCACAATACGTGGAAGGCCATGGAAGGCATCTTCATCAAGCCTAGTGTGGAGCCC
TCTGCAGGTCACGATGAACT**TGAG**TGTGTGGATGGATGGGTGGATGGAGGGTGGCAGGTGGG
GCGTCTGCAGGGCCACTCTTGGCAGAGACTTTGGGTTTGTAGGGGTCCTCAAGTGCCTTTGTG
ATTAAAGAATGTTGGTCTATGAAA

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FIGURE 488

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96857

><subunit 1 of 1, 221 aa, 1 stop

><MW: 23598, pI: 6.96, NX(S/T): 0

MWSAGRGGAAWPVLLGLLLIALLVPGGGAAKTGAELVTCGSVLKLLNTHHRVRLHSHDIKYGSG
SGQQSVTGVEASDDANSYWRIRGGSEGGCPRGSPVRCGQAVRLTHVLTGKNLHTHHFPSPLSN
NQEVSATFGEDGEGDDLDLWTVRCSGQHWEREAAVRFQHVGTSVFLSVTGEQYGSPIRGQHEVH
GMPSANTHNTWKAMEGIFIKPSVEPSAGHDEL

Important features of the protein:**Signal peptide:**

amino acids 1-28

Glycosaminoglycan attachment site.

amino acids 62-66

N-myristoylation sites.amino acids 16-22, 25-31, 27-33, 61-67, 71-77, 86-92, 87-93,
91-97, 190-196**Endoplasmic reticulum targeting sequence.**

amino acids 218-223

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FIGURE 489

CAGCAGCCGAGACAGCAGCTGAGACGGCAGCGGCAGCTTCTCAGGGCCGGAGCCAGTTCTTGGAGGAGACTCTGC
ACAGGGCATGGGATCACTGTGGTGCCCTTTTCTGTGCCTGTGCCTTCTGACTTTGCAGAATGCAACAACAGAGAC
ATGGGAAGAACTCCTGAGCTACATGGAGAATATGCAGGTGTCCAGGGGCCGGAGCTCAGTTTTTCTCTCGTCA
ACTCCACCAGCTGGAGCAGATGCTACTGAACACCAGCTTCCCAGGCTACAACCTGACCTTGACAGACCCACCAT
CCAGTCTCTGGCCTTCAAGCTGAGCTGTGACTTCTGTGGCCTCTCGCTGACCAGTGCCACTCTGAAGCGGGTGCC
CCAGGCAGGAGGTGAGCATGCCCGGGGTGAGCAGCCATGCAGTTCCCCGCCGAGCTGACCCGGGACGCCTGCAA
GACCCGCCCCAGGGAGCTGCGGCTCATCTGTATCTACTTCTCCAACACCCACTTTTTCAAGGATGAAAACAACCTC
ATCTCTGCTGAATAACTACGTCTTGGGGGCCAGCTGAGTCATGGGCACGTGAACAACCTCAGGGATCCTGTGAA
CATCAGCTTCTGGCACAACCAAAGCCTGGAAGGCTACACCTGACCTGTGTCTTCTGGAAGGAGGGAGCCAGGAA
ACAGCCCTGGGGGGGCTGGAGCCCTGAGGGCTGTGCTACAGAGCAGCCCTCCCCTCTCAGGTGCTCTGCCGCTG
CAACCACTCACCTACTTTTGTGTTCTCATGCAACTCTCCCAGCCCTGGTCCCTGCAGAGTTGCTGGCACCTCT
TACGTACATCTCCCTCGTGGGCTGCAGCATCTCCATCGTGGCCTCGCTGATCACAGTCTGCTGCACTTCCATTT
CAGGAAGCAGAGTGACTCCTTAACACGTATCCACATGAACCTGCATGCCTCCGTGCTGCTCCTGAACATCGCCTT
CCTGCTGAGCCCCGCATTGCAATGTCTCCTGTGCCCGGGTCAGCATGCACGGCTCTGGCCGCTGCCCTGCACTA
CGCGCTGCTCAGCTGCCTCACCTGGATGGCCATCGAGGGCTTCAACCTCTACCTCCTCCTCGGGCGTGTCTACAA
CATCTACATCCGCAGATATGTGTTCAAGCTTGGTGTGCTAGGCTGGGGGGCCCCAGCCCTCCTGGTGTGCTTTT
CCTCTCTGTCAAGAGCTCGGTATACGGACCCTGCACAATCCCCGTCTTCGACAGCTGGGAGAATGGCACAGGCTT
CCAGAACATGTCCATATGCTGGGTGCGGAGCCCCGTGGTGACAGTGTCTGGTCATGGGCTACGGCGGCCCTCAC
GTCCCTCTTCAACCTGGTGGTGTGCTGGCCTGGGCGCTGTGGACCCTGCGCAGGCTGCGGGAGCGGGCGGATGCACC
AAGTGTGAGGGCCTGCCATGACACTGTCACTGTGCTGGGCCTCACCGTGTGCTGGGAACACCTGGGCCTTGGC
CTTCTTTTCTTTTGGCGTCTTCTCTGCTGCCCGAGCTGTTCTCTTCAACCATCTTAAACTCGCTGTACGGTTTCTT
CCTTTTCTGTGGTTCTGCTCCCAGCGGTGCCGCTCAGAAGCAGAGGCCAAGGCACAGATAGAGGCCTTCAGCTC
CTCCCAAACAACACAGTAGTCCGGGCCTCCTGGCCTGGAATCCTCAGCCTCTCTGCCCCCAGTAGAGGCT
ACGGCTCCTGCTAGAGAGGGTGGCAGGCCTGCTGCTGGACCCAGAGGCCACTGTGACCGCCAAGGGGCCTTTTTC
CACTTCCACGGCCTCTCCAGGCACTGAGGGGAAGGCATTGCTCTACCTCTCCCTGACATTTTGTCTCCGGGGCAGA
TCCAACCTTACCTGGGGCAGCAAACTTTGTCTGTACCTGGGCCAGCTCGCCAGGGATGTGGGCAGAGCACC
GCCTGGGCATCAGGAAGCCAAGTTTCAAGGACTGTCTTTGAGTCTGTCTGTATGACCTTGGGCCTGCCACTTCTC
ACAGACCCTAGGTATCCACAGCTGTGACATGGGGGAAGCAGCTTTGTTTCAGCCTAACCAGGAGCTTAGTAAA
AATTGCATAAGACCAGGGGAAGAGTGTGACGTGGGGTGGGAATTCCCGCGGCCTCCACCTGCTTGCTAGGGGC
AGGATCTCATTAGGCTGCCCTGGAAGCACCTGCTTGGCCCTGCCACCTTCTCCAGGGGAGGGCCAGATGGCAT
CCTGGCTTGGGGCGGGTGGGACCTACCCAGGCTCTGAGACTTTACTGGCCTATGCCTGAGGCCTCTTTTCTTTTA
ACTCCCTAAATTATGATGACTCCAAGTCCAAGCCACCCTTCCCAAAGATTGGGAGGTTCCGCCGTTCCAGAGG
CTCCTCCTGCGGTGCTCCCAAGACTTCCATAGACCATCTGGACCAGTAGCCCATCCCGCAGTTTTCTTGGGGGCA
GAGGAAAACGCTTCTTTCTCTCCAGCTGAATCAGCTGGATCCCAGTGTCTGGCTGTTTGGTGATTGGGCAAGA
TTGAATTTGCCCAGGTAGGCGTGAGAGTGTGGGTTTTAAATTCGAAGCTCAGGCCATAGTTTCAGAGAATCACCC
TTACCCCAAGACCTTTCATGAGACAGTGTCTCATGAAGCCAGTGCGTTTCCAGAACGAACACTAGGCGGCACCGTTG
GTCCACACTCAGAGGCCCTTGGCGCCAAGACTGCATCTAGAATCGCTCAAACACCTGTTTGCAGACCCCATGCAC
CAGCTGGAGGGGCCGTAACCTGCAGGACTGCGCCTACTGAGTGACCCATTTCTCCAGGAGGAAAGGCAAGACAG
CTTACACGGCCATTTGTCTCTTTTCCCAATGCGGCGGTGCACTTTGCTCTTGGGGGCTGCACCCAGACATAGC
TGGCACCAGAGCAGGGTGTGAGGTGGTGGTGTGCTCAGGGCCCTGCCCGAGCCACTGGGCGGTTTTGATGACCT
CAAAGGTACAGGCAGAAAATAGGAGCAGGATTTCCCTGGGGAAAAGTTATCCTGGGACATCTTCTGCTCTTCT
GTACATTTCTAGATGCAATAACTCCTTACCAGGCAGTGAGTGGCGTAGGCTCTGGAGCCAGGCTGCCTGGGCT
CCAATGCCAGCTCTGCCACTTGTAGCTGTGAGACTGTGGACAAACCACTCAGCCTCTGTGTGCTCAGTTTTCC
TATTTGTAAATAGAGACCATAGTGGTACCTATTTTGAAGACTAAGTAAAAGAATTCAAATAAAGAGACTTGGCA
CAGAGTAAGTGCTCAGTAAAAA

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FIGURE 490

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96860
><subunit 1 of 1, 528 aa, 1 stop
><MW: 59000, pI: 8.73, NX(S/T): 9
MDHCGALFLCLCLLTQONATTETWEELLSYEMNQVSRGRSSVFSSRQLHQLEQMLLNTS
FPGYNLTQTPTIQSLAFKLSCDFSGLSLTSATLKRVPQAGGQHARGQHAMQFPAELTRD
ACKTRPRELRILICIYFSNTHFFKDENNSSLNNYVLGAQLSHGHVNNLRDPVNISFWHNQ
SLEGYTLTCVFWKEGARKQPWGGWSPGCRTEQPSHSQVLCRCNHLTYFAVLMQLSPALV
PAELLAPLTYISLVGCSISIVASLITVLLHFHFRKQSDSLTRIHMNLHASVLLLNIAFLL
SPAFAMSPVPGSACTALAAALHYALLSCLTWMAIEGFNLYLLLGRVYNIYIRRYVFKLG
LGWGAPALLVLLSLSVKSSVYGPCTIPVFDSEWNGTGFQNMSCWVRSPVHSLVMGYG
GLTSLFNLVVLAWALWTLRRLRERADAPSVRACHDTVTVLGLTVLLGTTWALAFFSFGVF
LLPQLFLFTILNSLYGFFLFLWFCSQRCRSEAEAKAQIEAFSSSQTTQ
```

Important features of the protein:**Signal peptide:**

Amino acids 1-21

Transmembrane domains:

Amino acids 244-264;290-309;316-344;358-376;411-431;468-491

N-glycosylation sites:Amino acids 18-22;58-62;65-69;146-150;147-151;173-177;
179-183;394-398;400-404**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 274-278

N-myristoylation sites:86 GLSLTS
101 GGQHAR
157 GAQLSH
255 GCSISI
311 GSACTA
420 GGLTSL
467 GTTWAL**Prokaryotic membrane lipoprotein lipid attachment sites:**

Amino acids 246-257;318-329

Eukaryotic thiol (cysteine) proteases histidine active site:

Amino acids 410-421

G-protein coupled receptors family 2 proteins:

Amino acids 273-302;314-343

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FIGURE 491

CTTGGCTGCCCCGACAACAAGCTCGCCACCTGCGCTGGGCGCATCCACCATCCAAGGCCAGCT
GAGGGGCACCAGACAGAGG**ATG**AGGAGAGAGAGTCCGACACGGGCTGCCCTGAGAGACATTTT
CATGGACATCCTCATGCTGCTTCTGCTTTTGTGTGTAATATATGGGAGATTTTCCCAAGATGA
ATACTCCCTCAATCAAGCTATCCGGAAAGAATTTACAAGAAATGCCAGAACTGCTTGGGTGG
CCTGAGAAACATCGCTGACTGGTGGGACTGGAGTCTGACCACACTTCTGGATGGCCTGTACCC
GGGAGGCACCCCGTCAGCCCGTGTGCCGGGGGCTCAGCCTGGAGCTCTTGGAGGAAAATGCTA
CCTAATAGGCAGTTCCGTAATTAGGCAGCTAAAAGTTTTTCTAGGCATTTATGCAAGCCTCC
CAGGCCATTTTTCAGCACTCATCGAAGACTCTATTCTACATGTAGTCCCGAAGTTGGAGGCCC
TGAGAACCCCTACCTGATAGACCCAGAGAACCAAAACGTGACCCTGAATGGTCCTGGGGGCTG
TGGGACAAGGGAGGACTGTGTGCTCAGCCTGGGCAGAACAAAGGACTGAAGCCCACACAGCCCT
GTCCCGACTCAGGGCCAGCATGTGGATTGACCGCAGCACCAGGGCTGTGTCTGTGCACTTCAC
TCTCTATAACCCTCCAACCCAACTCTTCACCAGCGTGTCCCTGAGAGTGGAGATCCTCCCTAC
GGGGAGTCTCGTCCCCTCATCCCTGGTGGAGTCATTGAGCATCTTCCGCAGCGACTCAGCCCT
GCAGTACCACCTCATGCTTCCCCAGCTGGTCTTCCTGGCACTCAGCCTGATCCACCTCTGTGT
TCAACTCTACCGTATGATGGACAAGGGCGTCCTCAGCTACTGGCGAAAGCCAAGGAACTGGCT
GGAGGTAGCCTCTCTTGTGTGTCATTTTCTTTTGAAAA**TA**ACAATAAACTGTTTATATCTTGAA
AAAATAATTTAAATAAGAAATTGATTATGCACTAGCTACTGCCAACATTATTGCAGTTTTCTC
CCTCTGTAGTGTTAATCTCAAAACAGCATTTGAGATCAGGTATCATTTAGTGTTGTACAGTT
ACCGTCATGTACCACACGAATTTAGCCAAAGGTGGTGGTCCCATAGATCATATGGTGCTAAG
AAATTTCTGTACCTAATGACATCTTGATTCTGACCTTGTATGTAGGCCTAGGCTAAATATGT
CTGTTTGTATCTTAGCTTTTAATAAAGAAGTTTAAAAATAAAAAA

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FIGURE 492

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96861
><subunit 1 of 1, 300 aa, 1 stop
><MW: 33649, pI: 9.26, NX(S/T): 1
MRRESRTRAALRDISMDILMLLLLCVIYGRFSQDEYSLNQAIRKEFTRNARNCLGGLRN
IADWWDWSLTTLDDGLYPGGTPSARVPGAQPGALGGKCYLIGSSVIRQLKVFPRLCKPP
RPFSAIEDSIPTCSPEVGGPENPYLIDPENQNVTLNGPGGCGTREDCVLSLGRTRTEAH
TALSRLRASMWIDRSTRAVSVHFTLYNPPTQLFTSVSLRVEILPTGSLVPSSLVESFSIF
RSDSALQYHMLPQLVFLALSLIHL CVQLYRMDKGVLSYWRKPRNWLEVASLVSFSEK
```

Important features of the protein:**Signal peptide:**

Amino acids 1-30

Transmembrane domain:

Amino acids 250-267

N-glycosylation site:

Amino acids 153-157

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 2-6

N-myristoylation sites:

Amino acids 56-62;75-81;79-85;80-86;88-94;92-98;160-166

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FIGURE 493

TCTCAGGGCTTCATACAGGAAATCTATTGCTGTGTCAAGTTCCAGAGAAAAGCTTCTGTTCGT
CCAAGTTACTAACCAGGCTAAACCACATAGACGTGAAGGAAGGGGCTAGAAGGAAGGGAGTGC
CCCCTGTTGATGGGGTAAGAGGATCCTGTACTGAGAAGTTGACCAGAGAGGGTCTCACCATG
CGCACAGTTCCTTCTGTACCTGTGTGGAGGAAAAGTACTGAGTGAAGGGCAGAAAAAGAGAAA
ACAGAAATGCTCTGCCCTTGGAGAACTGCTAACCTAGGGCTACTGTTGATTTTGACTATCTTC
TTAGTGGCCGAAGCGGAGGGTGCTGCTCAACCAACAACCTCATTAATGCTGCAAACTAGCAAG
GAGAATCATGCTTTAGCTTCAAGCAGTTTATGTATGGATGAAAAACAGATTACACAGAACTAC
TCGAAAGTACTCGCAGAAGTTAACACTTCATGGCCTGTAAAGATGGCTACAAATGCTGTGCTT
TGTTGCCCTCCTATCGCATTAAGAAATTTGATCATAATAACATGGGAAATAATCCTGAGAGGC
CAGCCTTCCTGCACAAAAGCCTACAGGAAAGAAACAAATGAGACCAAGGAAACCAACTGTACT
GATGAGAGAATAACCTGGGTCTCCAGACCTGATCAGAATTCCGACCTTCAGATTTCGTCCAGTG
GCCATCACTCATGACGGGTATTACAGATGCATAATGGTAACACCTGATGGGAATTTCCATCGT
GGATATCACCTCCAAGTGTTAGTTACACCTGAACTGACCCTGTTTCAAAACAGGAATAGAAT
GCAGTATGCAAGGCAGTTGCAGGGAAGCCAGCTGCGCAGATCTCCTGGATCCCAGAGGGCGAT
TGTGCCACTAAGCAAGAATACTGGAGCAATGGCACAGTGAAGTGTAAAGAGTACATGCCACTGG
GAGGTCCACAATGTGTCTACCGTGACCTGCCACGTCTCCCATTTGACTGGCAACAAGAGTCTG
TACATAGAGCTACTTCCTGTTCCAGGTGCCAAAAAATCAGCAAAATTATATATTTCCATATATC
ATCCTTACTATTATTATTTTGACCATCGTGGGATTCATTTGGTTGTTGAAAGTCAATGGCTGC
AGAAAAATATAAATTGAATAAAACAGAATCTACTCCAGTTGTTGAGGAGGATGAAATGCAGCCC
TATGCCAGCTACACAGAGAAGAACAATCCTCTCTATGATACTACAAACAAGGTGAAGGCATCT
CAGGCATTACAAAGTGAAGTTGACACAGACCTCCATACTTTATAAGTTGTTGGACTCTAGTAC
CAAGAAACAACAACAACGAGATACATTATAATTACTGTCTGATTTTCTTACAGTTCTAGAAT
GAAGACTTATATTGAAATTAGGTTTTCCAAGGTTCTTAGAAGACATTTTAATGGATTCTCATT
CATACCCTTGTATAATTGGAATTTTTGATTCTTAGCTGCTACCAGCTAGTTCTCTGAAGAACT
GATGTTATTACAAAGAAAATACATGCCCATGACCAAATATTCAAATTGTGCAGGACAGTAAAT
AATGAAAACCAATTTCTCAAGAAATAACTGAAGAAGGAGCAAGTGTGAACAGTTTCTTGTTG
TATCCTTTCAGAATATTTTAATGTACATATGACATGTGTATATGCCTATGGTATATGTGTCAA
TTTATGTGTCCCTTACATATACATGCACATATCTTTGTCAAGGCACCAGTGGGAACAATACA
CTGCATTACTGTTCTATACATATGAAAACCTAATAATATAAGTCTTAGAGATCATTTTATATC
ATGACAAGTAGAGCTACCTCATTCTTTTTAATGGTTATATAAAATTCCATTGTATAGTTATAT
CATTATTTAATTAAAAACAACCCTAATGATGGATATTTAGATTCTTTTAAGTTTTGTTTATTT
CTTTTAAGTTTTGTTTGTGGTATAAACAATACCACATAGAATGTTTCTTGTTTATATATCTCT
TTGTTTTGAGTATATCTGTAGGATAACTTTCTTGAGTGGAAATTGTCAGGTCAAAGGGTTTTGT
GCATTTTACTATTGATATATATGTTAAATTGTGTCAAATATATATGTCAAATTCCTCCAACA
TTGTTTTAATGTGCCTTTCCCTAAATTTCTATTTTAATAACTGTACTATTCTGCTTCTACAG
TTGCCACTTTCTCTTTTAAATCAACCAGATTAAATATGATGTGAGATTATAATAAGAATTATA
CTATTTAATAAAAATGGATTTATA

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FIGURE 494

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96866
><subunit 1 of 1, 348 aa, 1 stop
><MW: 39069, pI: 8.13; NX(S/T): 10
MLCPWRTANLGLLLIILTIFLVAEAEGAAQPNNSLMLQTSKENHALASSSLCMDEKQITQN
YSKVLAEVNTSWPVKMATNAVLCCPPIALRNLIITWEIILRGQPSCTKAYRKETNETKE
TNCTDERITWVSRPDQNSDLQIRPVAITHDGYRCIMVTPDGNFHRGYHLQVLVTPELTL
FQNRNRTAVCKAVAGKPAAQISWIPEGDCATKQEYWSNGTVTVKSTCHWEVHNVSTVTCH
VSHLTGNKSLYIELLPVPGAKKSAPLYIPYIILTIILTIIVGFIWLLKVNGCRKYKLNKT
ESTPVVEEDEMOPYASYTEKNNPLYDTTNKVKASQALQSEVDTLHTL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-24

Transmembrane domains:

Amino acids 78-98;267-286

N-glycosylation sites:Amino acids 31-35;60-64;69-73;116-120;122-126;185-189;
218-222;233-237;247-251;298-302**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 112-116

N-myristoylation sites:

Amino acids 103-109;259-265

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FIGURE 495

CCAGGTGCACAGCGCATCGCCCGAGGCTGTCACCGCCCTGCCCCGCCACCCCAGCTGTCCTG
GACCCAGGGGCAGGGAGAGGCTGGACGCCAGGTGCGCGGACACAGAAGCGTCTAAGCACAGCT
TCCTCCTTGCCGCTCCGGGAAGTGGGCAGCCAGCCAGGAACCAGTACCACCTGCACC**ATGGG**
GCTGTCCCGGAAGGAGCAGGTCTTCTTGCCCTGCTGGGGGCTCGGGGGTCTCAGGCCTCAC
GGCACTCATTCTCCTCCTGGTGGAGGCCACCAGCGTGCTCCTGCCACAGACATCAAGTTTGG
GATCGTGTGTTGATGCGGGCTCCTCCACACGTCCCTCTTCTGTATCAGTGGCCGGCGAACAA
GGAGAATGGCACGGGTGTGGTCAGCCAGGCCCTGGCCTGCCAGGTGGAAGGGCCTGGAATCTC
CTCCTACACTTCTAATGCTGCACAGGCTGGTGAGAGCCTGCAGGGCTGCTTGGAGGAGGCGCT
GGTGCTGATCCAGAGGGCCAGCATCGGAAAACACCCACGTTCTTGGGGGCCACGGCTGGCAT
GAGGTTGCTCAGCCGGAAGAACAGCTCTCAGGCCAGGGACATCTTTGCAGCAGTCACCCAGGT
CCTGGGCGGCTCTCCCGTGGACTTTTGGGGTGCCGAGCTCCTGGCCGGGCAGGCCGAAGGTGC
CTTTGGTTGGATCACTGTCAACTACGGCTTGGGGACGCTGGTCAAGTACTCCTTCACTGGAGA
ATGGATCCAGCCTCCGGAGGAGATGCTGGTGGGTGCCCTGGACATGGGAGGGGCTCCACCCA
GATCACGTTTCGTGCCTGGGGGCCCCATCTTGGACAAGAGCACCCAGGCCGATTTTCGCCTCTA
CGGCTCCGACTACAGCGTCTACACTCACAGCTACCTGTGCTTTGGACGGGACCAGATGCTGAG
CAGGCTCCTCGTGGGGCTGGTGCAGAGCCGCCCGCTGCCCTGCTCCGTCACCCGTGCTACCT
CAGCGGCTACCAGACCACACTGGCCCTGGGCCCGCTGTATGAGTCACCCCTGTGTCCACGCCAC
GCCCCCGCTGAGCCTCCCCCAGAACCTCACAGTTGAAGGGACAGGCAACCCTGGAGCCTGCGT
CTCAGCCATCCGGGAACTTTTCAACTTCTCCAGCTGCCAGGGCCAGGAGGACTGCGCCTTTGA
CGGGGTCTACCAGCCCCCGCTGCGGGGCCAGTTCTATGTGGAGGCCAGCTACCCTGGGCAGGA
CCGCTGGCTGCGGGACTACTGTGCCTCAGGCCTGTACATCCTCACCCCTCCTGCACGAGGGCTAC
GGTTTCAGCGAGGAGACCTGGCCCAGCCTCGAGTTCGAAAGCAGGCGGGCGGTGTGGACATT
GGCTGGACACTGGGCTACATGCTGAACCTGACCGGGATGATCCCGGCCGATGCGCCGGCTCAG
TGGCGGGCAGAGAGCTACGGCGTCTGGGTGGCCAAAGTGGTGTTCATGGTGCTGGCCCTGGTG
GCGGTGGTGGGGGCTGCCTTGGTCCAGCTCTTCTGTTGCAGGACT**AGT**GGGAAGGCGGAGGT
GGGCCCCCACAGAGCCACAGGCAGCTGCGTCCCGGATGCTGGAGGCTTCTGAGCCCTGAGC
GCCGTGGGGCCTTGCTCTGTGGCTCTGCCACGGTCAGGTGACAGCCACCTCCAGGGCACCGT
CAGGGTGGTGCTGGCCACAGAGGCTGCATGACCTCCCCTCCCGGCGTCCCTCCCCAACCTCC
TTCCGCAACTGGGCTTCCAGGGCCGTAGGTGCCTTTCTGCACACAGGCCGCCAGGACTCGTGG
TGTCTCCAGGCTGTGTGACTGCAGGGCCACATGCTGCCTGCAAACAGGGCAAGACCACGGAGG
CACAGGGGTCTTGCTCCTGATGGGGCCTCAGGAGGGGCGGAGAGGGGTGGAAGGGAGGGAGCT
GCCCCACCTGGACCCCCGCTCTCCCTGCTGTTGTCTGAGCAGATGGATGGAGTCCAGGCCTGG
GGGCTTCTGCTGGGCCAGCCCGCCTCCACACCCACTTGGAGGGTGAGACTGCAGTGGGGGT
TGTTTTTTATTAAAAGCATCATGGACACAGCAAAAAAAAAAAAAAAAAA

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FIGURE 496

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96870
><subunit 1 of 1, 458 aa, 1' stop
><MW: 49377, pI: 4.98, NX(S/T): 5
MGLSRKEQVFLALLGASGVSGLTALILLVLEATSVLLPTDIKFGIVFDAGSSHTSLFLYQ
WPANKENG TG VVSQALACQVEGPGISSYTSNAAQAGESLQGCLEEALVLIPEAQHRKTPT
FLGATAGMRLLSRKNSSQARDIFA AVTQVLGRSPVDFWGAELLAGQAEGAFGWITVNYGL
GTLVKYSFTGEWIQPPEEMLVGALDMGGASTQITFVPGGPILDKSTQADFRLYGSDYSVY
THSYLCFGRDQMLSRLLVGLVQSRPAALLRHPCYLSGYQTTLALGPLYESPCVHATPPLS
LPQNLTVEGTGNPGACVSAIRELENFSSCQGQEDCAFDGVYQPPLRGQFYVEASYPGQDR
WLRDYCASGLYILTLLHEGYGFSEETWPSLEFRKQAGGVDIGWTLGYMLNLTGMIPADAP
AQWRAESYGVVWAKVVFMVLALVAVVGAALVQLFWLQD
```

Important features of the protein:**Signal peptide:**

Amino acids 1-21

Transmembrane domain:

Amino acids 428-449

N-glycosylation sites:

Amino acids 67-71;135-139;304-308;325-329;410-414

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 133-137

N-myristoylation sites:Amino acids 50-56;123-127;165-171;207-213;234-240;
259-265;311-317;314-320;331-337;398-404;
413-419;429-435**GDA1/CD39 family of nucleoside phosphatases proteins:**

Amino acids 43-59;202-215

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FIGURE 497

GCCTTATAAAGTAGCCTCTGCATCTGCCTGCCTCGGGCAGAGGAGGGCTACCCTGGGGCTGAG
AGTTCACCTGTCTCAGGAACCACCTGAGCCACAGATCCTGTGGGCAGCGGCCAGGGCAGCCA
TGGCCTTGGGCAAGTAGGCTGGGCCTGCTGCTGGCACTGCTGCTGCCCCGTGGTGGTGCCTCCA
CGCCAGGCACCGTGGTCCGACTCAACAAGGCAGCATTGAGCTACGTGTCTGAAATTGGGAAAG
CCCCCTCTCCAGCGGGCCCTGCAGGTCACTGTCCCTCATTTCTGGACTGGAGTGGAGAGGCGC
TTCAGCCCACCAGGATCCGGATTCTGAATGTCCATGTGCCCCGCTCCACCTGAAATTCATTG
CTGGTTTCGGAGTGC GCCTGCTGGCAGCAGCTAATTTTACTTTCAAGGTCTTTCGCGCCCCAG
AGCCCCTGGAGCTGACGCTGCCTGTGGAAGTGTGGCTGACACCCGCGTGACCCAGAGCTCCA
TCAGGACCCCTGTGGTCAGCATCTCTGCCTGCTCTTTATTCTCGGGCCACGCCAACGAGTTTG
ATGGCAGTAACAGCACCTCCACGCGCTGCTGGTCTGGTGCAGAAGCACATTAAAGCTGTCT
TGAGTAACAAGCTGTGCCTGAGCATCTCCAACCTGGTGCAGGGTGTCAATGTCCACCTGGGCA
CCTTAATTGGCCTCAACCCCGTGGGTCTGAGTCCAGATCCGCTATTCCATGGTCACTGTGC
CCACTGTCACCAGTGACTACATTTCCCTGGAAGTCAATGCTGTTCTCTTCTGCTGGGCAACC
CCATCATCCTGCCCCAGGATGCCACCCCTTTTGTGTTGCCAAGGCATGTGGGTACCGAGGGCT
CCATGGCCACCGTGGGCCTCTCCAGCAGCTGTTTGACTCTGCGCTCCTGCTGCTGCAGAAGG
CCGGTGGCCTCAACCTGGACATCACAGGGCAGCTGAGGTGGATGACAACCTGCTGAACACCT
CTGCTCTGGGCCGGCTCATCCCGAGGTGGCCCGCCAGTTTCCCGAGCCCATGCCTGTGGTGC
TCAAGGTGCGGCTGGGTGCCACACCTGTGGCCATGCTCCACACAAACAACGCCACCCCTGCGGC
TGCAGCCCTTCGTGGAGGTCTGGCCACAGCCTCCAACCTCGGCTTTCAGTCCCTCTTCTCCC
TGGATGTGGTAGTGAAGTTGAGACTCCAGCTCTCTGTGTCCAAGGTGAAGCTTCAGGGGACCA
CGTCTGTGCTGGGGGATGTCCAGCTCACGGTGGCCTCCTCCAACGTGGGCTTCATTGATACAGAT
CAGGTGCGCACACTGATGGGCACCGTTTTTGAGAAGCCCCTGCTGGACCATCTCAATGCTCTC
TTGGCCATGGGAATTGCCCTCCCTGGTGTGGTCAACCTCCACTATGTTGCCCTGAGATCTTT
GTCTATGAGGGCTACGTGGTGATATCCAGTGGACTCTTCTACCAGAGCT**TGA**GGCAAGACCACT
GGGAGGCCTGAGAGTGGGCCAGCTCGCTGCTCAGGCGAATTTCTCATTTCAAGCCACTGGGGA
AACTGAGGCAAAACCATACTTAGTCATCACCAACAAGCTGGACTGCTTAGCTGGGCTGTTTTTA
TCTTCCCTGAGTGCCTGGGTCTCCCTCCCTCACTTCTGCCCTTTCCTTCCCTCCTCCTCTTCT
CCTCCCTCTTCCCTCATCTCCCCCTCCTTCTGCCCCACCCAGGGGGGAGCAGACTGCT
CCTCCAGGCTGTATAGACCTGCCCTCTTGCAATTAAACAACCTTCTCTTGAGCTGC

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FIGURE 498

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96872
><subunit 1 of 1, 458 aa, 1 stop
><MW: 49158, pI: 8.72, NX(S/T): 4
MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQRALQVTVPHFLDWS
GEALQPTRIRILNVHVPRLHLKFIAGFGVRLLAANFTFKVFRAPEPELELTLPVELLADT
RVTQSSIRTPVVSISACSLFSGHANEFDGSNSTSHALLVLVQKHIKAVLSNKLCLSISNL
VQGVNVHLGTLIGLNPVGPESQIRYSMVSVPTVTSDYISLEVNAVLFLLGNPIILPTDAT
PFVLPRHVGTEGSMATVGLSQQLFDSALLLLQKAGALNLDITGQLRSDDNLLNTSALGRL
IPEVARQFPEPMPVVLKVR LGATPVAMLHTN NATLRLQPFVEVLATASNSAFQSLFSLDV
VVNLRLQLSVSKVKLQGTTSVLGDVQLTVASSNVGFIDTDQVRTLMGTVF EKPLL DHLNA
LLAMGIALPGVVNLHYVAPEIFVYEGYVVISSGLFYQS
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

Transmembrane domain:

Amino acids 217-236

N-glycosylation sites:

Amino acids 96-100;151-155;293-297;332-336

N-myristoylation sites:

Amino acids 8-14;149-155;189-195;249-255;252-258;283-289

LBP / BPI / CETP family proteins:

Amino acids 22-50; 251-287

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FIGURE 499

TTGAAAATCTACTCTATCAGCTGCTGTGGTTGCCACCATTCTCAGGACCCTCGCC**ATG**GAAAGC
CCTTATGCTGCTCACCCCTGTCTGTTCTGCTCTGCTGGGTCTCAGCTGACATTCGCTGTCACCTC
CTGCTACAAGGTCCCTGTGCTGGGCTGTGTGGACCGGCAGTCCTGCCGCCTGGAGCCAGGACA
GCAATGCCTGACAACACATGCATACCTTGGTAAGATGTGGGTTTTCTCCAATCTGCGCTGTGG
CACACCAGAAGAGCCCTGTGAGGAGGCCTTCAACCAAAACCAACCGCAAGCTGGGTCTGACATA
TAACACCACCTGCTGCAACAAGGACAACCTGCAACAGCGCAGGACCCCGGCCCACTCCAGCCCT
GGGCCTTGTCTTCCTTACCTCCTTGGCTGGCCTTGGCCTCTGGCTGCTGCAC**TGA**ACTCATT
CCATTGGCTGCCCCCTCCTCCACCTGCCTTGGCCTGAGCCTCTCTCCCTGTGTCTCTGTATCC
CCTGGCTTTACAGAATCGTCTCTCCCTAGCTCCCATTTCTTTAATTAAACACTGTTCCGAGTG
GTCTCCTCATCCATCCTTCCACCTCACACCCTTCACTCTCCTTTTTCTGGGTCCCTTCCAC
TTCCTTCCAGGACCTCCATTGGCTCCTAGAAGGGCTCCCCACTTTGCTTCCTATACTCTGCTG
TCCCCTACTTGAGGAGGGATTGGGATCTGGGCCTGAAATGGGGCTTCTGTGTGTGTCCCCAGTG
AAGGCTCCCACAAGGACCTGATGACCTCACTGTACAGAGCTGACTCCCCAAACCCAGGCTCCC
ATATGTACCCCATCCCCATACTCACCTCTTCCATTTTGAGTAATAAATGTCTGAGTCTGGA
AAAAAAAAAAAAAAAAAAAA

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FIGURE 500

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96878
><subunit 1 of 1, 125 aa, 1 stop
><MW: 13821, pI: 8.60, NX(S/T): 2
MKALMLLTLSVLLCWVSADIRCHSCYKVPVLGCVDRQSCRLEPGQQCLTTHAYLGKMWVFSNL
RCGTPEEPCQEAFNQTNRKLGLTYNTTCCNKDNCNSAGPRPTPALGLVFLTSLAGLGLWLLH
```

Important features of the protein:**Signal peptide:**

amino acids 1-18

N-glycosylation sites.

amino acids 77-81, 88-92

N-myristoylation site.

amino acids 84-90

Ly-6 / u-PAR domain protein signature.

amino acids 85-98

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FIGURE 501

GGAGCCTCCTAATGCAGTCTTCTGCACAGTCCTGGGGACTGACTGACTGAATCACACCTCTGG
GGCTGGGGGCTGCTGACATGTGTGCCTTTCCTTGGCTGCTTCTTCTCCTGCTGCTCCAGGAGG
GCAGCCAAAGGAGACTCTGGAGATGGTGTGGATCCGAGGAAGTGGTTGCGGTCTTCAGGAGT
CCATCAGCCTCCCCCTGGAAATACCACCAGATGAAGAGGTTGAGAACATCATCTGGTCCTCTCAC
AAAAGTCTTGCCACTGTGGTGCCAGGGAAAGAGGGACATCCAGCTACCATCATGGTGACCAAT
CCACACTACCAGGGCCAAGTGAGCTTCCTGGACCCAGCTATTCCCTGCATATCAGCAATCTG
AGCTGGGAGGATTCAGGGCTTTACCAAGCTCAAGTCAACCTGAGAACATCCCAGATCTCTACC
ATGCAGCAGTACAATCTATGTGTCTACCATCCTAACTATGCTTCTGAGAAGCCTTCAACAGCC
TTCTGCCTCCTGGCCAAGGGATTGCTCATCTTCTTGCTCTTGGAATTCTGGCCATGGGACTC
TGGGTCATCCGAGTCCAGAAAAGACACAAAATGCCAAGGATGAAGAACTCATGAGAAACAGA
ATGAAATTGAGGAAGGAGGCAAAGCCTGGCTCCAGCCCTGCCTGACTGCTCCTTGGGAACCCC
AGTCCTGAGCTTGGTTTCTTCCCAGCACCCAGAGAATCCTTCCTCAGCTCTCTTCTTTCCAGG
GGAAGGAGGTGCTCAGGGGTGGGTATCCAGAGAGCCATACTTCTGAGGGAAGACTGGCTGGCA
ATAAAGTCAAATTAAGTGACCACA

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FIGURE 502

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96879
><subunit 1 of 1, 198 aa, 1 stop
><MW: 22584, pI: 9.40, NX(S/T): 1
MCAFPWLLLLLLLLLQEGSQRRLLWRWCGSEEVVAVLQESISLPLEIPPDEEVENIIWSSHKS
LATVVPGKEGHPATIMVTNPHYQGQVSFLDPSYSLHISNLSWEDSGLYQAQVNLRTSQIS
TMQQYNLCVYHPNYASEKPSTAFCLLAKGLLIFLLLVLAMGLWVIRVQKRHKMPRMKKL
MRNRMKLRKEAKPGSSPA
```

Important features of the protein:**Signal peptide:**

Amino acids 1-18

Transmembrane domain:

Amino acids 144-165

N-glycosylation site:

Amino acids 99-103

N-myristoylation site:

Amino acids 106-112

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FIGURE 503

ACGGGCCGCGAGCGGCAGTGACGTAGGGTTGGCGCACGGATCCGTTGCGGCTGCAGCTCTGCAG
TCGGGCCGTTTCCTTCGCCGCCGCCAGGGGTAGCGGTGTAGCTGCGCAGCGTCGCGCGCGCTAC
CGCACCCAGGTTTCGGCCCCGTAGGCGTCTGGCAGCCCCGGCGCCATCTTCATCGAGCGCC**ATGGC**
CGCAGCCTGCGGGCCGGGAGCGGCCGGGTACTGCTTGCTCCTCGGCTTGCAATTTGTTTCTGCT
GACCGCGGGCCCTGCCCTGGGCTGGAACGACCCTGACAGAATGTTGCTGCGGGATGTAAAAGC
TCTTACCCTCCACTATGACCGCTATACCACCTCCCGCAGGCTGGATCCCATCCACAGTTGAA
ATGTGTTGGAGGCACAGCTGGTTGTGATTCTTATACCCCAAAGTCATACAGTGTGAGAACAA
AGGCTGGGATGGGTATGATGTACAGTGGGAATGTAAGACGGACTTAGATATTGCATACAAATT
TGGA AAAACTGTGGTGAGCTGTGAAGGCTATGAGTCCTCTGAAGACCAGTATGTACTAAGAGG
TTCTTGTGGCTTGGAGTATAATTTAGATTATACAGAACTTGGCCTGCAGAACTGAAGGAGTC
TGGA AAGCAGCACGGCTTTGCCTCTTCTCTGATTATTATTATAAGTGGTCCTCGGCGGATTCT
CTGTAACATGAGTGGATTGATTACCATCGTGGTACTCCTTGGGATCGCCTTGTAGTCTATAA
GCTGTTCTTGAGTGACGGGCAGTATTCTCCTCCACCGTACTCTGAGTATCCTCCATTTTCCCA
CCGTTACCAGAGATTCACCAACTCAGCAGGACCTCCTCCCCAGGCTTTAAGTCTGAGTTCAC
AGGACCACAGAATACTGGCCATGGTGCAACTTCTGGTTTTGGCAGTGCTTTTACAGGACAACA
AGGATATGAAAATTTCAGGACCAGGGTTCTGGACAGGCTTGGGAAGTGGTGGAACTACTAGGATA
TTTGT TTGGCAGCAATAGAGCGGCAACACCCCTCTCAGACTCGTGGTACTACCCGTCCTATCC
TCCCTCCTACCCTGGCACGTGGAATAGGGCTTACTCACCCCTTCATGGAGGCTCGGGCAGCTA
TTCGGTATGTTCAAACCTCAGACACGAAAACCAGAACTGCATCAGGATATGGTGGTACCAGGAG
ACG**ATAA**AGTAGAAAGTTGGAGTCAAACACTGGATGCAGAAATTTTGGATTTTTCATCACTTT
CTCTTTAGAAAAAAAGTACTACCTGTTAACAATTGGGAAAAGGGGATATTCAAAGTTCTGTG
GTGTTATGTCCAGTGTAGCTTTTGTATTCTATTATTTGAGGCTAAAAGTTGATGTGTGACAA
AATACTTATGTGTTGTATGTCAGTGTAAACATGCAGATGTATATTGCAGTTTTTGAAAGTGATC
ATTACTGTGGAATGCTAAAAATACATTAATTTCTAAACCTGTGATGCCCTAAGAAGCATTAA
GAATGAAGGTGTTGTACTAATAGAACTAAGTACAGAAAATTTCAGTTTTAGGTGGTTGTAGC
TGATGAGTTATTACCTCATAGAGACTATAATATTCTATTTGGTATTATATTATTTGATGTTTG
CTGTTCTTCAAACATTTAAATCAAGCTTTGGACTAATTATGCTAATTTGTGAGTTCTGATCAC
TTTTGAGCTCTGAAGCTTTGAATCATTTCAGTGGTGGAGATGGCCTTCTGGTAACTGAATATTA
CCTTCTGTAGGAAAAGGTGGAAAATAAGCATCTAGAAGGTTGTTGTGAATGACTCTGTGCTGG
CAAAAATGCTTGAAACCTCTATATTTCTTTCGTTTCATAAGAGGTAAAGGTCAAATTTTCAAC
AAAAGTCTTTTAATAACAAAAGCATGCAGTTCTCTGTGAAATCTCAAATATTGTTGTAATAGT
CTGTTTCAATCTTAAAAAGAATCA

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FIGURE 504

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96889
><subunit 1 of 1, 339 aa, 1 stop
><MW: 36975, pI: 7.85, NX(S/T): 1
MAAACGPGAAGYCLLLGLHLFLLTAGPALGWNDPDRMLLRDVKALTLHYDRYTTSRRLDPIPQ
LKCVGGTAGCDSYTPKVIQCQNKGDGYDVQWECKTDLDIAYKFGKTVVSCEGYESSEDQYVL
RGSCGLEYNLDYTELGLOKLKESGKQHGFASFSDYKKWSSADSCNMSGITIVVLLGIAFVV
YKFLSDGQYSPPPYSEYPPFPHYRFTNSAGPPPPGFKSEFTGPQNTGHGATSGFGSAFTG
QQGYENSGPGFWTGLGTGGILGYLFGSNRAATPFSDSWYYPSYPPSYPGTWNRAYSPHGGSG
SYSVCSNSDTKTRTASGYGGTTRR

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 171-190

N-glycosylation site.

amino acids 172-176

Glycosaminoglycan attachment sites.

amino acids 244-248, 259-263, 331-335

Tyrosine kinase phosphorylation site.

amino acids 98-106

N-myristoylation sites.amino acids 68-74, 69-75, 131-137, 241-247, 247-253, 266-272,
270-276, 278-284, 312-318

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FIGURE 505

GCAAAAGGAAGGGAGGGAAGCACTCCATCATCTCACTGGGAAGAACGGCACGGGCATACCTGC
AGCTACTGGGGTTCCACTGGGCTTGAGGGTCGATTTTTTCACCTTTTGAAGGACAAG**ATG**CATT
GGAAGATGTTGCTGCTTCTGCTGTTGTATTACAATGCTGAGGCTTCTATGTGCCACAGGTGGA
GCAGGGCTGTGCTCTTCCCTGCCGCCACCGGCCAAAGAGGTCCTCATCACTGCCATTGAACC
CAGTCTTGCAGACCTCCCTGGAGGAGGTGGAGCTGCTCTACGAGTTCTGCTGGCCGAACCTTG
AGATCAGCCCTGACCTGCAGATCTCCATCAAGGACGAGGAGCTGGCCTCCTTGCGGAAGGCCT
CAGACTTCCGCACCGTCTGCAACAACGTCATCCCCAAGAGCATCCCAGACATCCGCCGGCTCA
GCGCCAGCCTCTCCAGCCACCCTGGCATCCTCAAGAAAGAAGACTTTGAAAGGACAGTGCTGA
CCCTGGCCTACACAGCCTACCGCACAGCCCTGTCCACGGCCATCAGAAGGACATCTGGGCGC
AGTCCCTCGTTAGCCTCTTCCAGGCCCTGAGGCACGACTTGATGCGCTCCTCACAGCCGGGAG
TACCTCCCT**TGA**GAGACTGGCCACACCAGGACCTCAGAGCAGGGACCAGCACAGTAATCCAGA
AAGTCTTCATTCTCTACTCCATTTACAGAGACCAGCAACAAAACACTTACCGCTGACACAGAG
CAGCAGAGATCAAACAGTAACCCCGATGCTCTTTTCTCCTTGAGTTTCCCTGGAAGACACATC
TGATTTCATGCCATCATGTGACCTGGGCTGGAAGAAAGGGCTGGAATGGTCATTCAAGACGCCT
CCATGGGCAGAATGGTTTGCCTATGGCAGGCAGAATTCTGATATGCTTCAACCCAGAGCAGTG
GCCACACACTCAAGAGTGAGAACAGGCGTGAGCCACCGTGCCTGGCCCAGGATCTAAAACTT
TCTAAGTTTCTCCATCGTTGGCATCCTCACAGCTATCTCCAATGTCACTCAAGAGACATCAA
CAGACATTTAACTGCTGCAGACTTCATTGCTCTGTCACCTCACCTTGAATCTAACAAATCAA
GTATTTCTGCAGGTCCAATGGTCTAAAATCAAATGCTTGTTAAATGACTTTTTTACAACACCCCTT
ACTTTCCTAATCCATTTCAATCTTATTTTTTTTTTATTGTGGTAAAAAACACATCACGTAAATG
TACCATCTTAACCATTTTTTAAGCATATGGTACAGCAGTGTTAACTCCATGCATGTTGTGAAAC
AGACCCCGGAACCTTCTCATCTTGTAATTCTGAAGTTCTATACCCACCGAACAACTCCTCTT
TTCCCTTCCCCCTGCCTGCCCCAGCTCTTGGCACCATTATTCTGCTTTCTGTTTTTGAGAGT
CTGACTACTTAAGATACCTCATACAAGCGGGATCTGGCTTACATTTCTTGAGCATTGTATTCT
GGAAAAGTGTTTCTTCTCTGAAAATGGGTAGAGTTCTGAAGGAGAACTACTGGTCTTATT
GTACACTTGCTGTACCTATTTTTTATTTAAACAAATATTCATCTATGGTATAATAAAGATGTCAT
GGTTGGAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 506

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96893
><subunit 1 of 1, 173 aa, 1 stop
><MW: 19733, pI: 8.78, NX(S/T): 0
MHWKMLLLLLLLYYNAEASMCHRWSRAVLFPAAHRPKRSSSLPLNPVLQTSLEEVELLYEF
LLAELEISPDQLQISIKDEELASLRKASDFRTVCNNVIPKSIPDIRRLSASLSSHPGILKK
EDFERTVLTLAYTAYRTALSHGHQKDIWAQSLVSLFQALRHDLMRSSQPGVPP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-17

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 36-40;84-88;105-109

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FIGURE 507

GGCGGCGGGCTGCGCGGAGCGGCGTCCCCTGCAGCCGCGGACCGAGGCAGCGGCGGCACCTGC
CGGCCGAGCAATGCCAAGTGAGTACACCTATGTGAACTGAGAAGTGATTGCTCGAGGCCTTC
CCTGCAATGGTACACCCGAGCTCAAAGCAAGATGAGAAGGCCAGCTTGTTATTAAGACAT
CCTCAAATGTACATTGCTTGTGTTTGGAGTGTGGATCCTTTATATCCTCAAGTTAAATTATAC
TACTGAAGAATGTGACATGAAAAAATGCATTATGTGGACCCTGACCATGTAAAGAGAGCTCA
GAAATATGCTCAGCAAGTCTTGCAGAAGGAATGTGTCCTCAAGTTTGCCAAGACATCAATGGC
GCTGTTATTTGAGCACAGGTATAGCGTGGACTTACTCCCTTTTGTGCAGAAGGCCCCCAAAGA
CAGTGAAGCTGAGTCCAAGTACGATCCTCCTTTTGGGTTCCGGAAGTTCTCCAGTAAAGTCCA
GACCCTCTTGGAACCTCTTGCCAGAGCACGACCTCCCTGAACACTTGAAAGCCAAGACCTGTCG
GCGCTGTGTGGTTATTGGAAGCGGAGGAATACTGCACGGATTAGAACTGGGCCACACCCTGAA
CCAGTTCGATGTTGTGATAAGGTTAAACAGTGCACCAGTTGAGGGATATTGAGAACATGTTGG
AAATAAACTACTATAAGGATGACTTATCCAGAGGGCGCACCCTGTCTGACCTTGAATATTAT
TCCAATGACTTATTTGTTGCTGTTTTATTGAAGAGTGTTGATTCAACTGGCTTCAAGCAATG
GTAAAAAAGGAAACCCTGCCATTCTGGGTACGACTCTTCTTTTGGGAAGCAGGTGGCAGAAAAA
ATCCCACTGCAGCCAAAACATTTTCAGGATTTTGAATCCAGTTATCATCAAAGAGACTGCCTTT
GACATCCTTCAGTACTCAGAGCCTCAGTCAAGGTTCTGGGGCCGAGATAAGAACGTCCCCACA
ATCGGTGTCATTGCCGTTGTCTTAGCCACACATCTGTGCGATGAAGTCAGTTTGGCGGGTTTT
GGATATGACCTCAATCAACCCAGAACACCTTTGCACTACTTCGACAGTCAATGCATGGCTGCT
ATGAACCTTCAGACCATGCATAATGTGACAACGGAAACCAAGTTCCTCTTAAAGCTGGTCAAA
GAGGGAGTGTTGAAAGATCTCAGTGGAGGCATTGATCGTGAATTTTGAACACAGAAAACCTCA
GTTGAAAAATGCAACTCTAACTCTGAGAGCTGTTTTTGACAGCCTTCTTGATGTATTTCTCCAT
CCTGCAGATACTTTGAAGTGCAGCTCATGTTTTTAACCTTTTAATTTAAAAACACAAAAAAAT
TTTAGCTCTTCCCACTTTTTTTTTTCTATTTATTTGAGGTCAGTGTTTGTGTTTGCACACCAT
TTTGTAATGAACTTAAGAATTGAATTGGAAGACTTCTCAAAGAGAATTGTATGTAACGAT
GTTGTATTGATTTTTAAGAAAGTAATTTAATTTGTAAACTTCTGCTCGTTTACACTGCACAT
TGAATACAGGTAACATAATTGGAAGGAGAGGGAGGTCACCTTTTGATGGTGGCCCTGAACCT
CATCTGCTGCCCTGCTGCGCTGCTTGGTGTGACCCACGGAGGATCCACTCCAGGATGACGT
GCTCCGTAGCTCTGCTGCTGATACTGGGTCTGCGATGCAGCGGCGTGAGGCCTGGGCTGGTTG
GAGAAGGTCACAACCCTTCTCTGTTGGTCTGCCTTCTGCTGAAAGACTCGAGAACCAACCAGG
GAAGCTGTCCTGGAGGTCCCTGGTGGAGAGGGACATAGAATCTGTGACCTCTGACAACTGTG
AAGCCACCCTGGGCTACAGAAACCACAGTCTTCCAGCAATTATTACAATCTTGAATTCCTT
GGGATTTTTTACTGCCCTTTCAAAGCACTTAAGTGTAGATCTAACGTGTTCCAGTGTCTGT
CTGAGGTGACTTAAAAAATCAGAACAAAACCTTCTATTATCCAGAGTCATGGGAGAGTACACCC
TTTCCAGGAATAATGTTTTGGGAAACACTGAAATGAAATCTTCCAGTATTATAAATTGTGTA
TTTAA

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FIGURE 508

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96897
><subunit 1 of 1, 362 aa, 1 stop
><MW: 41736, pI: 8.80, NX(S/T): 3
MRRPSLLLLKDILKCTLLVFGVWILYILKLNYTTEECMDKMKMHYVDPDHVKRAQKYAQQVL
QKECRPKFAKTSMAALLFEHRYSDLLPFVQKAPKDSEAESKYDPPFGFRKFSSKVQTLLE
LLPEHDLPEHLKAKTCRRCVVIGSGGILHGLELGHNTLNQFDVVIRLNSAPVEGYSEHVGN
KTTIRMTYPEGAPLSDLEYYSNDLFVAVLFKSVDFNWLQAMVKKETLPFWVRLFFWKQVA
EKIPLQPKHFRILNPVVIKETAFDILQYSEPQSRFWGRDKNVPTIGVIAVVLATHLCDEV
SLAGFGYDLNQPRTPPLHYFDSQCMAAMNFQTMHNVTTETKFLKLKLVKEGVVKDLSSGGIDR
EF
```

Important features of the protein:**Transmembrane domains:**

Amino acids 11-27;281-297

N-glycosylation sites:

Amino acids 30-34;180-184;334-338

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 2-6;109-113;223-227

N-myristoylation sites:

Amino acids 146-152;150-156;179-185;191-197

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FIGURE 509

GGGCGGACGCAGTGCAGTAAGAGCAGATGGGCGGACCCAAATTTCTTCGGCTTCACGATTTTG
CCGAGGTCTAGCCCTGCATCCAGCCTTGAAACAGGGTGGGGAGGAGGCAGAAAGGGGAGGGAC
TGCACTCCCTCTGAGCGTGCTAGCTCCGACTGCCTGACGGATCACCCCTCCGCTCCAACATGG
CTAGTTCCCTCAACGCCGTGACTCAAGCCTGTTGTGCCAGGCAGGGCGCACTCAGCAGCGCAGC
CCCACAGGTGGCGAAGGCTCCGCGAGAGGGTTCGCCGAGGCTAGACAGTGGAGTGCCGCACA
GCGCGCCTTCCAGCCTCGCAGCCGCCACCCTAGCGGTTCCGACCCGGCGCCAGCAGGCCTGCT
TGGTCGATCTTCGAGCCAAAGATGCGGGCGAGGCTGGAAGATGGCTCTGTCTGGGGGGCTGCGG
TGCTGCCGCCGGGTACTGTCCTGGGTGCCAGTGCTCGTTATTGTCCTCGTCGTGCTCTGGTCC
TACTATGCCTACGTCTTTGAACTCTGCCTGGTTATTTACCTCATACTCTACCATGCCATCTTT
GTGTTCTTTACCTGGACCTACTGGAAGTCTATCTTTACACTCCCACAGCAGCCAAACCAGAAG
TTCCACTTGTCTTACACAGACAAGGAGCGCTATGAAAATGAAGAAAGACCTGAGGTCCAGAAG
CAGATGCTTGTTGATATGGCCAAAAAGCTACCGGTTTACACAAGAACTGGAAGTGGAGGTCAG
TTCATCCAAAGGCAGCTAGAGAGGCAGCTCAGCAAGTATCTCAGAAAGGCTAAGTCATATATG
TTCTCAAACTAGCCCTTTTTTTTCCCTCCCATCTTCTGAAAACCACTATGGAGATTTTTCTCCA
CATTTTATTTCTAAAAAATTTTAAACACATATCAAAGCTGGAAGAATTGTATAGTAAACAAAC
TGTATACCCCAAACCTGGATTCTTCTGCTAACATTTTTCTGTGTTGCTATATCACATATCTATC
CACATATGCATACCTCTATTTATCTTTCGTCAAGCCATCTTATGTTTCTGATGCATTTCAAAG
TAAATAGCTGACATCAGTAAGACATCTACCTAAATATTTTATTCTGTTTTGTAAAATTTACA
TACAAAACATGCATAATCTTAAGGGTACCATTCCATGTATTTTGAAAAGTGACACATCTGT
GTAACATAACCCCAATAAAATTGCCATCACCTCAG

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FIGURE 510

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA98564
><subunit 1 of 1, 143 aa, 1 stop
><MW: 17255, pI: 9.99, NX(S/T): 0
MRRGWKMALSGGLRCCRRVLSWVPVLVIVLVVLWSYYAYVFELCLVIYLLILYHAIFVFFT
WTYWKSIFTLPQQPNQKFHLSYTDKERYENEERPEVQKQMLVDMAKKLPVYTRTGSGGQF
IQRQLERQLSKYLRKAKSYMFSN
```

Important features of the protein:**Transmembrane domain:**

Amino acids 24-45

N-myristoylation sites:

Amino acids 11-17;12-18

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FIGURE 511

CAGCCGGGGCG**ATG**GCGGGGCTCTGGCTGGGGCTCGTGTGGCAGAAGCTGCTGCTGTGGGGCG
CGGCGAGTGGCCTTTCCCTGGCCGGCGCCAGTCTGGTCCTGAGCCTGCTGCAGAGGGTGGCGA
GCTACGCGCGGAAATGGCAGCAGATGCGGGCCATCCCCACGGTGGCCCGCGCCTACCCACTGGTG
GGCCACGCGCTGCTGATGAAGCCGGACGGGCGAGGTAAGGGCCGGCGCTCCTCCTGGAGCGCA
ACGGGGTCCGCAGCCCCGTTCACCCCTCCGATCAGCCAGGAACCCGCTGCTTGTGGCGCTGG
CCGCAGGAGAGAGGAGCCTGTCACCCTGTGGAGAATGCACTCCCAGTTCTAGTCGTTGCCCT
TGGCACCCGCCGACACTGCTAGTGCCCCATCCCAAAGTGAGCATTCTTTGTGTGTAGCACA
GGATGCGGTATTTCCAAACCCCTGCCCTCGGTCTTTTCCACCTCACCGCTGCTCAGCTCTCA
AAGCCCTGCCGTTTCCCTCCTGCCTTGGCTTGGGAAGCCT**TAG**GAACAGAAGCTCCCTGGGAGC
ACAGAGCGGTTTTAAACTGGCCAACACCTTAACGCCAGAGCCGCCCTCCTCTCGCTGCCACT
TTGGAAAATAAGAGACTAGAGATTCAGTGGACGCTTCCTCCCGGCATCACAAGACTTGACTGC
TGCTTCAGTTCCCGCTTGACCTTCATACTTTAGCCCTTTAAAGGATGTTACATAATAACAATT
AAGAGACGGCAGGGCCCTTCAGGCAGACTTCTTTGGAGGGTGTCAAACGCCCTTGTTTATTAAAG
AGTGAATTTTTTAATTAAATCATGTTTTAAACAGAGATGGACATTTTATTGATGGAAAAA
ATCACGTAAAGTTAGAAAGCTCTCAAAGTACCTGGTATTTACAACCTCCCTGTCAGGGAGGGC
GAACTCGATCTCAGAGTTTTATTTTCATCAGGGATTACGTTGAGGTACCCAGAAATGAGAAGA
TTTGCCCAAATGGCATATTTTAAATTTGGCCAGACCAGAACCCAGTTTCCTCTGGGATTAT
TTGTTAGTAATCGTTTTACAGGCTGAGCATTAACTAACTCCAAAGCTTGAAGGACTTTTTCTC
ATTTTCACTTGTTTTCTCTAATAAAAATAATGCTGTAATTTCACTTCACAAGATGAGGCCTC
ATGGAAGAGTGTTTTACCAAATATTTAAATACTTTGACAGAAAAAATCAAGCGAACTCTTT
GCCAACCAAATATCATCATGACTGATGTAACAAGTAATCCAACACAGATATGAAAATCACTGG
TAAAATCATCTCAGTTAATTCTAAAAGCAGAGCTAACCACCCCTTTTGTCTTAAGGCTTTAT
GGTATTAATAAAATAAACTGTACAAAATATAGATTTTCCCCTATCCCCTACCCCTGGAAAGTA
ATATACTGAAGTCTCATCATACTGTTTTGGGGATTCCAGTAATTAATCTCTAGTGAACAAA
GACCTGTTTCAAACAACCTGTGAGCTGACTGGACTATTTAAAGTAATTCCTTGTTAGTCAC
TTTCAGAGTGAAGACAATGACGAATACTGTCTTTTACAAAGGGACTTTTTATTCCACCAACAA
ATTCTGGATTTTGGCATCAGGAAAACCACTGTTCAATTTCCAACACTATATCCAAGTTGTTTG
AGAAATTATTTAAACTCTTTAACTTAGAGGGTTTTCTTTCTCCTTTACTTGTTAAAGTGACT
ATATTACAGAGTCACTTTAAGGATTAAATTTATTGCATGCAAAGTTTCTAGATCACTGTCTAG
AAGTCAGTTAGAGTAAGTTCTTTAGTTGTCAATCAAGCATTTAGTAAGGCCCTGCTTTGTGCC
CAGTGTTGACCTCAACAAAGTTGGGGATATCAGAATATTCTAAGATACAGTCGTTGTTCCCAA
GAATCTTGCTTTTCATACATAAGAGGTGTTGCGTTTCATTTGCGGCTAATGTCCAAACGCTG
GCCTCAGCCATTTACCTTGAAGATTGCAGTTGGCTTCCAACCTGGCCTCTAACTCTAATCTA
GCATTTTCCAGTCCATTGTGACAAAGTCTGCCTTCCCAGCTACTCCCAGCTGTTGGACCTGC
TGCCTTAGAACACAGATTGGTACCTCGTGCC

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FIGURE 512

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA107443
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19353, pI: 10.97, NX(S/T): 0
MAGLWLGVLVWQKLLLWGAASALSLAGASIVLSLLQRVASYARKWQQMRPIPTVARAYPLV
GHALLMKPDGRGKGRSSWSATGSAAPFPPSDQPGTRCLWRWPQERGACHPVENALPVLV
VAPWHPPTLLVPHPKVSIFFVCSTGCGISKPLPSVFSHLTAAQLSKPCRFLLPWLGKP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-25

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 75-79

N-myristoylation sites:

Amino acids 3-9;17-23;145-151

Amidation site:

Amino acids 73-77

Leucine zipper pattern:

Amino acids 8-30

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FIGURE 513

GGCGGCTGGACGAGGACGCTCAGAGCCCAGCTCTCGAGAGTTCAAGCAACCGACGGTTCC
CCACTGCTCCCAGGAGCGGTTACCTGGGCACTCTGTGCCCCCTCCTTCCTGTTGGGGCCCA
GGCCGAGGACCTGCCAGTAGGGCTCAGTTGCCTGGAGCCCGTTAGCCCCATCCCCAGTT
CACTTTGCTTGTGGGATCTCCCCGTTGCTCCTGCCCCTGGACTGAGTGGCAGGCCATCCT
ACAAGCACCCGGACACTTGACATCAGTGGTGTCAAGACAACCTCTAAGAAGGTTTTCCGTG
ATCCTGCAAGCCCTGCCTTCCTTCCTGGGATCCTGCCTTCAATTTGATTGCACAGGTACC
ACAGCAAGCCAGTGCTGTGTGCTCCGAGTTCAGGGCGTCTCCAGCTCAGCCACTGCAC
TGAGAACAATGGACTCTCTGTGGGGCCAGGAGCCGGGAGTCACCCCTTTGGGGTCCACAA
CACCCGGCTGTCCCCAGACTTGTGTCCAGGGAAGATAGTGTGAGGGCCCTCAAGGAGAG
CGGGGCAGGGATGCCTGAGCAGGACAAGGACCCTAGAGTCCAAGAGAATCCTGGTGATCA
GAGAAGGGTCCCCGAGGTACCCGGGGATGCACGGTCTGCATTTGCGCCCCCTGCGGGACAA
TGGAGGCCCTCTCTCCCTTTGTGCCGGGGCCCGGGCCTCTGCAGACAGACCTCCATGCCCA
GAGGTCAAGAAATCAGATATAACCAGACATCCCAGACCTCCTGGACGAGCTCCTGCACCAA
CCGAAATGCCATCTCCAGCTCCTACAGCTCCACGGGAGGCTTGCTGGGGCTAAAGCGGAG
GAGGGGGCCAGCCTCATCCCACTGCCAGCTGACCCTCAGTTCTCTCAAAGACAGTGAGTGA
GGACAGGCCTCAGGCTGTCTCTCAGGTACACCCAGTGTGAAAAGGCAGCAGATATAGC
ACCAGGGCAGACACTCACCTCAGGAATGACTCCTCCACATCCGAGGCCTCTAGGCCCAG
TACACACAAGTTTCCCCTGCTGCCACGCAGGCGAGGGGAGCCTTTGATGCTGCCACCTCC
CTTAGAGCTGGGGTACCGGGTCACTGTTGAAGACCTGGACCGGGAGAAGGAGGCGGCCTT
CCAGCGCATCAACAGTGCCTGCAGGTTGAGGACAAGGCCATCTCGGACTGCAGACCCCTC
ACGGCCTTCCCACACTTTGTCTCTCACTTGCAACAGGGGCTTCTGGTCTGCCTGCCGTTTC
TAAAGCACCCAGTATGGATGCACAGCAGGAGACACACAAGTCCCAAGACTGCCTGGGCCT
ACTGGACCCCTTAGCATCTGCTGCAGGGGTCCCCTCTACAGCTCCCATGTCTGGGAAGAA
GCACAGACCACCAGGCCCCCTGTTCTCCTCCTCAGATCCCCTTCTGCCACCTCTTCTGA
TTCCCAGGACTCAGCCCAGGTACCTCGCTGATTCTCTGCCCCCTTCCCAGCTGCAAGCAT
GGATGCGGGCATGAGAAGAACAAGGCATGGCACTTCTGCTCCTGCAGCTGCCGCAGCAGC
CCCTCCCCGCTCCACATTGAACCCACGTTGGGGTCACTACTGGAGTGGATGGAGGCCCT
TCACATTTCTGGGCCTCAGCCACAGCTGCAGCAGGTGCCAGAGGTGAGAACCAGAGATC
CCAGACCTCCTGGACCAGCTCGTGCCCCAAATGAATGCCATCTCGAGCCCCCTACAGCTC
TACGGGAGGCCTCCCGGAACAAAAGCGGAAGAGGGGCCAGCCTCATCCCACTGCCAGCTG
ACCCTCAGTTCTCTCAAACACAGTGAGTGAGGACGGACCTCAGGCTGTCTCTCGGGTCA
ACCCAGTGTGAAAAGACGGCAGATACAGCACCAGGGCAGACACTCGCCTCCAGGGGTGGC
TCCCCCAGATCCCAGGCCTCTAGGCCCCGTATATGCAAGTTTCCCCTGCTGCCACGCAGG
CGAGGGGAGCCTTTGATGCTGCCACCTCCCTTAGAGATGGGGTACCGGGTCACTGCTGAA
GACCTGGACCGGGAGAAGGAGGAGGCATTCCAGCGCATCAACAGTGCCTGCAGGTTGAG
GACCAGGCCATCTAGGACTGCAGACCCTCACGGCCTTCCCACACTTTGTCTCACTTGCA
ACAGGGGCTTCTGGTCTGCCTGCCGTTTCTAAAGCACCCAGTATGGATGCACAGCAGGAG
ACACACAAGTCCCAAGACTGCCTGGGCCTAGTGGCCCCCTGCATCTGCTGCACAGGCCT
GTAGTCCCAGCTACTTGGGAGGCTGAGGCAGGAGAACGGCATAAACCCGGGAGGCAGAGC
TTGCAGTGAGCTGAGATCGCGCCACTGCACTCCAGCCTGGGTGACAGAGCGAGACTCCGT
CTC

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FIGURE 514

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA107786
><subunit 1 of 1, 428 aa, 1 stop
><MW: 45450, pI: 9.28, NX(S/T): 3
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VPEVTGDARSAFRPLRDNGGLSPFVPGPGPLQTDLHAQRSEIRYNQTSQTSWTSSCTNRN
AISSSYSSSTGGLLGLKRRRGPASSHCQLTLSSSKTVSEDRPQAVSSGHTQCEKAADIAPG
QTLTLRNDSSSTSEASRPSTHKFPLLPRRRGEPLMLPPPPELGYRVTVEDLDREKEAAFQR
INSALQVEDKAISDCRPSRPSHTLSSLATGASGLPAVSKAPSMDAQQETHKSQDCLGLLD
PLASAAGVPSTAPMSGKKHRPPGPLFSSSDPLPATSSDSQDSAQVTS LI PAFPAASMDA
GMRRTRHGTSAPAAAAAAPPRSTLNPTLGSLLLEWMEALHISGPQPQLQOVPRGQNQRSQT
SWTSSCPK .
```

Important features of the protein:**N-glycosylation sites:**

Amino acids 105-109;187-191

Glycosaminoglycan attachment site:

Amino acids 38-42

N-myristoylation sites:

Amino acids 15-21;130-136;180-186;307-313;361-367

Amidation site:

Amino acids 315-319

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 106-117

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FIGURE 515

GTCAGGGCCAGGGTGAGCGCCCGACTCCGAGCTGTCCCCGCTCCCGGCGCGGCGCTCCGCTCT
CAGCCACCTCACGGCTGCCAGGAGTGCGCGGGAGTTTGCCCCGGAGCGCGGGGAAGTTTCCTC
CGAAGCTGCGCTCCTGGAACAGCAGCACCTGCAAGCGCCCGGCAGCGGGCCCGCGAGGTTACTT
TATGGAATTGGGCTCTTAGAGAACAAGAAAAGACTGAAGTTTACGGGAAAACAAATCATGTG
GTCTTCAGATTCTGAAATAAGGAGAAATGCAGCCATCTGAAATGGTCATGAACCCCAAACAAG
TCTTCCTCTCTGTGCTGATATTTGGAGTAGCTGGGCTACTCCTCTTCATGTATTTGCAAGTCTGG
ATTGAAGAACAACATACAGGGAGAGTGGAGAAGAGAAGAGAACAAAAAGTAACTTCAGGATGG
GGACCAGTGAAGTACTTGCGGCCTGTACCCAGAATCATGAGTACAGAAAAAATCCAGGAACAT
ATCACCACCAGAACCCCAAGTTTACATGCCTGAGGATGTACGAGAAAAAAGGAAAATCTT
CTACTCAATTCTGAGAGATCTACTAGGCTCTTAACAAAGACCAGTCATTACAAAGGAGGGGAT
CAAGCTTTAAGTAAGTCCACAGGGTCAACACAGAGAAGTTGATTGAAAAACGTCAAGGAGCT
AAGACTGTTTTTAAACAAGTTCAGCAACATGAATTGGCCAGTGGACATTCACCCTTTAAACAAA
AGTTTAGTCAAAGATAATAAATGGAAGAAAAGTGAAGAGACCCAAGAGAAACGAAGGTCTTTC
CTTCAGGAGTTTTTGCAAGAAATACGGTGGGGTGAGTCATCATCAGTCACATCTTTTTCATACA
GTATCCAGAATCTATGTAGAAGATAAACACAAAAATCTTATATTGTGAGGTACCTAAGGCTGGC
TGTTCCAATTGGAAGAAGATTCTGATGGTACTAAATGGATTGGCTTCCCTCTGCATACAACATC
TCCCACAATGCTGTCCACTACGGGAAGCATTTGAAGAAGCTAGATAGCTTTGACCTAAAAGGG
ATATATACCCGCTTAAATACTTACACCAAAGCTGTGTTTGTTCGTGATCCCATGGAAAGATTA
GTATCAGCCTTTAGGGACAAATTTGAACACCCCAATAGTTATTACCATCCAGTATTCGGAAAG
GCAATTATCAAGAAATATCGACCAAATGCCTGTGAAGAAGCATTAATTAATGGATCTGGAGTC
AAGTTCAAAGAGTTTATCCACTACTTGCTGGATTCCCACCGTCCAGTAGGAATGGACATTCAC
TGGGAAAAGGTCAGCAAACCTCTGCTATCCGTGTTTGATCAACTATGATTTTGTAGGGAAATTT
GAGACTTTGGAAGAAGATGCCAATTACTTTTTACAGATGATCGGTGCTCCAAAGGAGCTGAAA
TTTCCCAACTTTAAGGATAGGCACCTCTCCGATGAAAGAACCAATGCTCAAGTCGTGAGACAG
TATTTAAAGGATCTGACTAGAAGTGAAGAGACAATTAATCTATGACTTTTATTACTTGGACTAT
TTAATGTTTAATTATACAACCTCACTTTTTGTAGTTTTGCATTCATTTTCTAAAACCCTGTATAT
ACTTAATGATGATAAGTTCAAATCAGCTGTAATTTTTCTATAATTCTCTGTATGACAGAAATT
TAACCAAGTGCAGTTGTCTTGATTTAATGTAGATTTTTACCAAATAGTATGACACCAATTGGC
ACAAAGTTATAGGAAAATCACCTACAGGAGATGTAAACAACCTTGAGTTGCTCTAAAATGTTTG
GAAAAGAGCTGCTTTTGCAATTATGAATTATATTGTTGAAGCAATAACCTAGCCAGCTGTTGCA
TTAGCTAAAGCAGCCTCTTGCAATGGTAGGAAAAAAGGATCTCAAATAGCATGAGTGTATGTC
TATATCCTGAAATTTATTGTCTAAAATGCATGAATATATTTTTAGCAGTCTGTGGCATATTAA
TCAAACGTGTGAATTGTTTTCTTACACCCTGGAAATCTTCTATCAACTATAATGATAAATCC
ATTTTGAAGTGATATTTTGGACTTAGGCATTTTACTTTAGATTGGAAGGCATTATGTGATTTACA
ATATGAGAATATAGCAGAAAAACCA

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FIGURE 516

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><subunit 1 of 1, 443 aa, 1 stop
><MW: 52021, pI: 9.63, NX(S/T): 4
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LRPVPRIMSTEKIQEHITNQNPKFHMPEDVREKKENLLLNSERSTRLLTKTSHSQGGDQA
LSKSTGSPTEKLIKROGAKTVFNKFNSNMNWPVDIHPLNKS LVKDNKWKKTETQEKRRS
FLQEFCKKYGGVSHHQSHLFHTVSRIVYEDKHKILYCEVPKAGCSNWKRLMVLNGLASS
AYNISHNAVHYGKHLKKLDSFDLKGITYTRLNTYTKAVFVRDPMERLVSAFRDKFEHPNSY
YHPVFGKAIKKYRPNACEEALINGSGVKFKEFIHYLLDSHRPVGMDIHWEKVS KLCPYPC
LINYDFVGKFETLEEDANYFLQMIGAPKELKFPNFKDRHSSDERTNAQVVRQYLKDLTRT
ERQLIYDFYYLDYLMFNYYTPLL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-24

N-glycosylation sites:

Amino acids 159-163;243-247;324-328;437-441

Glycosaminoglycan attachment site:

Amino acids 53-57

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 177-181

Tyrosine kinase phosphorylation site:

Amino acids 329-337

N-myristoylation sites:

Amino acids 116-122;236-242

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FIGURE 517

GGAACCTTCCCAGGCACCCTGTGTGGCCGCACTGCTCCCTCTGGCCCAACCATGCCTCTGTCCAGCCACCTGCTGC
CCGCTTGGTTCCTGTTCCCTGGCAGGGTCCTCAGGCTGGGCTGGGTCCCCAACCCTGCAGGAGCCCTGGCCAGG
CCGTGTGCAACTTCGTGTGTGACTGCAGGGACTGCTCAGATGAGGCCAGTGTGGTTACCACGGGGCCTCGCCCA
CCTGGGCGCCCCCTTCGCTGTGACTTCGAGCAGGACCCCTGCGGCTGGCGGGACATTAGTACCTCAGGCTACA
GCTGGCTCCGAGACAGGGCAGGGGCCGCACTGGAGGGTCCTGGGCTCACTCAGACCACACACTGGGCACCGACT
TGGGCTGGTACATGGCCGTGGAAACCACCGAGGGAAAGAGGCATCCACCGCAGCCCTGCGCTCGCCAACCCTGC
GAGAGGCAGCCTCCTCTTGAAGCTGAGGCTCTGGTACCACGCGCCCTCTGGAGATGTGGCTGAACTGCGGGTGG
AGCTGACCCATGGCGCAGAGACCTGACCCTGTGGCAGAGCACAGGGCCCTGGGGCCCTGGCTGGCAGGAGTTGG
CAGTGACCACAGGCCGCATCCGGGTGACTTCCGAGTGACCTTCTCTGCCACCCGAAATGCCACCCACAGGGGCG
CTGTGGCTCTAGATGACCTAGAGTTCTGGGACTGTGGTCTGCCACCCCCAGGCCAACTGTCCCCGGGACACC
ACCAGTGCCAGAACAAGGTCTGCGTGGAGCCCCAGCAGCTGTGCGACGGGGAAGACAACCTGCGGGGACCTGTCTG
ATGAGAACCCTACTCACCTGTGGCCGCCACATAGCCACCGACTTTGAGACAGGCCTGGGCCCATGGAACCGCTCGG
AAGGCTGGTCCCGGAACCACCGTGCTGGTGGTCTGAGCGCCCTCCTGGCCACGCGCTGACCACAGCCGGAACA
GTGCACAGGGCTCCTTCCCTGGTCTCCGTGGCCGAGCCTGGCACCCCTGCTATACTCTCCAGCCCCGAATTCCAAG
CCTCAGGCACCTCCAACCTGCTCGCTGGTCTTCTATCAGTACCTGAGTGGGTCTGAGGCTGGCTGCCTCCAGCTGT
TCCTGCAGACTCTGGGGCCCGGCCCCCCGGGCCCCCGTCTGCTGCGGAGGCGCCGAGGGGAGCTGGGGACCG
CCTGGGTCCGAGACCGTGTGACATCCAGAGCGCTACCCCTTCCAGATCCTCCTGGCCGGGCAGACAGGCCCGG
GGGGCGTCTGGGTCTGGACGACCTCATCTGTCTGACCACTGCAGACCAGTCTCGGAGGTGTCCACCTGCAGC
CGCTGCCTCCTGGGCCCCGGGCCCCAGCCCCCAGCCCTGCCGCCAGCTCGCGGCTCCAGGATTCTTGAAGC
AGGGGCATCTTGCCTGCGGGGACCTGTGTGTGCCCCGGAACAACCTGTGACTTCGAGGAGCAGTGCAGAGGGG
GCGAGGACGAGCAGGCCTGTGGCACCACAGACTTTGAGTCCCCGAGGCTGGGGGCTGGGAGGACGCCAGCGTGG
GGCGGCTGCAGTGGCGCGTGTCTCAGCCCAGGAGAGCCAGGGGTCCAGTGCAGCTGCTGCTGGGCACTTCTGT
CTCTGCAGCGGGCCTGGGGCAGCTAGGCGCTGAGGCCCGGTCTCACACCCCTCCTTGGCCCTTCTGGCCCCA
GCTGTGAACTCCACCTGGCTTATTATTTACAGAGCCAGCCCCGAGAGGTCTCCTGTAACCTTTGAGCGGGACACAT
GCAGCTGGTACCCAGGCCACCTCTCAGACACACACTGGCGTGGGTGGAGAGCCGCGGCCCTGACCACGACCACA
CCACAGGCCAAGGCCACTTTGTGCTCCTGGACCCACAGACCCCTGGCCTGGGGCCACAGTGGCCACCTGCTCT
CCAGGCCCCAGGTGCCAGCAGCACCACGGAGTGTCTCAGCTTCTGGTACCACCTCCATGGGCCCCAGATTGGGA
CTCTGCGCCTAGCCATGAGACGGGAAGGGGAGGAGACACACCTGTGGTGCGGTCAAGCACCCAGGGCAACCCT
GGCAGAGGCCTGGGCCACCCCTTTCCACAGCCTGGCTCCCATGCCAGTACCAGTGTCTGTCGAGGGCCTCC
GGGACGGATACACGGCACCATGGCGCTGGACGATGTGGCCGTGCGGCCGGGCCCTGCTGGGCCCCAATTACT
GCTCCTTTGAGGACTCAGACTGCGGCTTCTCCCTGGAGGCCAAGGTCTCTGGAGGCGGAGGCCAATGCCTCGG
GCCATGCTGCCTGGGGCCCCCAACAGACCATAACCTGAGACAGCCCAAGGGCACTACATGGTGGTGGACACAA
GCCCAGACGCACTACCCCGGGGCCAGACGGCCTCCCTGACCTCCAAGGAGCACAGGCCCTGGCCAGCCTGCTT
GTCTGACCTTCTGGTACCACGGGAGCCTCCGCAGCCAGGCACCCTGCGGGTCTACCTGGAGGAGCGCGGGAGGC
ACCAGGTGCTCAGCCTCAGTGCCACGGCGGGCTTGCTGGCGCCTGGGCAGCATGGACGTGCAGGCCGAGCGAG
CCTGGAGGGTGGTGTGAGGCGAGTGGCCGAGGCGTGGCACACTCCTACGTGGCTCTGGATGATCTGCTCCTCC
AGGACGGGCCCTGCCCTCAGCCAGGTTCTGTGATTTTGAAGTCTGGCCTGTGTGGCTGGAGCCACCTGGCCGGG
CCGGCCTGGGCGGATACAGCTGGGACTGGGGCGGGGAGCCACCCCTCTCGTTACCCCGAGCCCTGTGGACC
ACACCTGGGCACAGAGGCAGGCCACTTTGCCTTCTTTGAACTGGCGTGTGGGCCCCGGGGGCCGGCCGCT
GGCTGCGCAGCGAGCCTCTGCCGGCCACCCAGCCTCCTGCCTCCGCTTCTGGTACCACATGGGTTTCTCTGAGC
ACTTCTACAAGGGGGAGCTGAAGTACTGCTGCACAGTGTCTAGGGCCAGCTGGCTGTGTGGGGCGCAGGCGGGC
ATCGGCGGCACCAAGTGGCTGGAGGCCAGGTGGAGGTAGCCAGTGCCAAGGAGTTCCAGATCGTGTGGAAGCCA
CTCTGGGCGGCCAGCCAGCCCTGGGGCCATTGCCCTGGATGACGTGGAGTATCTGGCTGGGCAGCATTGCCAGC
AGCCTGCCCCCAGCCCGGGGAACACAGCCGCACCCGGGTCTGTGCCAGCTGTGGTTGGCAGTGGCCTCCTATTGC
TCATGCTCCTGGTGTCTGGGACTTGGGGACGGCGCTGGCTGCAGAAGAAGGGGAGCTGCCCTTCCAGAGCA
ACACAGAGGCCACAGCCCTGGCTTTGACAACATCCTTTCAATGCGGATGGTGTACCCCTCCCGGCATCTGTCA
CCAGTGATCCGTAGACCACCCAGACAAGGCCCGCTTCTCAGTGACATCCAGCACTTGGTCAGACCCCTAGCC
AGGACCGGACACCTGCCCCGCCAGGCTGGGACAGGCTCAGGCTCAGGATATGCTGAGGCTGGCGTTCC
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AAAAAAAAAAAAA

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FIGURE 518

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108684
><subunit 1 of 1, 1137 aa, 1 stop
><MW: 122776, pI: 6.00, NX(S/T): 4
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GAPFACDFEQDPCGWRDISTSGYSWLRDRAGAALGPGPHSDHTLGTDLGWYMAVGTHRG
KEASTAALRSPTLREAASSCKLRLWYHAASGDVAELRVELTHGAETITLWQSTGPWGPWG
QELAVTTGRIRGDFRVTFSTRNATHRGAVALDDLEFWDCGLPTPQANCPPGHHHCQNKV
CVEPQQLCDGEDNCGDLSDENPLTCGRHIATDFETGLGPWNRSEGSRNHRAGGPERPSW
PRRDHSRNSAQGSFLVSVAEPTGPAILSSPEFQASGTSNCSLVFYQYLSGSEAGCLQLFL
QTLGPGAPRAPVLLRRRRRGELGTAWVRDRVDIQSAYPFQILLAGQTGPGGVVGLDDLILS
DHCRPVSEVSTLQPLPPGPRAPAPQPLPPSSRLQDSCKQGHLAGDLCVPPEQLCDFEEQ
CAGGEDEQACGTTDFESPEAGGWEDASVGRQLQWRRVSAQESQGSSAAAAGHFLSLQRAWG
QLGAEARVLTPLLGPSPGSCELHLAYYLSQSPREVSCNFERDTCWYPGHLSDTHWRWVE
SRGPDHDHTTGQGHFVLLDPTDPLAWGHSALHLSRPQVPAAPTECLSFYHLHGPGQIGTL
RLAMRREGEETHLWSRSGTQGNRWHEAWATLSHQPGSHAQYQLLFEGLRDGYHGTMALDD
VAVRPGPCWAPNYCSFEDSDCGFSPGGQGLWRRQANASGHAAGPPTDHTTETAQGHYMV
VDTSPDALPRGQTASLTSKEHRPLAQPACLTFWYHGSLRSPGTLRVYLEERGRHQVLSLS
AHGGLAWRLGSMVDVQAERAWRVFEAVAAGVAHSYVALDDLLQLDGPQPGSCDFESGL
CGWSHLAGPGLGGYSWDWGGGATPSRYQPPVDHTLGTGAGHFAFFETGVLGPGGRAAWL
RSEPLPATPASCLRFWYHMGFPEHFYKGELKVLLHSAQGQLAVWGAGGHRRHQWLEAQVE
VASAKEFQIVFEATLGGQPALGPALDDVEYLAGQHCCQPAPSPGNTAAPGSVPAVVGSA
LLLLMLLVLLGLGRRWLQKKGSCPFQSNTEATAPGFDNILFNADGVTLPASVTS DP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

Transmembrane domain:

Amino acids 1075-1092

N-glycosylation sites:

Amino acids 203-207;281-285;339-343;756-760

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 514-518;1100-1104

N-myristoylation sites:Amino acids 32-38;55-61;61-67;106-112;116-122;336-342;350-356;409-415;
523-529;540-546;678-684;707-713;791-797;870-876;921-927;
937-943;954-960;1036-1042;1071-1077**Amidation site:**

Amino acids 1093-1097

Cell attachment sequence:

Amino acids 191-194

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FIGURE 519

GCAGGGGAGCTCCGAGTGTCCACAGGAAGGGAACTATCAGCTCCTGGCATCTGTAAGG**ATG**CT
GTCCATGCTGAGGACAATGACCAGACTCTGCTTCCTGTTATTCTTCTCTGTGGCCACCAGTGG
GTGCAGTGCAGCAGCAGCCTCTTCTCTTGAGATGCTCTCGAGGGAATTCGAAACCTGTGCCTT
CTCCTTTTCTTCCCTGCCTAGAAAGCTGCAAAGAAATCAAGGAACGCTGCCATAGTGCAGGTGA
TGGCCTGTATTTTCTCCGCACCAAGAATGGTGTGTCTACCAGACCTTCTGTGACATGACTTC
TGGGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCACGAGAATGACATGCGTGGGAAGTGCAC
GGTGGGTGATCGCTGGTCCAGTCAGCAGGGCAACAAAGCAGACTACCCAGAGGGGGATGGCAA
CTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCGATGACTACAAGAACCC
TGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCATGTGCCCAACAAGTCCCCAT
GCAGCATTGGAGAAACAGCGCCCTGCTGAGGTACCGCACCAACACTGGCTTCCTCCAGAGACT
GGGACATAATCTGTTTGGCATCTACCAGAAATACCCAGTGAAATACAGATCAGGGAAATGTTG
GAATGACAATGGCCCAGCCATACCTGTGGTCTATGACTTTGGTGATGCTAAGAAGACTGCATC
TTATTACTCACCGTATGGTCAACGGGAATTTGTTGCAGGATTCGTTTCAGTTCGGGGTGTTTAA
TAACGAGAGAGCAGCCAACGCCCTTTGTGCTGGGATAAAAGTTACTGGCTGTAACTGAGCA
TCACTGCATCGGTGGAGGAGGGTTCTTCCACAGGGCAAACCCGTCAGTGTGGGGACTTCTC
CGCCTTTGACTGGGATGGATATGGAATCACGTTAAGAGCAGCTGCAGTCGGGAGATAACGGA
GGCGGCTGTACTCTTGTTCATAGAT**TGA**GACAGAGCTCTGCGGTGTCAGGGCGAGAACCCATC
TTCCAACCCCGCTATTTGGAGACGAAAAACTGGAATTCTAACAAGGAGGAGAGGAGACTAA
ATCACATCAATTTGCA

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FIGURE 520

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108701
><subunit 1 of 1, 325 aa, 1 stop
><MW: 36212, pI: 8.68, NX(S/T): 1
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HSAGDGLYFLRTKNGVVYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGNKA
DYPEGDGNWANYNTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSALLR
YRTNTGFLQRLGHNLFGIYQKYPVKYRSGKCWNDNGPAIPVVYDFGDAKKTASYYSYGQ
REFVAGFVQFRVFNNERAANALCAGIKVTGCNTEHHCIIGGGGFFPQGKPRQCGDFSADFWD
DGYGTHVKSSCSREITEAAVLLFYR
```

Important features of the protein:**Signal peptide:**

Amino acids 1-26

Glycosaminoglycan attachment site:

Amino acids 86-90

N-myristoylation sites:

Amino acids 23-29;88-94;127-133;136-142;265-271

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FIGURE 521

GATCAGTGTGTGAGGGAACCTGCCATCATGAGGTCTGACAAGTCAGCTTTGGTATTTCTGCTCCTGCAGCTCTTCT
GTGTTGGCTGTGGATTCTGTGGGAAAGTCCTGGTGTGGCCCTGTGACATGAGCCATTGGCTTAATGTCAAGGTCA
TTCTAGAAGAGCTCATAGTGAGAGGCCATGAGGTAACAGTATTGACTCACTCAAAGCCTTCGTAAATTGACTACA
GGAAGCCTTCTGCATTGAAATTTGAGGTGGTCCATATGCCACAGGACAGAACAGAAGAAAATGAAATATTTGTTG
ACCTAGCTCTGAATGTCTTGCCAGGCTTATCAACCTGGCAATCAGTTATAAAATTAATGATTTTTTTGTTGAAA
TAAGAGGAACTTTAAAAATGATGTGTGAGAGCTTTATCTACAATCAGACGCTTATGAAGAAGCTACAGGAAACCA
ACTACGATGTAATGCTTATAGACCCTGTGATTCCCTGTGGAGACCTGATGGCTGAGTTGCTTGCAGTCCCTTTTG
TGCTCACACTTAGAATTTCTGTAGGAGGCAATATGGAGCGAAGCTGTGGGAACTTCCAGCTCCACTTTCCTATG
TACCTGTGCCTATGACAGGACTAACAGACAGAATGACCTTTCTGGAAAGAGTAAAAAATTCATGCTTTCAGTTT
TGTTCCACTTCTGGATTACGATTACGACTATCATTTTTGGGAAGAGTTTATAGTAAGGCATTAGGAAGGCCCA
CTACATTATGTGAGACTGTGGGAAAAGCTGAGATATGGCTAATACGAACATATTGGGATTTTGAATTTCCCTCAAC
CATACCAACCTAATTTGAGTTTGTGGAGGATTGCACTGTAAACCTGCCAAAGCTTTGCCTAAGGAAATGGAAA
ATTTTGTCCAGAGTTCAGGGGAAGATGGTATTGTGGTGTCTCTGGGGTCACTGTTTCAAAATGTTACAGAAG
AAAAGGCTAATATCATTGCTTCAGCCCTTGCCAGATCCCACAGAAGGTGTTATGGAGGTACAAAGGAAAAAAC
CATCCACATTAGGAGCCAATACTCGGCTGTATGATTGGATACCCAGAATGATCTTCTTGGTCATCCCAAAACCA
AAGCTTTTATCACTCATGGTGGAATGAATGGGATCTATGAAGCTATTTACCATGGGGTCCCTATGGTGGGAGTTC
CCATATTTGGTGATCAGCTTGATAACATAGCTCACATGAAGGCCAAAGGAGCAGCTGTAGAAATAAACTTCAAAA
CTATGACAAGCGAAGATTTACTGAGGGCTTTGAGAACAGTCATTACCGATTCTCTTATAAAGAGAATGCTATGA
GATTATCAAGAATTCACCATGATCAACCTGTAAAGCCCCCTAGATCGAGCAGTCTTCTGGATCGAGTTTGTCTATGC
GCCACAAAGGAGCCAAGCACCTGCGATCAGCTGCCCATGACCTCACCTGGTTCCAGCACTACTCTATAGATGTGA
TTGGGTTCTGCTGACCTGTGTGGCAACTGCTATATTCTTGTTCACAAAATGTTTTTTATTTTCTGTCAAAAAT
TTAATAAACTAGAAAGATAGAAAAGAGGGAATAGATCTTTCCAAATTCAGAAAAGACCTGATGGGGTAATCCTG
TTAATTCAGCCACATAGAAATTTGGTGAAAACCTTGCTATTTTCATATTATCTATTCTGTTATTTTATCTTAGCT
ATATAGCCTAGAATTCATGATCATGAGGTTGTGAGTATATCTCATTCTTTTCGTTGTATTTTCTTAGGTGTCTTT
ACTCTCTTCTCTCACTTTGTGACACAAGGACATGAATACATCTAAATTTTCTATTTCTGATATGACTGTTTTGA
TGATGTCACTTACTTCTATAACCTTAAGTGATAGGGTGACATGCAATATGATTATTCCTGGTGTGCGCCCAACAC
ATGGATATAAAGAGGTAAAAAATTAATTCACAAAATTCAGTAAACCACACAAATCAGGTAAGTGTCTATGA
GATTAGCTGGCTATGAGAAACATAATGATGTTTCTTTTTCAATTTAAATAAGCCTTTCTACATAGCCAGCATCAG
TGATCTCAGAAAATAAATTGCTAATAATGATGACATGGCATTATGCTTAGAAAAGTTTGTGTATTTCCATAGAC
CTCATCTAGATGTGATGGCCTACATTTCTGCCATCACTCAACCAATACTTTTTTCTGTTTTCTTGATGATAAAAA
GACCTTTCTCATGATTGCCATCAAATAACAAAAGAACTATTTTTTTCTCACATAGAGAACATGTCAGTAAGAT
ATTCAGGTGAACAGATATTTTTGGGATTAGTAACCTATTTGAAATATGTGGTGATAATTACTGAGTTTATAAAAT
TTATTTGATAGTACACTTAAAGAAGATTTATATGTTTATTCTTTAAAAATGATGAATACTCATAATTCCTATCTC
TATAATCAAAAGTATAATTTACTGTAGAAAAATAAGAGATGCTTGTTCTGAAAGTAAGATCAGTGAAGTGCCTT
TCAGTCTCAATCTTTGAGAAATGTAAATTCATCAAATAATGCTTACATAGTAAAAATTTAAGGTATTAGAAAAC
CTGCATAACAAATAGTATTATATATTAATATTTTGATATGTAAAGCTCTACACAAAGCTAAATATAGTGTAATA
ATGTTTACACTAGTAAGCAATATGTTAATCTTCTCATTTTTTTTACTGTGATATAATCTTAGTGATATGCCTATT
AATAGTTTTAAATAAATAAATTGGCTTATCTGGCTTTTTGAAAATTTTGAATTTCTTACAGATGTTGATTAGGTA
TATCTACAAATTAATTTCAATTTTAAATGATGATATAAAAAATAAATAAGTATTTTCTTGTGTATGTATACA
ATAAATATAAATAAATTTGTTTACTGTTTTGAAAGTTTCTTAAGTTTTA

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FIGURE 522

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108720
><subunit 1 of 1, 527 aa, 1 stop
><MW: 60284, pI: 8.31, NX(S/T): 3
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LKMMCESFIYNQTLMKKLQETNYDVMLIDPVI PCGDLMAELLAVPFVLTLRISVGGNMER
SCGKLPAPLSYVPVPM TGLTDRMTFLERVKNSMLS VLFHFWIQDYDYHFWEEFYKALGR
PTTLCETVGKAEIWLIRTYWDFEFPQPYQPNFEFVGGLHCKPAKALPKEMENFVQSSGED
GIVVFSLSLGFQNVTEEKANIIASALAQIPQKVLWRYKGKKPSTLGANTRYDWIPQNDL
LGHPKTKAFITHGGMNGIYEAIYHGVPVMGVPIFGDQLDNIAHMKAKGAAVEINFKTMTS
EDLLRALRTVITDSSYKENAMRLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRSA AHD
LTWFQHYSIDVIGFLLTCVATAIFLFTKCF LFSCQKFNKTRKIEKRE
```

Important features of the protein:**Signal peptide:**

Amino acids 1-21

Transmembrane domain:

Amino acids 489-510

N-glycosylation sites:

Amino acids 131-135;313-317;518-522

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 67-71;340-344

Tyrosine kinase phosphorylation sites:

Amino acids 122-131;136-144

N-myristoylation sites:

Amino acids 19-25;276-282;373-379;377-383

Amidation site:

Amino acids 338-342

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FIGURE 523

GGCTGCGGGGTGCGGCACGGAAG**ATG**CACGCGAGGCTCCTGGGGCTCTCGGCCCTGCTGCAGGC
GGCCGAACAGAGCGCGCGCCTTTACACCGTGGCTTACTACTTCACCACAGGACGGCTTCTGTG
GGGGTGGCTGGCCCTTGCTGTCCTCCTGCCCGGGTTCTTGGTCCAGGCCCTGAGCTACCTGTG
GTTCCGAGCAGACGGGCATCCAGGGCATTGCTCCTTGGTGATGCTGCACCTCTACAGCTTGG
TGTTTGAAGCGGCACTGGGACGCTGCACTGACCAGTCTGCAGAAGGAAGTGGAGGCTCCCCA
CCGAGGCTGGCTGCAGCTGCAGGAGGCCGACCTGTCGGGCCCTTCGACTCTTGGAGGCCCTGCT
GCAGACTGGGCCCCACCTGCTGCTTCAGACATATGTTTTTCTAGCCTCAGACTTCACAGATATT
GTGCCAGGGGTGAGCACCTGTTTTCTGGTCCTCACTCTCCTGGGCACTGGTGTCTTACACT
CGCTTCATGGGCTTCATGAAGCCAGGCCACCTGGCCATGCCATGGGCCCGCCCTCTTCTGCCAG
CAGCTCTGGAGGATGGGCATGTTGGGAACCCGCGTGCTGAGTCTGGTTCTGTTCTACAAAGCC
TACCACTTTTGGGTTTTTGTGGTTGCAGGTGCCCACTGGCTGGTGATGACATTCTGGCTTGTG
GCCCAGCAGAGTGACATCATCGACAGCACCTGCCACTGGAGGCTGTTCAACCTGCTCGTGGGG
GCCGTGTACATCCTCTGCTACCTCAGCTTCTGGGACAGCCCTTCTAGAAATAGGATGGTCAG
TTCTACATGGTTCATGCTGTTGGAGAACATCATCCTGTTGCTGTTGGCCACCGACTTCTCCAG
GGGGCATCGTGGACCAGCCTGCAGACCATAGCTGGGGTCTGTCTGGATTCTGATTGGCAGT
GTCTCACTGGTAATTTATTACAGCCTGCTGCATCCAAATCCACAGACATCTGGCAGGGCTGC
CTAAGGAAGTCCTGTGGCATTGCAGGAGGTGATAAAACAGAGAGAAGAGATTCTCCCCGGGCC
ACAGACTAGCTGGGAAGAGAACCGAGAGCTCAGGCTCATGCCAAGGGGCAAGTTATGAACCA
ACCATTTTAGGGAAGCCCCCTACCCCTGAGCAGGTCCCCCAGAGGCTGGGCTGGGGACCCAG
GTTGCTGTGGAGGACTCTTTCCTCAGTCATCACCCTGGCTGTGGGTGAACTTGCCCTAAAA
ACAGGAAATGTGTCTAAGATCAATGCCGCCTTTGGAGATAACAGTCCTGCCTATTGTCCACCT
GCATGGGGGTTGAGTCAACAGGACTACCTGCAGAGAAAGGCCTTGTCTGCCAGCAAGAGCTC
CCATCCTCATCCCGTGACCCCTCAACCTTAGAGAACAGCTCTGCGTTTGAAGGTGTCCCTAAA
GCAGAGGCCGACCCATTGGAAACCTCAAGTTACGTATCTTTTGCCAGCGATCAGCAGGATGAA
GCACCTACCCAGAACCCAGCAGCCACGCGAGGGGGAGGGCACCCCAAAGGAAGGAGCTGACGCT
GTTTCTGGGACACAGGGGAAGGGGACAGGTGGGCAGCAGAGAGGAGGGGAAGGACAGCAGAGT
TCCACGTTGTACTTCAGCGCCACTGCAGAAGTGGCCACATCCTCACAACAAGAAGGCAGCCCA
GCTACTCTGCAAACGGCCCACTCTGGAAGGAGGCTGGGAAAGAGCAGCCCTGCCAGCCTGCA
TCGCCCCACCCAGTGGGCTTGGCGCCCTTCCCCGACACCATGGCCGACATTAGCCCCATCCTA
GGCACAGGCCCATGTAGAGGCTTCTGCCCCAGTGCAGGCTTCCCTGGAAGAACCCTCAGTATC
TCAGAGCTAGAGGAGCCGCTGGAGCCCCAAAGGGAGCTAAGTCACCATGCAGCTGTTGGTGTG
TGGGTGTCATTGCCACAGCTGAGGACTGCCCATGAGCCCTGCCTCACGTCCACCCCTAAGTCT
GAGTCTATCCAAACGGACTGCAGCTGCAGGGAACAGATGAAGCAAGAGCCGAGTTTTTTCATC
TGACCACAGTCATGGTGGGATAAGACAACAGGCTGACAAACCAAGCTGGCCATTTGGTACCGT
GAGAAAGGAAATCCCACTTCTGACACCTGTGTCTTGGGCACATCACTGTCACCTCTGAATCT
CCATCTGCATCCCTGAAAAATGAAGAAACAGGGCTGGATGATTTTGCAGGTCCAATGCAAACA
TCACAGACCCCAACCCATGCATAGGAGAGACTCTAACATACTTTAGAGGAGGAGAAAGAGATTC
CAGTCAAAATTGTCTGCTACCTTTTATGAGCTGTAGGTTCCCTTATTTTATCTTTTGTCTGTG
GCTTCTAGGAAACACAAAGGTAAAACCCAGATTCTTATTTTATTTGAGGTTCTTGTTACAATT
AGCTTTGCCTCACATTTAGCGGTTATGAATCTCATTTTAAATATATTCTAACTGTATTATGTTA
TGAAATCTCTTGGTAAGATAATTTGCATGCTTTCTGGGAGTAGGTAAGGCCTGTGTGCTTGTA
ATAACTAACATAACTGAAAGTGCAAATGTCA

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FIGURE 524

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108726
><subunit 1 of 1, 686 aa, 1 stop
><MW: 74981, pI: 6.60, NX(S/T): 2
MHARLLGLSALLQAAEQSARLYTVAYYFTTGRLWGWLALAVLLPGFLVQALSYLWFRAD
GHPGHCSLVMHLHLLQLGVWKRHWDAALTSLQKELEAPHRGWLQLQEADLSALRLLEALLQ
TGPHLLLQTYVFLASDFTDIVPGVSTLFSWSSLSWALVSYTREMGFMKPGHLAMPWAALF
CQQLWRMGMLGTRVLSLVLFYKAYHFWVFVAGAHWLVMTFWLVAQQSDIIDSTCHWRFL
NLLVGAVYILCYLSFWDSPSRNRMVTFYVMMLLENIILLLLATDFLQGASWTSLOTIAGV
LSGFLIGSVSLVIYYSLHHPKSTDIWQGLRKSCGIAGGDKTERRDS PRATDLAGKRTE
SGSCQGASYEPTILGKPPTPEQVPPEAGLGTQVAVEDSFLSHHHWLWVKLALKTGNVSKI
NAAF GDNSPAYCPPAWGLSQQDYLQRKALSAQQELPSSSRDPSTLENSSAFEGVPKAEAD
PLETSSYVSFASDQQDEAPTQNPAAATQGEPTKEGADAVSGTQKGKTGGQQRGEGQQSS
TLYFSATAEVATSSQQEGSPATLQTAHSGRRLGKSSPAQPASPHVGLAPFPDTMADISP
ILGTGPCRGCPSAGFPGRTL SISELEEPLEPKREL SHHAAGVGVWSLPQLRTAHEPCLT
STPKSESIQTDCSCREQMKQEPSFFI
```

Important features of the protein:**Signal peptide:**

Amino acids 1-17

Transmembrane domains:

Amino acids 35-50;269-287;293-313

N-glycosylation sites:

Amino acids 416-420;467-471

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 344-348

N-myristoylation sites:Amino acids 188-194;288-294;299-305;335-341;338-344;362-368;
390-396;473-479;529-535;536-542;558-564;603-609;
643-649**Amidation sites:**

Amino acids 354-358;568-572

Leucine zipper pattern:

Amino acids 112-134

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FIGURE 525A

AGTGCCCTCTGTCATTTAATCTCCACGGAGTCCTGAAGGTGCTTCCCAGGTTTGTCCCCATCACACAGATGAGGC
AATCGTTCTGTTAAGACTGTCCTTGGGTCAATTATGTCAGCAATGAAATCGGTGCTGCCATTACTAAACCCTTACT
GTGTGCTGGCATTGTGTATGCATGCATGTGTGTGCGTGACACGTTGTGTGTTTGCCTGTACATGTGCATGTGTGTG
TTGTGTGCTGTGTGTGCACATGTAGAAAGAAAGTGATGTGTGGGAATGGAGAATTCCAACCCAGGAGAGACTG
TGCTGGGGCTGCCACGAGAAGTGGTGACACTTCGAGAAACGGGTTCCAAATGCACGTTGCCTTCAATCTCTCTG
TGTGACCTTGGGCAAGTCACCTCAGCTCCCTGAGCTTTGTTTTTAAAAATATTTTTTAAATGTATAAAACCATGG
ACCATTACATATGAAGAGAAATGTGTGTGCAAACATTCAGTTAATAATCACAAGGTGGAGGAGTGCCTGCTCAGA
CCCAGAGCTGCACAGGGAACTCTCCAGAAGGCTGCAGGGCTTCCCTCCCAACCCTCCAACGGCCCACTTGCTG
AGCCCGTGCTTATCTGTTCACTGGAAATGCCATGTGCCACGTTCCCTCAGAAGTAAAGCCACTAGGTAAGTGTGAC
ACTCTGTGCCAGCTTGGTGCAAAGCCCCCTTGTGTGTGCTATCTTATTGACCTCCCAATAGCATGGTAAGGTCA
GTACTGTCACTTCCCCCACTTTGAAGATGAGGAGAGCACAATTTCTAGATGGAAATGGAGGTCACGCAGTGGAAA
TAGGATCCAGACAGATTAATCCAATCTCAAGCCTGAATTTCTCCATTCCACGCTACGCTGAAGCTCAATCTCTC
TTCTGCTGTTGATTCTCCCCACTTCCCCACCCCCAGATATATCCCATCGCTGCTTGGTGGACAGTAGCCATGACTG
GGTTTTGGTAAAGGTTGCTGAATAATCAGGCTGCTGGTTAGTTTTACATTTACCTTTCCAGTGAAATGGGGC
CCCATGAAAAAGGCAGCTCAAGTTGTAAATTAATCAAAGGAAGGACAGAAAGGCTTCTGTTTGCACCTACCCTA
AGGATTTGGGGTAGACACTGGGAATTTACTAATTATGAATTCAGTGCTTTCCTTGCTGAAAGAGAGGGCGTGGAA
TCAACGCTGAGTGAAGGCATCAAGTTAAGCTGCTAATTACTTCTGATCATGCAGAATAAAAGCTACGTCCTT
ATCAGTGCTAATATAGAAAAAGCTAGTATTTATTGGGCTTATTAGATTTTGTAGTCTGAATCCTCACAACCTTACG
AACCCTCCATAAACAAAAGGAACACCCAGCTGTGAGAACTGGCTTCTCAGCATTCGTCCAGCAGAGGCTCTTC
CGGGGCCAGCCCTGGAAGAACCCATCAGGGTCTGATGGTTGCCCTGTTTCAGCACAGCCCTTATTGGCAGGCAG
ACGGCTACGGGCACAGCCACAGGCTGAAGGTGAGTCCAGCACACAACCTTCTGACAGTGAACAGGAGTAAACATG
GGACCCACCCGAAACCTTTGCTGTTGACTTCTTAGCAAATGGAGGCAGCTCTAGGCTCTGGAGAGTTCGGGTAT
AGGAGACCATGACTTGAGCAGACTGATATAAGTGGAAATGCAACATATTTAGATGGCACAACCTTAATTTAGATTT
ATCAGTGCTAATATAGAAAAAGCTAGTATTTATTGGGCTTATTAGATTTTGTAGTCTGAATCCTCACAACCTTACG
AGGGGGTTGTTTTACAGACTATGATCTTGCATGATTTCCCAAGATGCTCATTAAGTATATGGTGAAGTAGA
ATTTGAATACAGAAGACCTGGTCTGCTACTTTCTGTGTTTCTATTTGGTTCAAACAGCCCTTTCTCTTTCAA
ACAACCTTCAGTGCAATTCATGGTTTTGGAAAATAAACTTGATTTTGAGATTCAGACAATAAGTGCATTTTTAATG
TTTATTCTTTTATCTTGA AAAACTGATATATTTATGAAATGATATGTGCTCACTCAGTGTCAACACTTCAAACAA
CACAGACAGTACAATGACAAATGGAGATCAGCTCTAATCTCGGCCCAATTTAATGCATTGCTGAATATTTCTT
CTGAACATAGTCCATCCCACACTGTCCCATGACACAAGACGCTCCAAGGGGCTGAAGATAGAGGGACTTCTGCAG
TCAAGAGAGCTGGGAAACTCTTGGACAGTCACAATGTGCATTTGGGTATTAAAGGCTCTGCAAAGTTCTGCACCA
AATAAACCTTGGATTGGCTTGATCCAATGCCATGTTTCCAAAACCTACTTGCCCGTGGGACACCTTAGTCCATA
ACACAGGTTGGCATTCTTCTAGAGAGTGTGCTGTGAAAAACACTGGTCTCACAGCACCGTGCATTTCATCCAGCA
GGTATTTACCAAGCAGGGACTTTGGGCCAGGTCCGTGCTAGGCTCTGCAGGTGGACCAGCCAGCCCTGACCTCCA
TGGTGTCTCTTCTCATGGGAGAGGCTGCACAGCAGTCATTGAGAAAACGAAGAAACACACAGGTACTTTCAGATG
CTGATAATGACTACCATGTGCTAAAAGAGCTCCAGGTGTTGTCTGTTTTGAGACAATCTTCTCGACAATGAGATA
GAATGAACCATGCAAACCTTTGGGGGCTACGATGGTTTTAGGAAAGAGCTAGAGTGA AAAATCCTTTGACATATAT
ACATACAAATAAAGATACATGTGTATAATTTTATGTAATTGACATCACATTATATGCTGGCACCTGCCTTTTTTG
CTTAATGAAAATGTCAAAGTAATATTACCAATCAATCAATATATTTACCATCGTGTTTAATTTCTGCAGAGCA
CTTATTCAAGCACATACTGCATTTTTCTTAGTCACTCACTGGTGGGAATAGAAAGTTTTCTCAGGCATGCATTTT
TCCCACTTCTGAAATGATCTCCTTAGAATAAATCCCCAAATGTATTGCTGGGTTCAAAGGCATGAACATTTTA
CATTTTTATACAATAATGTCAAACCTACCTTCCGGAATGATGCTCACTTTACTTTCCCTCCAAGACTGTGTGAAA
ATGCCCATTTTTCTAAATGCTTACTATGACTGGTTTTCCAACCTACATTTAATTTCTTGTTCATCTGATAGGCAAA
AAATGATATTTAATTTTTATTTGATTGATAATGACCTTGAACGTGCCCATTAGCCTTTTGCATGTATTCTTTTAT
GAAACATCTGTTTCTATCCTTCGTCAATGTTTCTTCTATATGTTAACTTTTCTTATTGATTTGTTAGAGCACTT
TGTATATTGTGAATATTAGCTTTTGTGATCAGAATTATGGAATTGTTGTTGTCTTTAGTTTTGCTTATCAAGTTT
AAAGCCATTACAGAGATGTTGTAATGTGTATGTTGTTAAATTTATGTCTTATTTTGTGTTTTCTGATGCTCATAT
GTTTAGAATGGTCAAGCAATCCCACTTATGATTACATAAATTTCTCCATATTTGCTCTTAGCATTTTTTTTC
TTTTCATGTAACCTTTGTTCTTTTCAAGAAATTTACTTTGCGGTAAGAAATGGGCTGGCTTCCAGTTTTATGTTT
CCAAATGGTGATTGAGCTGTTCCATTTCCATATTTCTCCCTTATTAGAAATGACCACTATATTATGTTCTAAAATA
TCTGCGTACTTGTGTCCCTTCTATAATCTCAGTTCATCTCTTTGAGCTATCTTTTGATTCTTTTTCAAACCAC
ACTGCTTTACTGAAGTGTATCTTATACATTTTTTAATCTCAGCAAGACAAGTTTCTCAATGCCACTCTTTT
TCAGAGTTTTTCTGGTGGTTGTAAGATGTTTATTCTTCTGGATAAACTTTAGAATCACTCTTTTTGTCCAAGGTA
AAATATATCCCACATTGAGATCATCTGAATATACAGACTAATTCAGGAAAAATGTATGCTTTATTGCATTGA
GTCTTCTTATCCAATAAAAAAGATATGAATTTCCATGTATTGAAATCTTCACTGAGACTTATTTTTGGCTTTTCA

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FIGURE 525B

CATGTCCTGCAAATGTATTGTTAAATTTATTTTATAGGTATTTAGGGGAAATGATTTTCTAAAGTTTGTATTTTC
TAGCTTGTTATAATTTACATATGAGATAGTCATTGTTGTATATTATTTATAACTGATCATATTACTGTATTTGTA
TTGTTTTAATAGTTTTTCTATTATTTTGGGTTTTCTGGAATACAACCTTATTATCTACAAATTATGATTGTTTT
GCCTTTTCCAATGTTTCATAACTGTTTTATATTCTTGTCTGATTGCTTTGTTTCAGCACTTCTAGAATAAAGTCAT
GCAATACTAATGA

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FIGURE 526

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108728
<subunit 1 of 1, 100 aa, 1 stop
<MW: 10922, pI: 8.81, NX(S/T): 0
MSAMKSVLPLLNPYCVLAFVYACMCVRAHVVCVYMCMCVLCACVCTCRKKVMCGNGEFQ
PRRRLCLGLPREVVTLRETGSKCTLPSSSLCDLGQVTSAP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-28

N-myristoylation sites:

Amino acids 80-86;94-100

Prokaryotic membrane lipoprotein lipid attachment sites:

Amino acids 13-24;34-45

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FIGURE 527

GTGAGACTTCTTTCTTCATTGTGGCTAGCTTTGAAAAGACCCTCTGAACTTCCTAAAGATATC
AAG**ATG**ATATCACCAGACTTGCCCTTTTTGACAATTGTCTTGATCATAGTTAGTTGGACAACCT
TGTGGAGCACTAGCCATACTTCTTTCTTATCTTTACTATGTGTTTAAGGTTGTTTCATCTGCAA
GCCAGCTTAACAACCTTTTAAGAATAGCCAGCCTGTGAATCCCAAACACTCTAGAAGAAGTGAA
AAGAAATCCAATCATCATAAAGACTCCTCAATACACCATCTTCGTTTATCTGCCAACGATGCT
GAAGATAGCCTTCGCATGCACAGTACTGTGATTAACTTACTAACATGGATTGTATTACTCAGC
ATGCCTTCTCTAATTTATTGGCTAAAGAATCTTAGGTATTATTTTAACTTAATCCTGATCCA
TGTAACCTTTGGCATTATCCTTATTCCGACTATGGCAATTCTTGGAATACTTACACTGTT
TCAATAAAATCAAGTAAATTGTTGAAGACTACTTCACAATTTCCACTTCCTCTGGCTGTTGGT
GTGATTGCTTTTGGGTCAGCACATTTATATAGGCTTCCATGCTTTGTCTTCATTCCTCTTTTA
CTCCATGCATTATGCAACTTTATG**TAA**GATTGGACTTAAGGAATGATGAAGATAATTTATGTG
TTTAGGGCCAGTGATAAGAGGGAACACACAGATCCATCAGTATGGACAGCAAGATCCTTTGGA
GAAGACAAGTCTATTTTTACAATATTGAAAATAGGAAATTAGTTTTGTAATGTTTGAGGGAAG
TAGTTGAAGCATGGTTTTGTTTTGTGGTGTGGAATCCATGTACTAATCATTTTTGAAAAATTC
ATGAAGGGATATATGGTGATCACTATCATTGAGGACTCCTGTGCATATAAAATAGTCTGTTTT
ATCAACTGTAAA

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FIGURE 528

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108738
><subunit 1 of 1, 196 aa, 1 stop
><MW: 22225, pI: 9.90, NX(S/T): 0
MISPDLPFLTIVLIIVSWTTCGALAILLSYLYYVFKVVHLQASLTTFKNSQPVNPKHSRR
SEKKSNNHHKDSSIHHLRLSANDAEDSLRMHSTVINLLTWIVLLSMPSLIYWLKNLRYYYFK
LNPDPCKPLAFILIPTMAILGNTYTVSIKSSKLLKTTSQFPLPLAVGVIAFGSAHLYRLP
CFVFIPLLLHALCNFM
```

Important features of the protein:**Signal peptide:**

Amino acids 1-25

Transmembrane domains:

Amino acids 91-108;128-143;167-186

N-myristoylation site:

Amino acids 141-147

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FIGURE 529

GCGAGCCGGGTCCCACCATGGCCGCGAATTATTCCAGTACCAGTACCCGGAGAGAACATGTCA
AAGTTAAAACCAGCTCCCAGCCAGGCTTCCTGGAACGGCTGAGCGAGACCTCGGGTGGGATGT
TTGTGGGGCTCATGGCCTTCCTGCTCTCCTTCTACCTAATTTTCACCAATGAGGGCCGCGCAT
TGAAGACGGCAACCTCATTGGCTGAGGGGCTCTCGCTTGTGGTGTCTCCCGACAGCATCCACA
GTGTGGCTCCGGAGAATGAAGGAAGGCTGGTGCACATCATTGGCGCCTTACGGACATCCAAGCTT
TTGTCTGATCCAAACTATGGGGTCCATCTTCCGGCTGTGAAACTGCGGAGGCACGTGGAGATG
TACCAATGGGTAGAACTGAGGAGTCCAGGGAGTACACCGAGGATGGGCAGGTGAAGAAGGAG
ACGAGGTATTCTTACAACACTGAATGGAGGTCAGAAATCATCAACAGCAAAAACTTCGACCGA
GAGATTGGCCACAAAAACCCAGTGCCATGGCAGTGGAGTCATTCATGGCAACAGCCCCCTTT
GTCCAAATTGGCAGGTTTTTCTCTCTCGTCAGGCCTCATCGACAAAGTCGACAACTTCAAGTCC
CTGAGCCTATCCAAGCTGGAGGACCCCTCATGTGGACATCATTCGCCGTGGAGACTTTTTCTAC
CACAGCGAAAATCCCAAGTATCCAGAGGTGGGAGACTTGCCTGTCTCCTTTTCTATGCTGGA
CTGAGCGGCGATGACCCTGACCTGGGCCAGCTCACGTGGTCACTGTGATTGCCCCGCGAGCGG
GGTGACCAGCTAGTCCCATTTCTCCACCAAGTCTGGGGATACCTTACTGCTCCTGCACCACGGG
GACTTCTCAGCAGAGGAGGTGTTTCATAGAGAACTAAGGAGCAACTCCATGAAGACCTGGGGC
CTGCGGGCAGCTGGCTGGATGGCCATGTTTATGGGCCTCAACCTTATGACACGGATCCTCTAC
ACCTTGGTGGACTGGTTTTCTGTTTTCCGAGACCTGGTCAACATTGGCCTGAAAGCCTTTGCC
TTCTGTGTGGCCACCTCGCTGACCCTGCTGACCGTGGCGGCTGGCTGGCTCTTCTACCGACCC
CTGTGGGCCCTCCTCATTGCCGGCCTGGCCCTTGTGCCCATCCTTGTTGCTCGGACACGGGTG
CCAGCCAAAAAGTTGGAGTGAAGAACCCCTGGCACCCGCCGACACCTGCGTGAGCCCTGAGG
CTGGTTGTACAATGCCACGCCTGCCTGGCTGCTTTACCTGGGAGTGCTTTCGATGTGGGCA
CCTGGGCTTCCTAGGGCTGCTTCTGAGTGGTTCTTTACGTGTTGTGTCCATAGCTTTAGTCT
TCCTAAATAAGATCCACCCACACCTAAGTCACAGAATTTCTAAGTTCCCCAACTACTCTCACA
CCTTTTTAAAGATAAAGTATGTTGTAACCAGGACGTCTTAAATGATTCTTTGTGTACCTTTTC
TGTATATTTCAGAAACCGTTCTGTGCCTGCTGGGAGTAATTCTTTAGCAATTAAGTATTTGG
TAGCTGAATAAGGGGTGAGAACTTCTGAAACCAGAGATCTGTAATCATCTCTATTGGCCTGGG
GTGCCTGTGCTATAAATGAGTTTCTTACATGAAAAACACAGCCAGCCCAAGATGACTTATCT
GGGTTTAGGATTCAATAGTATTTCACTAACTGCTTATTACATGAGCAATTTTCATCAAATCTCCA
AACTCTTAAAGGATGCTTTTCGGAAAACACGCTGTATACCTAGATGATGACTAAATGCAAAATC
CTTGGGCTTTGGTTTTTTTTCTAGTAAGGATTTTAAATAACTGCCGACTTCAAAGTGTCTTA
AAACGAAAGATAATGTTAAGAAAAATTTGAAAGCTTTGGAAAACCAAATTTGTAATATCATTG
TATTTTTTATTAAAAGTTTTGTAATAAATTTCTAAATTATCA

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FIGURE 530

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108743
><subunit 1 of 1, 400 aa, 1 stop
><MW: 44876, pI: 8.32, NX(S/T): 2
MAANYSSSTSTRREHVKVKTSSQPGFLERLSETSGGMFVGLMAFLLSFYLIIFTNEGRALKT
ATSLAEGLSLVSPDSIHSVAPENEGRLVHIIGALRTSKLLSDPNYGVHLPVKLRRHVE
MYQWVETEEESREYTEDGQVKKETRYSYNTEWRSEIINSKNFDREIGHKNPSAMAVESFMA
TAPFVQIGRFFLSSGLIDKVDNFKSLSLSKLEDPHVDIIRRGDFFYHSENPKYPEVGDLR
VSFSYAGLSGDDPDLGPAHVVTVIARQRGDQLVPFSTKSGDTLLLLHHGDFSAAEEVFHRE
LRNSMKTWGLRAAGWMAMFMGLNLMTRILYTLVDWFPVFRDLVNIGLKAFACVATSLT
LLTVAAGWLFYRPLWALLIAGLALVPILVARTRVPAKKE
```

Important features of the protein:**Transmembrane domains:**

Amino acids 34-53;365-388

N-glycosylation site:

Amino acids 4-8

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 140-144

Tyrosine kinase phosphorylation sites:

Amino acids 99-107;220-227

N-myristoylation sites:

Amino acids 35-41;93-99;310-316

Cell attachment sequences:

Amino acids 221-224;268-271

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FIGURE 531

AAAAAAAAAAAAAAAAAAGAAGCTCTTATGCCAGGAACCTGGAATGGAGACCAAATATATATTG
GTTATATCATAGTATCACAGGGTTACTTTGGCATTGTTGGGAACTTGAGAGAAATGGGCAATAA
CTGTTACTTTAAAAGCTTGGGTGCTGTGATTCTGCCTTCAGCCTCAGCCACTTTTGTGGTGCT
TTGCGTGGCATCAGTACCTCCACTGATTCTTCTGTCTTTCCTCTCTCTTCCCCCCTCTT
CCCTTCTGTTTTTCTCAGATCTAAGGGTTATAATGGAGGGGCAAACCTGCCTGGCTATTTCAGA
TAAGACTTCACTGAGTGACTGTTTCAGCCCATGATTTACCCTGCAGTTTAACAGGCTCAGGAAT
TAGGTCGCATCAGTTGAGCGCGGGTCACTTAGGCCTATAATCATCATCAGACGGCAATTAAAG
GACCATTTCTGCCTTTTTCACTATTACATCCCCCGCCTGTAGCCAGCCTGCCATACAGTAGA
TACTCAATAAATATTTGCTGAATGATAACCAATAA

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FIGURE 532

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108758
<subunit 1 of 1, 100 aa, 1 stop
<MW: 10316, pI: 8.52, NX(S/T): 0
MGNNCYFKSLGAVILPSASATFVVLCDVASVPPLILLSFLSLFPPSFPSVFLRSKGYNGGA
NCLAISDKTSLSDCSAHDLPCLTGGSGIRSHQLSAGHLGL

Important features of the protein:**Signal peptide:**

Amino acids 1-47

N-myristoylation site:

Amino acids 58-64

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FIGURE 533

CGGGGTGTACGAAAGAGAAACCCGGAGGGCGCCGGGGGACTGGGCGGGGTCTGCAGGGCTCAG
CTGAGCCCATGAGCTCCCAGAGCTAACCCCTGAACACCCAGGCGGGCAAAGGGCTGATGTTCGG
TAGTCCCCATCCTGGAGGGGCAGGCTCTGCGCATCTGCTCCTGGC**ATG**GCGCTGCGGCACCTC
GCCCTCCTGGCTGGCCTTCTCGTGGGAGTCGCCAGCAAGTCCATGGAGAACACGGCCCAGCTG
CCCGAGTGCTGTGTGGATGTGGTGGGCGTCAACGCCAGCTGCCAGGCGCAAGTCTGTGTGGT
CCAGGCTGTTACAGGCGCTGGAACGCGGACGGGAGCGCCAGCTGCGTCCGCTGTGGGAACGGA
ACCTCCCAGCCTACAACGGCTCCGAGTGTAGAAGCTTTGCTGGCCCGGGTGCGCCATTCCCC
ATGAACAGAAGCTCAGGGACCCCCGGGCGGCCACATCCTGGGGCTCCGCGCGTGCGCCGCTCC
CTCTTCTGGGCACGTTCTTCATTAGCTCCGGCCTCATCCTCTCCGTAGCTGGGTCTTCTAC
CTCAAGCGCTCCAGTAAACTCCCCAGGGCCTGCTACAGAAGAAACAAAGCTCCGGCCCTGCAG
CCTGGCGAAGCCGCTGCAATGATCCCCCGCCACAGTCTCAGACGTGGGGTCTGCAGGAAAG
GAGGACCCACCACGACAGGGCAGACCCCCAATACCTGCTCCTCCT**TGA**AGTCCAGCTCCACCC
GAGGACAGACGCAGCCGGCCTCCGCCAGGGCCTCCTGAGCAGCCATCGCTTCAGTGGTGCTGG
GTCAGGCGGACCCAAGAGTCAGCCCGTACGGAAGCCGCGCTACGTACAGGCGGGAGCGGCCCT
GGACAGGGCCACGGATCCCGCTGCCTTCCCGGGGGAGGCCCCTATCAGCAATGTCTGACCTGG
AGGCCGAGACCACGCCACGCACTTGGCGGCAGGGACCCGGAGGCCGACCCCTTGGCGGGAACC
AGCACAAAGTGTTGGCATCGCCCGGCGCCCGGGACAGTCTTGGGCACAGCCTCGGCTCTGGGT
CCCTCCGCCTCCCAGCGACGGACGCCAAAGGGTCCCGGGCCGCCTGAGGCTCCTCCCCACCAC
AGCCATCTCGTTTATCGGACCAGGAGCAGGCATCCATGAGACCTCAGAGCTTCAGATCGAGGC
CTTGGGGGGTCCGGGCCCCCCCCAGGAAACACGGTGAGGCCCCAGCGCTGCAGCCAAAGCTGG
CACGATCTATGGGGCAGGTGCCGCTCTGCCTAGAAAAGCCAGGGGCTCTGCTGCCGTGCCCTC
CAGAGCCCACAGCGGGCAGGACTCCTCCAGCACACCACACCCAGTGGCCCCGAGACCCCTCTG
AGAACAGTGAGGCTGGTCTCGTGCCGTTCCAGCCGGTGCCCGGCCAGTGGGGAGGACACAGC
CTAGGAACCAGCTGCCTGAGACCAGGGTGCCCTCTGGGCTGTCTCCCGCGTGGCGGAGACCCC
AAGCACGCAGCCACCCATTTCCGGAGCTGCAGGATAGAGCTTCCTCTTGATCTCTGTTTTTAAG
CAGAAATTCATTGTGCAGAAAAGTCTCCTCCAGAGCTCTGTGGCCCCGCTCGGATCCGCTGGACC
CCCATGCCTGGCTGATCCCTGCCCACGTGGGGCAGGCCACATCTAACCCCCACAAGTCACTG
CCTCACTGCACCTGCCAAGGCTGCCCTGGCGCTGAGTCTGGGGTCCCTCCCGGAGTTCCTGG
GAGAAAGGCGCCGTCGTGGCCGCCTCCCGCACGCCAGGCCCGGGCTCCACCGTGGGTCTCAGA
CGCCCTGCGGCACCGGCACCGTCTGCTTTAGCATGGGACCCCCATCTGAGGGGTGGCCTGGCC
TTCGGGGTCCCCACGCTCCTTTGCGAAGTCCACTGTGGGTGCCATCATGGTCTCCGGGACCTG
GGCCAGCGGGAACGTGGGGGCACTGGGTGTGCTGATATAAAGTCGGCATTACTCAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 534

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108765
><subunit 1 of 1, 189 aa, 1 stop
><MW: 19464, pI: 9.60, NX(S/T): 4
MALRHLALLAGLLVGVASKSMентаQLPECCVDVVGVNASCPGASLCGPGCYRRWNADGS
ASCVRCGNGTLPAYNGSECRSFAGPGAPFPMNRSSGTPGRPHPGAPRVAASLFLGTTFFIS
SGLILSVAGFFYLKRSSKLPRACYRRNKAPALQPGEEAAMI PPPQSSDVGSAGKEDPPRQ
GRPPI PAPP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-18

Transmembrane domain:

Amino acids 111-129

N-glycosylation sites:

Amino acids 38-42;68-72;75-79;92-96

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 134-138

N-myristoylation sites:

Amino acids 11-17;36-42;43-49;59-65;69-75;122-128

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FIGURE 535

TGGATCTGCGGGAATGTGGGCTGGAGAGGTCCTGCCGTGGTACCAGCCTCCAGCCTGCCCCCA
GGAAGTCCCCCTGACCCAGGCGCGCCCGCTGCTCGGTGGCAGGAGGGCCGGCGGAGCGCC**ATGG**
CCTGCATCCTGAAGAGAAAGTCTGTGATTGCTGTGAGCTTCATAGCAGCGTTCCTTTTCCTGC
TGGTTGTGCGTCTTGTAAATGAAGTGAATTTCCCATTTGCTACTAAACTGCTTTGGACAACCTG
GTACAAAGTGGATAACCATTCCTACACATACAGGCGGCCCTTCGAACTCACTATGGATACA
TAAATGTGAAGACACAAGAGCCTTTGCAACTGGACTGTGACCTTTGTGCCATAGTGTCAAACCT
CAGGTCAGATGGTTGGCCAGAAGGTGGGAAATGAGATAGATCGATCCTCCTGCATTTGGAGAA
TGAACAATGCCCCACCAAAGGTTATGAAGAAGATGTCGGCCGCATGACCATGATTCGAGTTG
TGTCCCATACACAGCGTTCCTCTTTTGCTAAAAAACCTGATTATTTTTTCAAGGAAGCGAATA
CTACTATTTATGTTATTTGGGGACCTTTCCGCAATATGAGGAAAGATGGCAATGGCATCGTTT
ACAACATGTTGAAAAAGACAGTTGGTATCTATCCGAATGCCCAAATATACGTGACCACAGAGA
AGCGCATGAGTTACTGTGATGGAGTTTTTAAGAAGGAACTGGGAAGGACAGTACAGAG**TGAC**
CATGCAGTGTTGATTGATCGAACAGCAACCACCACATACATGTCCTGCCCCACCACAAAAGGA
AGGAAGGAATAAAAGAAAGAAAGAAAGAAACAAACAAACAAACAAACAAACTAAGCAAGACA
AAACAAATACCCATGTCAGTGGTTCAAAGATTAAGATTGTGGCTTTGTGTAAAGTTCTTTCCC
TTTGTAGACTTGCTGCATAATTATTCAGGTATGATGGTTACAGTTTTTAAAAAGGAAGGGAAA
TTGTGGTATGTGGTATGTAAATATTTTAAATGTTGTCTCTCTGTTTTGATCAGTTTTTGT
TATTCAATTTGTCTTTATTAAATCTTATCAAAGCA

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FIGURE 536

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108783
><subunit 1 of 1, 210 aa, 1 stop
><MW: 24022, pI: 9.51, NX(S/T): 1
MACILKRKSVIAVSFIAAFLLVRLVNEVNFPLLLNCFGQPGTKWIPFSYTYRRPLRT
HYGYINVKTQEPLQLDCDLCAIVSNSGQMVGQKVGNEIDRSSCIWRMNNAPTKGYEEDVG
RMTMIRVVSHTSVPDLLKNPDYFFKEANTTIYVIWGPFRNMRKDGNGIVYNMLKKTVGIIY
PNAQIYVTTEKRMSYCDGVFKKETGKDSTE
```

Important features of the protein:**Signal peptide:**

Amino acids 1-27

N-glycosylation sites:

Amino acids 148-152

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 6-10;191-195;201-205

N-myristoylation sites:

Amino acids 41-47;87-93;91-97;167-173;178-184

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FIGURE 537

GTTTTATTGACAATACATGCATCATATCTTTTGACTTTGAAGGATATCTCATGTCAAAGGAAT
CAAGTTATGATTTATAGAGGATTCAGCTGGAATACCTTGTGGGTGCTGGCTGAGGGTGGCAAA
ACGCCTACCGAGACATGAAGGTTTTAGCCACTAGTTTTGTCTTGGGAGCCTGGGGTTGGCCT
TCTACCTGCCTTTGGTGGTGACTACACCTAAAACACTGGCCATCCCTGAGAAGCTGCAAGAAG
CTGTGGGGAAAGTTATCATCAATGCCACAACCTGTACTGTACCTGTGGCCTTGGCTATAAGG
AGGAGACCGTCTGTGAGGTGGGCCCTGATGGAGTGAGAAGGAAATGTCAGACTCAGCGCTTAGAA
TGTCTGACCAACTGGATCTGTGGGATGCTCCATTTACCATTCTCATTGGCAAGGAATTTGAG
CTTAGCTGTCTGAGTTCAGACATCTTGGAGTTTGGACAGGAAGCTTTCGGGTTACCTGGAGA
CTTGCTCGAGGTGTCATCTCCACTGACGATGAGGTCTTCAAACCCTTTCAAGCCAACCTCCAC
TTTGTGAAGTTTAAATATGCTCAGGAGTATGACTCTGGGACATATCGCTGTGATGTGCAGCTG
GTAAAAAAGTTGAGACTTGTCAAGAGGCTCTATTTTGGGTTGAGGGTCCTTCCTCCTAACTTG
GTGAATCTGAATTTCCATCAGTCACTTACTGAGGATCAGAAGTTAATAGATGAGGGATTGGAA
GTTAATCTGGACAGCTACTCCAAGCCTCACCACCCAAAGTGGAAGAAGGTGGCGTCAGCC
TTGGGAATAGGAATTGCCATTGGAGTGTTGGTGGCGTGTTGGTGAGGATTGTCTCTGTGCG
CTAAGGGGGGGCCTGCAGCAGTGAAGCTTCAAGAACTTAACAGCCTTGCTCCTGAAGAACTG
GCTGCCCAGGAAGCCAAGCTAGCTTTTTAGGGGAGTGTTCCAGCTGCTGGTAGTGGATCAGCT
TAGAGGGAACTACTCCACAGCCAAAAGAATGAGTGGGAGAAATGGAGGGGACAATCTCCTGGG
AGCTATGCGCAGTAACCTAAGCTTCTTATGTCCCATGGATCTCTCCTGATCTTCCCTGCCA
TTGGGTACCCAGGAACTGCAAGCATTGCCTGTGTTCTTGGGAAGAGTTCTAAGAAGCTTGCA
TTCATTTTCTACCCTTTATGACTTGGATGCCTCCCCACCTCCATTTCCCCTCTTCTGAGCTGT
GTATTCATGTAGAGGGATGTATTCAGCCTTTTTAGTGAACATTTTTTTTCAATAAAAGTAATT
CACAGTAA

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FIGURE 538

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108789
><subunit 1 of 1, 255 aa, 1 stop
><MW: 28440, pI: 8.92, NX(S/T): 1
MKVLATSFVLGSLGLAFYLPVVVTPKTLAIPEKLQEAVGKVIINATTCTVTCGLGYKEE
TVCEVGPDGVRRKCQTQRLECLTNWICGMLHFTILIGKEFELSCLSSDILEFGQEAFT
WRLARGVISTDDEVFKPFQANSHFVKFYAQEYDSGTYRCDVQLVKNLRLVKRLYFGLRV
LPPNLVNLNFHQSLTEDQKLIDEGLEVNLDSYKPHHPKWKKKVASALGIGIAIGVVGGV
LVRIVLCALRGGLQQ
```

Important features of the protein:**Signal peptide:**

Amino acids 1-30

Transmembrane domain:

Amino acids 225-244

N-glycosylation site:

Amino acids 45-49

N-myristoylation sites:

Amino acids 126-132;156-162;204-210;229-235;231-237;235-241

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FIGURE 539

GCGCTCATCACTGGCTGGGGACAGAGCCGGGCACCAAGGAGCGACAGGATCCCGAAGAGAGAG
AGAGAAGGCAGCGAGGGAAGGAGGACCCCGGCAGGCAGCAGCATGAAATTTCAGCCCAGCGCAC
TACCTGCTGCCTCTCCTGCCTGCGCTGGTCCTCAGCACCCAGACAGGACTATGAAGAGCTAGAA
AAGCAGCTGAAAGAAGTCTTTAAGGAGCGAAGCACCATTTCTTCGTCAGCTGACAAAGACATCA
AGAGAACTTGATGGAATTAAAGTCAATCTTCAGTCCTTAAAAAACGATGAGCAGTCTGCCAAA
ACTGATGTTTCAGAACTTCTGGAATTAGGACAGAAACAAAGAGAAGAAATGAAGTCTCTTCAG
GAGGCCCTGCAAAATCAGCTTAAGGAGACATCAGAGAAAGCAGAAAAACACCAGGCTACTATT
AATTTTTTAAAGACTGAAGTTGAAAGAAAGAGCAAAATGATCCGAGACCTCCAGAATGAGGAT
TCAAGGAAGAGACCAAGAGATCTCCAGTGGAAGATAGTCTCCATGAGGACCATGTCAATATAC
TTATTGATGTATCTCTAGTACCTAGAATAGTGGAGATTTATATTAGATACAAAATAAATATGT
GTGGAATTAATTAATAA

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FIGURE 540

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108806
><subunit 1 of 1, 159 aa, 1 stop
><MW: 18865, pI: 9.76, NX(S/T): 0
MKFSPAHYLLPLLPAVLSTRQDYEELEKQLKEVFKERSTILRQLTKTSRELDGIKVNLO
SLKNDEQSAKTDVQKLLELGQKQREEMKSLQEALQNQLKETSEKAEKHQATINFLKTEVE
RKSKMIRDLQNEDSRKRPRDLQWKIVSMRTMSIYLLMYL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-22

N-myristoylation site:

Amino acids 54-60

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FIGURE 541

[illegible]

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FIGURE 542

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108936
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19472, pI: 5.71, NX(S/T): 0
MSPSGRLCLLTIVGLILPTRGQTLKDTTSSSSADSTIMDIQVPTRAPDAVYTELQPTSPT
PTWPADETPQPQTQTQQLEGTDGPLVTDPEETHKSTKAAHPTDDTTTLSERPSPSTDVQTD
PQTLKPSGFHEDDPFFYDEHTLRKRGLLVA AVLFITGIIILTS GKCRQLSRLCRNRCR
```

Important features of the protein:**Signal peptide:**

Amino acids 1-21

Transmembrane domain:

Amino acids 147-162

Tyrosine kinase phosphorylation site:

Amino acids 45-52

N-myristoylation site:

Amino acids 146-152

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FIGURE 543

CGGCTCGAGGTGAGAAGGAACTGCAAGAGTGGGGCAGAGAACCAGAGTGTGAGAGCAAAACC
TCCTCTATCTGCACATCCTGGGGACGAACCGGGCAGCCGGAGAGCTGCGGCCGGCCCAGTCCC
GCTCCGCCCTTTGAAGGGTAAAACCCAAGGCGGGGCCCTTGGTTCTGGCAGAAGGGACGCT**ATGA**
CCGCAGAATTCCTCTCCCTGCTTTGCCTCGGGCTGTGTCTGGGCTACGAAGATGAGAAAAAGA
ATGAGAAACCGCCCAAGCCCTCCCTCCACGCCTGGCCCAGCTCGGTGGTTGAAGCCGAGAGCA
ATGTGACCCTGAAGTGTGAGGCTCATTCCAGAATGTGACATTTGTGCTGCGCAAGGTGAACG
ACTCTGGGTACAAGCAGGAACAGAGCTCGGCAGAAAACGAAGCTGAATCCCCCTTCACGGACC
TGAAGCCTAAGGATGCTGGGAGGTACTTTTGTGCCTACAAGACAACAGCCTCCCATGAGTGGT
CAGAAAGCAGTGAACACTTGCAGCTGGTGGTCACAGATAAACACGATGAACTTGAAGCTCCCT
CAATGAAAACAGACACCAGAACCATCTTTGTGCGCCATCTTCAGCTGCATCTCCATCCTTCTCC
TCTTCCTCTCAGTCTTCATCATCTACAGATGCAGCCAGCACGGTTCATCATCTGAGGAATCCA
CCAAGAGAACCAGCCATTCCAACTTCCGGAGCARGAGGCTGCCGAGGCAGATTTATCCAATA
TGGAAAGGGTATCTCTCTCGACGGCAGACCCCCAAGGAGTGACCTATGCTGAGCTAAGCACCA
GCGCCCTGTCTGAGGCAGCTTCAGACACCACCCAGGAGCCCCCAGGATCTCATGAATATGCGG
CACTGAAAGTGT**TAG**CAAGAAGACAGCCCTGGCCACTAAAGGAGGGGGGATCGTGCTGGCCAAG
GTTATCGGAAATCTGGAGATGCAGATACTGTGTTTCCTTGCTCTTCGTCCATATCAATAAAAT
TAAGTTTCTCGTCTTA

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FIGURE 544

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119510
><subunit 1 of 1, 236 aa, 1 stop
><MW: 26079, pI: 5.05, NX(S/T): 3
MTAEFLSLLCLGLCLGYEDEKKNEKPPKPSLHAWPSSVVEAESNVTLKCOAHSQNVTFVL
RKVNDSGYKQEQSSAENEAEFPFTDLKPKDAGRYFCAYKTTASHEWSESSEHLQLVVTDK
HDELEAPSMKTDTRTIFVAIFSCISILLFLSVFIIYRCSQHGSSEESTKRTSHSKLPE
QEAAEADLSNMERVSLSTADPQGVTYAELSTSALSEAASDTTQEPPGSHEYAALKV
```

Important features of the protein:**Signal peptide:**

Amino acids 1-16

Transmembrane domain:

Amino acids 135-153

N-glycosylation sites:

Amino acids 44-48;55-59;64-68

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 171-175

Tyrosine kinase phosphorylation sites:

Amino acids 61-69;87-95

N-myristoylation sites:

Amino acids 12-18;203-209

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FIGURE 545

GGCGGCCCGGAGCTGGGAGCGCGGGGAAGGCGGTTGGGGTTCTGACAGCTGCGCGCGATCCTG
CTCTCTCTCAGCCGCCTGTGGACATGCGCAAAGGGCCCTCTCCTGAGTCCAG**ATG**ATGCTCAT
ACCAATGGCTTCAGTGATGGCGGTGACTGAACCGAAATGGGTCTCGGTCTGGAGCCGCTTCCT
CTGGGTGACGCTGCTGAGCATGGTGCTGGGGTCCCTGCTGGCCCTGCTGCTGCCGCTGGGGGC
TGTGGAGGAGCAGTGCTTGGCTGTGCTCAAAGGCCTCTACCTGCTCAGGAGCAAACCGGACAG
GGCGCAGCATGCCGCCACCAAGTGCACCAGCCCGTCCACGGAGCTCAGCATCACCTCCAGGGG
CGCGACGCTGCTGGTGGCCAAGACCAAGGCCTCTCCAGCGGGTAAGTTGGAAGCCAGAGCTGC
CCTGAACCAGGCCCTGGAGATGAAGCGCCAGGGCAAGCGGGAAAAAGCCCCAAAAGCTCTTCAT
GCACGCCCTCAAGATGGACCCGGACTTCGTGGACGCGCTCACCGAGTTTGGCATCTTCTCGGA
AGAAGACAAGGACATCATCCAGGCGGACTACTTGTACACCAGAGCATTGACCATCTCACCTA
CCATGAGAAAGCACTGGTCAACCGCGATCGGACACTGCCTCTTGTGGAAGAGATCGACCAGAG
GTATTTTCAGCATCATCGACAGCAAAGTGAAGAAGGTCATGTCCATCCCCAAGGGGAACTCAGC
TCTGCGCAGGGTCATGGAGGAGACCTACTACCATCACATCTACCACACAGTGGCCATCGAGGG
CAACACCCTCACCTCTCGGAAATCAGGCACATCCTGGAGACCCGCTACGCCGTGCCCGGGAA
GAGCCTGGAGGAGCAGAACGAGGTCATAGGCATGCATGCAGCCATGAAGTACATCAACACGAC
TCTGGTTTCGCGCATCGGCTCCGTACCATCAGCGACGTGCTGGAGATCCACAGGCGGGTGCT
GGGCTACGTGGACCCCGTGGAAGCCGGCAGGTTTCGGACAACACAGGTCCTGGTCGGACACCA
CATCCCTCCCCATCCGCAGGATGTGGAAAAGCAGATGCAGGAGTTTGTACAGTGGCTCAACTCC
GAGGAAGCCATGAACCTGCACCCAGTGGAGTTTGCAGCCTTAGCCCATTTATAAACTCGTTTAC
ATCCACCCTTTTCATTGATGGCAACGGGAGGACCTCCCGTCTGCTCATGAACCTCATCCTCATG
CAGGCGGGCTACCCGCCCATCACCATCCGCAAGGAGCAGCGGTCCGACTACTACCACGTGTTG
GAAGCTGCCAACGAGGGCGACGTGAGGCCTTTTCATTGCTTCATCGCCAAGTGTACTGAGACC
ACCCTGGACACCCTGCTTTTTGCCACAACCTGAGTACTCGGTGGCACTGCCAGAAGCCCAACCC
AACCACTCTGGGTTCAAGGAGACGCTTCCTGTGAAGCCCT**TAA**CCCTAGAAATCCTCAGTGACA
AAGGCTGTCTGAGGTAGGAAA

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FIGURE 546

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119517
><subunit 1 of 1, 458 aa, 1 stop
><MW: 51778, pI: 7.81, NX(S/T): 2
MMLIPMASVMAVTEPKWVSVWSRFLWVTLLSMVLGSL LALLPLGAVEEQCLAVLKGLYL
LRSKPDRAQHAATKCTSPSTELSITSRGATLLVAKTKASPAGKLEARAALNQALEMKRQG
KREKAQKLFMHALKMDPDFVDALTEFGIFSEEDKDIIQADYLYTRALTISPYHEKALVNR
DRTLPLVEEIDQRYFSIIDSKVKVMSIPKGN SALLRRVMEETYYHHIYHTVAIEGNTLTL
SEIRHILETRYAVPGKSLEEQNEVIGMHAAMKYINTTLVSRIGSVTISDVLEIHRRVLGY
VDPVEAGRFRFTTQVLVGHHIPPHQDVEKQM QEFVQWLNSEEAMNLHPVEFAALAHYKLV
YIHPFIDGNGRTSRLLMNLILMQAGYPPITIRKEQRSDYYHVLEAANECDVRPFIRFIK
CTETTLDTLLFATTEYSVALPEAQP NHSGFKETLPVKP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-46

N-glycosylation sites:

Amino acids 275-279;446-450

Tyrosine kinase phosphorylation sites:

Amino acids 216-225;217-225;244-232

N-myristoylation sites:

Amino acids 35-41;235-241;266-272;368-374

Amidation site:

Amino acids 119-123

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FIGURE 547

CCTCTGTCTGTGCTCCCATCCCAGGGAGTATAGGTGGAGCCTCCAGAGCCCATGGACAGGGCA
TGCTGGGGCTGGGCCAGCCCCAGCGGTGTCTCTAAGGCACCCCTGGGATCCCCACTGAGCTGG
CCTACTTCAGACAGCCAGGGCCCCACCCCTCTGGCCCCCTTAGTGTCCAGCTCGTGGCCCCCTTG
GCATTTCCACAAGACGCCAAG**ATG**GAGATTCCCATGGGGACCCAGGGCTGCTTCTCAAAGAGC
CTCCTGCTCTCAGCCTCAATCCTGGTCTCTGGATGCTCCAAGGCTCCCAGGCAGCTCTCTAC
ATCCAGAAGATTCCAGAGCAGCCTCAAAAGAACCAGGACCTTCTCCTGTCAGTCCAGGGTGTC
CCAGACACCTTCCAGGACTTCAACTGGTACCTGGGGGAGGAGACGTACGGAGGCACGAGGCTA
TTTACCTACATCCCTGGGATACAACGGCCTCAGAGGGATGGCAGTGCCATGGGACAGCGAGAC
ATCGTGGGCTTCCCCAATGGTTCCATGCTGCTGCGCCGCGCCAGCCTACAGACAGTGGCACC
TACCAAGTAGCCATTACCATCAACTCTGAATGGACTATGAAGGCCAAGACTGAGGTCCAGGTA
GCTGAAAAGAATAAGGAGCTGCCCAGTACACACCTGCCACCAACGCTGGGATCCTGGCGGCC
ACCATCATTGGATCTCTTGCTGCCGGGGCCCTTCTCATCAGCTGCATTGCCTATCTCCTGGTG
ACAAGGAAGTGGAGGGGGCCAGAGCCACAGACTGCCTGCTCCGAGGGGGCCAGGGATCTCTGTCC
ATCTTGCTCGGCTGTATCCCCAGTGCCTTCAGTGACGCCCAGCACATGGATGGCGACCACA
GAGAAGCCAGAATTGGGCCCTGCTCATGATGCTGGTGACAACAACATCTATGAAGTGATGCCC
TCTCCAGTCCTCCTGGTGTCCCCCATCAGTGACACAAGGTCCATAAACCCAGCCCGGCCCTG
CCCACACCCCCACACCTGCAGGCGGAGCCAGAGAACCACCAGTACCAGCAGGACCTGCTAAAC
CCCGACCTGCCCCCTACTGCCAGCTGGTGCCAACCTTCC**TGAT**GGGTCTGGGCCAGGCCAGC
CAGGGAGAAGACAAGGCCCCAGCCCTCCTCTGGGAGCCTCACACCTGAGACCAGCAGGACAAG
GCCATTGGGGGCTGTGGGGCCGATGAGGTGGACTCAGCCAAAGACTCAGCAGCACATGGGGCA
GGTGTCTTGGCAGGGGGACAGGAGACTGTAACAGGCCCAGGTCTTGTGCAGCCCCCTGAATGC
ACGCCCCGCTTCGGTCTGTTCCCTCAAGCAAGCTGGCCTGGGCCATGTGCCTGTGAAAGGCAG
GCTCTGGCCCCCTTTCCATGCCAAAGTCCCCCAAGATCTGGATATCTGGGGACAAGATGGTGGC
CTCAGGCCTGCCTCCCAGGCAGTTGGCTGGGCTCCCAACTGTCTGTCTCAATGCCCTACCCC
AACTCCACTAGTGACCCTCAGAGTCTTCTCCCTTAGGACAAGGCAGACACCCCACCATGCGG
GCCTCAGGTGGCAGAGAGGGCCAGCCTCACAGGCCTGTGGCCCCACACACCAGTCCCAGCAAG
GTGACCACGGCTGCTGGACCCCTTCCCTGTTCAAGCAGGCCCAGCCCCCTCTCAGAACCTGCTG
CCAGCTGCTGGTCTTGGCCCCCACCCTGAATCTTACTGAGTCCCTCTGGGCAGCAGCTCCCTT
CTCCACCCCACCCCAGCACCCGTCCCAATGTGGCCTCAGCTTGTCTCCCTTCCCCAACT
ATGCATTTCATTCAGCAATAAATGAGCCTTTGCTGCA

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FIGURE 548

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119535
><subunit 1 of 1, 300 aa, 1 stop
><MW: 32638, pI: 6.02, NX(S/T): 1
MEIPMGTOGCFSKSLLLSASILVLWMLQGSQAALYIQKIPEQPQKNQDLLLSVQGVPDF
QDFNWYLGEETYGGTRLFTYIPGIQRPQRDGSAMGQRDIVGFPNGSMLLRRAQPTDSGT
YQVAITINSEWTMKAKTEVQVAEKNKELPSTHLPTNAGILAATTIGSLAAGALLISCIAYL
LVTRNWRGQSHRLPAPRGQGSLSILCSAVSPVPSVTPSTWMATTEKPELGPAGDAGDNNI
YEVMPSPVLLVSPISDTRSINPARPLPTPPHLQAEFENHQYQQDLLNPDAPYQCQLVPTS
```

Important features of the protein:**Signal peptide:**

Amino acids 1-32

Transmembrane domain:

Amino acids 159-178

N-glycosylation site:

Amino acids 104-108

N-myristoylation sites:

Amino acids 6-12;29-35;55-61;91-97;157-163;165-171

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FIGURE 549

GCCACTCACACCATCTGCTAATGGGACAGCTCACTCTTCCCTCCAAACCATGGCCTTGGCTCA
AGAGCTTCCTTGTTTCTGGAATGTTCTTTCCTCCAGCTCCAGGTGTTGAAATTCTGCCTGGTC
TGGGTCTCCTGTTGAAGGACGCCCTCCACTGGGAAGGATCCTCTTGCCTTCACCACTTGTCTT
CACCAGCCCCCTGCTCCCCCTCTTCTCTTGGGGCTGTTGTCGTTGTTGATACTTTTTTTTTTGT
GTGTTTGACACACATCTTCTTCTCACCCCTCTAACACAGTTCTCAACCACAGCACTTTTGTCCC
TGGAGATGTTGGCAGTGTCCAGAGGCGTGTTGATGGTCCCCTGGGGTGGGGGTGCTGCTGGCA
CCAGATGGTAGGGAGATGCCAGGGGTGCTGCTCCACACCCCTATGGGACACTGCACAGTACACC
TGGCCTGTGTCCCCACAGCGAGAGCTGGCCCTGGGCAGGCGTGGTCCCTGCGGTGTGTGTTG
GTTGGGATCCTCCACAGTGACAGACGGTGCGCTCTGCCACGTTTCCACACAGCTCTTTTGCT
TGTGGAGCTCACCCCTTTCAGAGAGCTCATTTCCCTGCGGTCTTTGGCCTGCAGAAGTAAAA
TGAGGGGTGGTGAATTACACCCCTGCTGGTTACACATGGAAACTCAGGAGTGAGAATTTTGT
GGAGAGCAAGAGAGGTGAGACTGGGGTGCTGGCTGCCAGCCAGGCGGTCCCTCAGCCCCCTGGA
GAAGCGGGGTGGGGCCTGCACACCGAGTCCTTCCAGTGAGTCCAGTGATGCTCTCTCCTCTTC
CTCCAGTCACCTTCTCTCCAGTGCCACTACTGCGCTTTCGATGCAGAATAATTCAGTATTT
GGCGACTTGAAGTCGGACGAGATGGAGCTGCTCTACTCAGCCTACGGAGATGAGACAGGCGTG
CAGTGTGCGCTGAGCCTGCAGGAGTTTGTGAAGGATGCTGGGAGCTACAGCAAGAAAGTGGTG
GACGACCTCCTGGACCAGATCACAGGCGGAGACCACTCTAGGACGCTCTTCCAGCTGAAGCAG
AGAAGAAATGTTCCCATGAAGCCTCCAGATGAAGCCAAGGTTGGGGACACCCTAGGAGACAGC
AGCAGCTCTGTTCTGGAGTTCATGTGATGAAGTCCTATCCCGACGTTTCTGTGGATATCTCC
ATGCTCAGCTCTCTGGGGAAGGTGAAGAAGGAGCTGGACCCTGACGACAGCCATTTGAACTTG
GATGAGACGACGAAGCTCCTGCAGGACCTGCACGAAGCACAGGCGGAGCGCGGCGGCTCTCGG
CCGTGCTCCAACCTCAGCTCCCTGTCCAACGCCTCCGAGAGGGACCAGCACCACTGGGAAGC
CCTTCTCGCCTGAGTGTGCGGGAGCAGCCAGACGTCACCCACGACCCCTATGAGTTTCTTCAG
TCTCCAGAGCCTGCGGCCTCTGCCAAGACCTAACTCTAGACCACCTTCAGCTCTTTTATTTTA
TTTTTTTAGTTTTATTTTGCACGTGTAGAGTTTTTGTGTCATCAGACAAGGACTTTGATCCTGTC
CCCTTTGGCATGCGGGAAGCAGCCGCGGGGAGGTAATGAATTGTCTGTGGTATCATGTCAGCA
GAGTCTCCAAGCCCCACGAACCCTGAGGAGTGGAGTCATACGCGAAGGCCATATGGCCATCGT
GTCAGCAGAGAGAGTCTCTGTACACAGCCCCGTGAACCCTGAGGAGTGGAGTCATACACGAAG
GGCGTGTGGCCATCGTGTGAGCAGAGAGAGTCTCTGTACACAGCCCCGTGAACCCTGAGGAGTGG
AGTCATACGCGAAGGGTGTGTGGCCAGGCTGCAGAGCTGCGTGCCGTTTGTGTCCGAGCATCA
CGTGTGGCTCCAGCCCTTGTCTGCCAGTGTAGACACCTCTGTCTGCCCCACTGTCCTGGGG
TCGCTCTTGGGAGGCACAGGCATGGGTGTGTCTGGCCTCATTCTGTATCAGTCCAGTGTGTTT
CTGTATAGTTTTGTGTCTCCAGGCAGGCCATGGTAGGGGCCTCGCAGGGGCCATTGGGGAGC
ACAGGGCCAGGCTGGGGTGAGGAGAGCTCCCCTGTTTTCTGTTTAATTGATGAGCCTGGGAAA
GGAGTGTGTTCTGCCTGCCCGTTACAGTGGAGCGTTCGTTCCATAAAACGTTTTCTAACTG
GGAA

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FIGURE 550

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119537
><subunit 1 of 1, 104 aa, 1 stop
><MW: 11136, pI: 8.20, NX(S/T): 0
MLAVSRGVLMVPLGLGVLLAPDGREMPGVLLHTLWDTAQYTWPVSPPTARAGPGQAWSLRC
VLVGILHSDRRRCALPTFPHSSFACGAHPFAESSFPCGLWPAEVK
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

N-myristoylation sites:

Amino acids 53-59;64-70;97-103

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 74-85

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FIGURE 551

CGCCCTTAGCATGGGGTTTCTGCCGAGCGCCCTGCACCCGCTGTCTCTCTGGTGCAGGCCATCATGCTGGCCAT
GACCCTGGCCCTGGGTACCTTGCCCTGCCTTCTACCCCTGTGAGCTCCAGCCCCACGGCTGGTGAAGTGAAGTGA
GCTGTTCTCTGAAGTCTGTGCCCCACTTCTCCATGGCAGCACCCCGTGGCAATGTCACCAGCCTTTCTTGTCTCTC
CAACCGCATCCACCACCTCCATGATTCTGACTTTGCCACCTGCCAGCCTGCGGCATCTCAACCTCAAGTGGAA
GTGCCCCGCGGTTGGCCTCAGCCCCATGCACTTCCCCTGCCACATGACCATCGAGCCCAGCACCTTCTTGGCTGT
GCCCCACCTGGAAGAGCTAAACCTGAGCTACAACAACATCATGACTGTGCCTGCGCTGCCAAATCCCTCATATC
CCTGTCCCTCAGCCATACCAACATCCTGATGCTAGACTCTGCCAGCCTCGCCGGCCTGCATGCCCTGCGCTTCT
ATTCATGGACGGCAACTGTTATTACAAGAACCCTGCAGGCAGGCCTGGAGGTGGCCCCGGGTGCCCTCCTTGG
CCTGGGCAGCCTCACCCACCTGTCACTCAAGTACAACAACCTCACTGTGGTGGCCCCGAACCTGCCTTCCAGCCT
GGAGTATCTGCTGTTGTCTTACAACCGCATCGTCAAACCTGGCGCCTGAGGACCTGGCCAATCTGACCGCCCTGCG
TGTGCTCGATGTGGGCGGAAATTGCCGCGCTGCGACCAGCCTCCCAACCCCTGCATGGAGTGGCCTCGTCACTT
CCCCAGCTACATCCCGATACCTTCAGCCACCTGAGCCGTCTTGAAGGCCTGGTGTGAAGGACAGTTCTCTCTC
CTGGCTGAATGCCAGTTGGTTCCGTGGGCTGGGAAACCTCCGAGTGTGGACCTGAGTGAGAAGTTCTCTACAA
ATGCATCACTAAAACCAAGGCCCTCCAGGGCCTAACACAGCTGCGCAAGCTTAACCTGTCTTCAATTACAAAA
GAGGGTGTCTTTGCCACCTGTCTCTGGCCCCCTTCTTCCGGAGCCTGGTCCGCCCTGAAGGAGCTGGACATGCA
CGGCATCTTCTTCCGCTCACTCGATGAGACCAGCCTCCGGCCACTGGCCCGCTGCCCATGCTCCAGACTCTGCG
TCTGCAGATGAAGTTCAACAACAGGCCAGCTCGGCATCTTCAGGGCCTTCCCTGGCCTGCGCTACGTGGACCT
GTCGGACAACCGCATCAGCGAGCTTCGGAGCTGACAGCCACCATGGGGGAGGCAGATGGAGGGGAGAAGGTCTG
GCTGCAGCCTGGGGACCTTGCTCCGGCCCCAGTGGACACTCCAGCTCTGAAGACTTCAGGCCCAACTGCAGCAC
CCTCAACTTCACCTTGGATCTGTACGGAACAACCTGGTGACCGTGCAGCCGGAGATGTTTGGCCAGCTCTCGCA
CCTGCAGTGCCTGCGCCTGAGCCACAACCTGCATCTCGCAGGCAGTCAATGGCTCCAGTTCTTCCGCTGACCGG
TCTGCAGGTGCTAGACCTGTCCCACAATAAGCTGGACCTTACCACGAGCACTCATTACGGAGCTACCACGACT
GGAGGCCCTGGACCTCAGCTACAACAGCCAGCCCTTTGGCATGCAGGGCGTGGGCCACAACCTTCAGCTTCGTGGC
TCACCTGCGCACCCCTGCGCCACCTCAGCCTGGCCACAACAACATCCACAGCCAAGTGTCCCAGCAGCTCTGCAG
TACGTGCTGCGGGCCCTGGACTTCAGCGGCAATGCACTGGGCCATATGTGGGCCGAGGGAGACCTCTATCTGCA
CTTCTTCCAAGGCCTGAGCGGTTTGATCTGGCTGGACTTGTCCCAGAACCAGCCTGCACACCCTCCTGCCCCAAC
CCTGCGCAACCTCCCCAAGAGCCTACAGGTGCTGCGTCTCCGTGACAATTACCTGGCCTTCTTTAAGTGGTGGAG
CCTCCACTTCTGCCCCAACTGGAAGTCTCGACCTGGCAGGAAACCAGCTGAAGGCCCTGACCAATGGCAGCCT
GCCTGCTGGCACCCGGCTCCGGAGGCTGGATGTGAGCTGCAACAGCATCAGCTTCGTGGCCCCCGGCTTCTTTTC
CAAGGCCAAGGAGCTGCGAGAGCTCAACCTTAGCGCCAACGCCCTCAAGACAGTGGACCACTCCTGGTTTGGGCC
CCTGGCGAGTGGCCTGCAATACTAGATGTAAGCGCCAACCTCTGCACTGCGCCTGTGGGGCGGCCCTTTATGGA
CTTCTGCTGGAGGTGCAGGCTGCCGTGCCCGGTCTGCCAGCCGGGTGAAGTGTGGCAGTCCGGGCCAGCTCCA
GGCCTCAGCATCTTTGCACAGGACCTGCGCCTCTGCCTGGATGAGGCCCTCTCCTGGGACTGTTTCGCCCTCTC
GCTGCTGGCTGTGGCTCTGGGCCTGGGTGTGCCATGCTGCATCACCTCTGTGGCTGGGACCTCTGGTACTGCTT
CCACCTGTGCTGGCCTGGCTTCCCTGGCGGGGGCGGCAAGTGGGCGAGATGAGGATGCCCTGCCCTACGATGC
CTTCGTGGTCTTCGACAAAACGAGAGCGCAGTGGCAGACTGGGTGTACAACGAGCTTCGGGGGAGCTGGAGGA
GTGCCGTGGGCGCTGGGCACCTCCGCCTGTGCTGGAGGAACGCGACTGGCTGCCTGGCAAAACCTCTTTGAGAA
CCTGTGGGCTCGGTCTATGGCAGCCGCAAGACGCTGTTTGTGCTGGCCACACGGACCGGGTCAAGTGGTCTCTT
GCGCGCCAGCTTCTGCTGGCCAGCAGCGCCTGCTGGAGGACCGCAAGGACGTCGTGGTGTGGTATCCTGAG
CCCTGACGGCCGCGCTCCCCTACGTGCGGCTGCGCCAGCGCCTCTGCCGCCAGAGTGTCTCTCTGGCCCCA
CCAGCCCAGTGGTCAGCGCAGCTTCTGGGCCAGCTGGGCATGGCCCTGACCAGGGACAACCACCACTTCTATAA
CCGGAAGTTCTGCCAGGGACCCACGGCCGAATAGCCGTGAGCCGGAATCCTGCACGGTGCCACCTC

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FIGURE 552

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119714
><subunit 1 of 1, 1032 aa, 1 stop
><MW: 115799, pI: 8.61, NX(S/T): 12
MGFCRSALHPLSLLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWLFLKSVPHFMSMAA
PRGNVTSLSLSSNRIHHLHDSDFAHLPSLRHLNLKWNCPVGLSPMHFPCMTIEPSTFL
AVPTLEELNLSYNNIMTVPALPKSLISLSLSTNIMLMLDSASLAGLHALRFLFMDGNCY
KNPCRQALEVAPGALLGLGSLTHLSLKYNNTLVVPRNLPSSLEYLLLSYNRIVKLAPEDL
ANLTALRVLDVGGNCRRCDHAPNPCMECPRHFPQLHPDTFSHLSRLEGLVLKDSSLSWLN
ASWFRGLGNLRVLDLSENFYKCIKTKALQGLTQLRKLNLSFNYQKRVSAHLSLAPSF
GSLVALKELDMHGIFFRSLDETTLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRYV
DLSDNRISGASELTATMGEADGGEKVWLQPGDLAPAPVDTPSSEDFRPN CSTLNFTLDLS
RNNLVTVQPEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQVLDLSHNKLDLYHEHS
FTELPRLEALDLSYNSQPPFGMQGVGHNFSAHLRTRLRHLSLAHNNIHSQVSQQLCSTSL
RALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDDLSQNRHLTLTPQTLRNLPKSLQVRL
RDNYLAFFKWWSLHFLPKLEVLDLAGNQLKALTNGSLPAGTRLRRLDVSCNSISFVAPGF
FSKAKELRELNLSANALKTVDSWFGPLASALQILDVSANPLHCACGA AFMDFLLEVQAA
VPGLPSRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCFALSLLAVALGLGVPMLHHL CG
WDLWYCFHLCLAWLPWRGRQSGRDEDALPYDAFVVFDKTQSAVADWVYNELRGQLEECRG
RWALRLCLEERDWLP GKTLFENLWASVYGSRKTLFVLAHTDRVSGLLRASFLLAQQRLL E
DRKD VVVVLVILSPDGRRSRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGMALTRDNH HF
YNRNFCQGPTAE
```

Important features of the protein:**Signal peptide:**

Amino acids 1-30

Transmembrane domain:

Amino acids 818-835

N-glycosylation sites:Amino acids 64-68;129-133;210-214;242-246;300-304;340-344;
469-473;474-477;513-517;567-571;694-698;731-735**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 347-351

Tyrosine kinase phosphorylation site:

Amino acids 863-871

N-myristoylation sites:Amino acids 27-33;41-47;63-69;193-199;361-367;409-415;
563-569;607-613;695-701;794-800;929-935;945-951;
1010-1016**Amidation site:**

Amino Acids 974-978

Leucine zipper patterns:

Amino acids 204-226;644-666;814-836

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FIGURE 553

GGCGTGGGACGTGCTGCGGCGTCCTAGCTGGCTTACAGGGCGGCGGGGGTGTGTGTCTCTCT
GTTAAGAGTGCTACTCGCCCGGGGTTGATCTGTGCATGCCACTCCTGGGTGAGACGGTGAGGT
CGGCGTCTGCGAGGACGCGGCGGTGGAGTAGAAGGGCAGCCGGAGACAGGCCCGGCGCCCCCTT
CCGAGGCTAGACGGCCCCAGCTTCGCGGGGATC**ATGG**CATTGCTGGTGGACCGAGTGCGGGGC
CACTGGCGAATCGCCGCGGGGCTCCTGTTCAACCTGCTGGTGTCCATCTGCATTGTGTTCCCTC
AACAAATGGATTTATGTGTACCACGGCTTCCCCAACATGAGCCTGACCCTGGTGCACCTTCGTG
GTCACCTGGCTGGGCTTGTATATCTGCCAGAAGCTGGACATCTTTGCCCCAAAAGTCTGCCG
CCCTCCAGGCTCCTCCTCCTGGCCCTCAGCTTCTGTGGCTTTGTGGTCTTCACTAACCTTTCT
CTGCAGAACAAACACCATAGGCACCTATCAGCTGGCCAAGGCCATGACCACGCCGGTGATCATA
GCCATCCAGACCTTCTGCTACCAGAAAACCTTCTCCACCAGAATCCAGCTCACGCTGATTCCCT
ATAACTTTAGGTGTAATCCTAAATTCTTATTACGATGTGAAGTTTAATTCCTTGGAATGGTG
TTTGCTGCTCTTGGTGTTTTAGTTACATCCCTTTATCAAGTGTGGGTAGGAGCCAAACAGCAT
GAATTACAAGTGAACCAATGCAGCTGCTGTACTACCAGGCTCCGATGTCATCTGCCATGTTG
CTGGTTGCTGTGCCCTTCTTTGAGCCAGTGTGGGAGAAGGAGGAATATTTGGTCCCTGGTCA
GTTTCTGCTTTGCTTATGGTGCTGCTATCTGGAGTAATAGCTTTCATGGTGAACCTTATCAATT
TATTGGATCATTGGGAACACTTCACCTGTCACCTATAACATGTTCCGACACTTCAAGTTCTGC
ATTACTTTATTCGGAGGATATGTTTTATTTAAGGATCCACTGTCCATTAATCAGGCCCTTGGC
ATTTTATGTACATTATTTGGCATTCTCGCCTATACCCACTTTAAGCTCAGTGAACAGGAAGGA
AGTAGGAGTAAACTGGCACAACGTCCT**TAA**TTGGGTTTTTGTGGAGAAAAGAATGTTGTCCCA
AGAAGATAAAAAATATTGTTAAGTGTGCAAGTTATTA

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FIGURE 554

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125170
><subunit 1 of 1, 313 aa, 1 stop
><MW: 35066, pI: 9.39, NX(S/T): 5
MALLVDRVRGHWRIAAGLLENLLVSICIVFLNKWIYVYHGFNMSLTLVHFVVTWLGLYI
CQKLDIFAPKSLPPSRLLLLALSFCGFVVFETNLSLQNTTIGTYQLAKAMTTPVIIAIQTF
CYQKTFESTRIQLTLIPITLGVILNSYYDVKFNFGLGMVFAALGVLVTSLYQVWVGAKQHEL
QVNSMQLLYYQAPMSSAMLLVAVPFFEPVFEGGGIFGPWSVSALLMVLLSGVIAFMVNLS
IYWIIGNTSPVTYNMFGHFKFCITLFGGYVLFKDPLSINQALGILCTLFGILAYTHFKLS
EQEGSRSKLAQRP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-27

Transmembrane domains:

Amino acids 46-60;75-90;153-167;192-208;221-237

N-glycosylation sites:

Amino acids 43-47;92-96;97-101;238-242

N-myristoylation sites:

Amino acids 17-23;57-63;140-146;155-161;162-168;283-289

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FIGURE 555

GTTAGGCAGAGCCAAGGTGGTTGCAGACCTGGAATCAGAACAGCTTTTAGACCAACCTGAAAG
CAGGAATGTAAGCACTGTTACAGAGATTTTCGTCTTTGGCTTATTGTGCCTGCAGAGTCTAG
TGCTTCTTTGCCAGCTGTGCTGACTCAGCACTCC**ATG**CCTGTTTTCTGGAACCAAGTCCCTGGA
GCTGGGCCATGTTTTGATTGACAGTGTGGAGCTAGCCCAGCAAGTACTCTACATGCAACCCCC
CACCCAGGCACTACCTCTGCTCCTCCTCCATGGCCTCCTGCTACACCGGCAGCTCTATGGAAC
AAGGCTGCAGGCACACAGGGGGCGCTGGAGTCAAGTGAAGTCTAACCAGGTTCTTCAGACCCA
AGACCAGCTGTGGGCAAGTCTTAGCAATCCCCGTGCTGCCATGCAAGAGCTGGCTGCTTCAGT
TTTCTACGGGGTCTCTGCGGGGACACTGAGGACAGGGAGGCCCTGATTAGCCTCACACAAGC
CTGCCTGAGCCCCAGTAGTGGGAGCTGGGTCCAGCCACACACACCTCAGTCTTTGCTGGCCAC
GCTCATGCCCCCTCCAGCTAAGGGAGCTGGATGCAATGGCAGAGTGCAAGGCCCAAGATGCACC
TACTGCCCTCACACCT**TGA**ACCCCGGCTCTGCGGACTGAGTGAGGGCCCCAAGCCTGGCTGT
TGCGACGCCAGAGTCGCGCTCTCTTGAGTGCCTGTCAGCGGAGTTCACCCGTGTGGGTTCTCTG
AGTCTCGAAGAGGGCGCCAGCTTGCGGAAAGGCGACTGCGGCAACGCCTAGTGCAAGTCAACCG
GAGGCTGGAGTCACTGCAGGATCTGCTGACCCACGTGATTCGCCAAGACGAGTCCGACGCCCC
GTGGTCAGTGCTGGGGCCAAATGCACGGCGGCCTCTGGAGGGCGTCTTAGAGACCGAGGCTCT
AGAAGTGAAGCCAGTTGGTGGGCACGCTACAACGCGACCTTGATTGCCTGTTGCAGCAGCTGAA
GGGCGACCCCCGTGCCCCCTCCCGCCGCTGTGCTGCGGTGGCCACGCTCTCTGGACTGGCCG
CCTACCCCTTGCCCTGGCGACCTCATGCGCCGGCCGCTCCGCAGCCGCCCTGGCACTGGCTGCG
ACAGTTGTCGCGCCGTGGGCAACTGTTGGTTCGTTACTTGGGCGTGGGCGCGGACGCGAGCAG
TGATGTACCAGAGCGCGTCTTCCACCTGTCAGCCTTTCGCCACCCGCGCCGCTGCTGCTGGC
ATTGCGTGGGGAAGCTGCCCTGGACCAGAATGTGCCAGCTCGAATTTCCCTGGTAGCCGAGG
CTCGGTCTCCAGTCAGCTCCAGTATAAACGTCTGGAGATGAACAGCAACCCTCTGCACTTCAG
GGTGGAGAATGGTCCAAATCCCACGGTTCCAGAGAGAGGGCTGCTGCTGATCGGGCTACAGGT
CCTACATGCGGAGTGGGACCCAATAGCTGGAGCCTTGCAAGACAGTCCTTCCAGCCAACCCAG
CCCTCTGCCTCCCGTCAGCATCAGCACACAGGCCCCGGGCACCAGTGACCTGCCAGCCCCAGC
CGACCTGACTGTGTACTCGTGTCTGTGTACATGGGAGGGCCCCCTTGGCACCGCTAAGCTGCA
GAGCAGGAACATCGTGATGCATCTGCCTTTACCCACCAAGCTCACCCCCAACACCTGTGTCCA
AAGGAGGGTCCATGTGTGCAGCCCACCCCTGTCTTGAGCCCGTCTACCAAATAAAGTTGTAG
TGATTCCA

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FIGURE 556

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA129594
><subunit 1 of 1, 162 aa, 1 stop
><MW: 17598, pI: 6.58, NX(S/T): 1
MPVFWNQSLELGHVLIDSVELAQQVLYMQPPTQALPLLLHGLLLHRQLYGTRLQAHRGR
WSQVTILTQVLQTQDQLWASLSNPRAAMQELAASVFYGGPLGDTEAREALISLTQACLSPS
SGSWVQPHTPQSLLATLMPLPAKGAGCNGRVQGPDAPTALT
```

Important features of the protein:**Signal peptide:**

Amino acids 1-45

N-glycosylation site:

Amino acids 6-10

N-myristoylation sites:

Amino acids 97-103;144-150

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FIGURE 557

GACCTTGAGCCCTCGAAAGCGAC**ATG**GCGGTTCTCTTAAAGCTGGGCGTTCTCTGCAGTGGCC
AAGGAGCTCGAGCTCTCCTACTCCGAAGCCGGGTGGTCAGACCCGCTTATGTGTCAGCATTTC
TCCAGGACCAGCCTACCCAAGGACGGTGTGGTACCCAGCACATTACCTGTCACCAAGCCACC
ACTCTGGTTCCAAGGCTGCATCTCTCCACTGGACCAGTGAGAGGGTTGTCAGTGTCTGCTCT
TGGGGCTGATCCCTGCTGGGTACTTGAATCCCTGCTCTGTGGTGGACTACTCTCTGGCTGCAG
CCCTCACCCCTGCACAGTCACTGGGGCCTTGGACAAGTGGTTACCGACTACGTTTCATGGGGACA
CCCTGCCGAAGGCTGCCAGGGCAGGCCTCTTGGCACTCTCAGCTTTGACCTTTGCTGGGCTTTGC
TACTTCAATTACCACGATGTCGGCATCTGCAGAGCGGTTGCCATGCTGTGGAAGCT**CTGA**CCT
GGGTGCAGCACTTTGATTGTGTGCCTCCTTGCCTCTGCTTTACCAATGCCGTTACCTCGCAG
TGAGGGGGGATGAAGGATAAGCCCATTGGTGGGCAGAATGTCTTCTAATTACATGGTTATTTT
CAGAATTTATTTGTTGAGGAAGAGGTTTGAGGAGTTAGGTTGACCATTCGTGAGTCTGTGTT
CCATACTCCACTGAGTGTGGGCAGTAGCTCACAGCCTCGCGGTGAGACTGAACATTTTCATGAG
CTCATGTTGCCTTTGACCACCATTTCTTAAGGAGAGCCAGCTGATTGCTGTCAGGATAAGAGC
ATCTCTTCAGCCAGGAGGGAGGCCTGTTCCCTCCTGAGTTAGACTTTGCATGAAGCTCGAAAG
TATTCCTTTTGGAACCTCCCATTCTTGTTCAGGTGACACCAGCTCTGTTGATGGCTCTGCTTC
TAGGGAACATTTAATCAGGAGATGCTCTCAATGACTAATTTGTCTAAGTCTTAGGAAGGAGGT
TGAGGAAAGCTGGATTTAGACAAGTTCAATTTAGGGAGTTCTCCTTGTTTGTGGATTAAAATA
TGACAGATTGCAAACAGACTACTCTTCAAATGTATCTCAATTGTGCAGAAGTGAGCTGTCCAA
AAGTATAAGACTAAGTGATAAACTGTCTTCCCACCGTGGGAGTTGTTAATGAGAAAGAAAGTG
TACTCTGAAAAACAAGGGGG

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FIGURE 558

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA129793
><subunit 1 of 1, 159 aa, 1 stop
><MW: 17014, pI: 9.38, NX(S/T): 0
MAVLLKLGVLCSGQGARALLRSRVVRPAYVSAFLQDQPTQGRCGTQHIHLSPSHHSGSK
AASLHWTSERVVSLLLLGLIPAGYLNPCSVVDYSLAAALTLHSHWGLGQVVTDYVHGDTL
PKAARAGLLALSALTFAGLCYFNYHDVGICRAVAMLWKL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-15

Transmembrane domains:

Amino acids 71-88;126-140

Glycosaminoglycan attachment site:

Amino acids 12-16

N-myristoylation sites

Amino acids 8-14;58-64;78-84;108-114;148-154

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FIGURE 559

CCCAGCCCCGCGTTTCGGCTGCTCTCGAGGAGGCCGGAGTCCCCGGAGACGATGCGCCCCGCGC
AGCCGCCTGCGCCTGCGGGAGCCGGCTGCCCTTGAGATGGAGTTGCTGCCTCTTTGGCTCTGC
CTGGGTTTTTCACTTCCTGACCGTGGGCTGGAGGAACAGAAGCGGAACAGCCACAGCAGCCTCC
CAAGGAGTCTGCAAGTTGGTGGGTGGAGCCGCTGACTGCCGAGGGCAGAGCCTCGCTTCGGTG
CCCAGCAGCCTCCCGCCCCACGCCCGGATGCTCACCCCTGGATGCCAACCCCTCTCAAGACCCTG
TGGAATCACTCCCTCCAGCCTTACCCTCTCCTGGAGAGCCTCAGCCTGCACAGCTGCCACCTG
GAGCGCATCAGCCGCGGCGCCTTCCAGGAGCAAGGTCACCTGCGCAGCCTGGTCCTGGGGGAC
AACTGCCTCTCAGAGAACTACGAAGAGACGGCAGCCGCCCTCCACGCCCTGCCGGGCCTGCGG
AGGCTGGACTTGT CAGGAAACGCCCTGACGGAGGACATGGCAGCGCTCATGCTCCAGAACCTC
TCCTCGCTGCGGTCCGTGTCCCTGGCGGGGAACACCATCATGCGGCTGGACGACTCCGTCTTC
GAGGGCCTGGAGCGTCTCCGGGAGCTGGATCTGCAGAGGAACTACATCTTCGAGATCGAGGGC
GGCGCTTTCGACGGCCTGGCTGAGCTGAGGCACCTCAACCTGGCCTTCAACAACCTCCCCTGC
ATCGTGGACTTCGGGCTCACGCGGCTGCGGGTCCTCAACGTCAGCTACAACGTCCTGGAGTGG
TTCCTCGCGACCGGGGGAGAGGCTGCCTTCGAGCTGGAGACGCTGGACCTGTCTCACAACCAG
CTGCTGTTCTTCCCGCTGCTGCCCCAGTACAGCAAGTTGCGGACCCTCCTGCTGCGCGACAAC
AACATGGGCTTCTACCGGGACCTGTACAACACCTCGTCGCCGAGGGAGATGGTGGCCAGTTTC
CTCCTCGTGGACGGCAACGTGACCAACATCACCACCGTCAGCCTCTGGGAAGAATTCTCCTCC
AGCGACCTCGCAGATCTCCGCTTCCTGGACATGAGCCAGAACCAGTTCCAGTACCTGCCAGAC
GGCTTCCTGAGGAAAATGCCTTCCCTCTCCACCTGAACCTCCACCAGAATTGCCTGATGACG
CTTCACATTCGGGAGCACGAGCCCCCGGAGCGCTCACCGAGCTGGACCTGAGCCACAACCAG
CTGTGCGAGCTGCACCTGGCTCCGGGGCTGGCCAGCTGCCTGGGCAGCCTGCGCTTGTTCAAC
CTGAGCTCCAACCAGCTCCTGGGCGTCCCCCTGGCCTCTTCGCCAATGCTAGGAACATCACTAC
ACTTGACATGAGCCACAATCAGATCTCACTTTGTCCCTGCCAGCTGCCTCGGACCGGGTGGG
CCCCCTAGCTGTGTGGATTT CAGGAATATGGCATCTTTAAGGAGCCTGTCTCTGGAGGGCTG
TGGCCTGGGGGCATTGCCAGACTGCCCATTTCCAAGGGACCTCCCTGACCTACTTAGACCTCTC
AAGCAACTGGGGGGTTCTGAATGGGAGCCTCGCCCCACTCCAGGATGTTGCCCCCATGTTACA
GGTCCTGTCTCTCAGGAACATGGGCCTCCACTCCAGCTTTATGGCGTTGGACTTCTCTGGGTT
TGGGAATCTCAGGGACTTAGATCTGTGCGGGGAATTGCTTGACCACCTTCCCAAGGTTGGGGG
CAGCCTGGCCCTGGAGACCCTGGATCTCCGTAGAACTCGCTCACAGCCCTTCCCCAGAAGGC
TGTGTCTGAGCAGCTCTCGAGAGGTCTGCGGACCATCTACCTCAGTCAGAATCCATATGACTG
CTGTGGGGTGGATGGCTGGGGGGCCCTGCAGCATGGGCAGACGGTGGCCGACTGGGCCATGGT
CACCTGCAACCTCTCCTCCAAGATCATCCGCGTGACGGAGCTGCCGGAGGTGTGCCTCGGGA
CTGCAAGTGGGAGCGGCTGGACCTGGGCCTGCTCTACCTCGTGCTCATCCTCCCCAGCTGCCT
CACCTGCTGGTGGCCTGCACTGTCTCGTCTCACTTTTAAGAAGCCTCTGCTTCAGGTCAT
CAAGAGCCGCTGCCACTGGTCCCTCCGTTTACTGACCTGGCTGTGTGCCAAGACTCGAAATTCTG
GTCCGCACACAACAGGACACTTTCTCTGCCAGCTTTCAAGATGTGATGCAGAGGCCAAGTCTG
ACGAATTGAAGTTTCAATTAAAATTTAATATGTTTCCATTCCCTCATCGCCACCCCAACCCCG
CCCCACCACCGCCCAAGTTCTTTTCCATCATTATAATTATCCTTATTATCTTGGTAAAT
ATTTATTAAGTGACTTTTTCAGAAATAAAAGGCAACGTGTCTCATAAATATTTTTTAAAAAA
AAAAAAAAAAAAAA

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FIGURE 560

><subunit 1 of 1, 692 aa, 1 stop
><MW: 76366, pI: 6.07, NX(S/T): 11
MELLPLWLCCLGFHFLTIVGWRNRSQTATAASQGVCKLVGGAADCRGQSLASVPSSLPPHAR
MLTLDANPLKTLWNHSLQPYPLLESLSLHSCHLERISRGAFQEQGHLRSLVLGDNCLSEN
YEETAALHALPGLRRLDLSGNALTEDMAALMLQNLSSLRSVSLAGNTIMRLDDSVFEGL
ERLRELDLQARNYIFEIEGGAFDGLAELRHLNLAFFNNLPCIVDFGLTRLRLVNLVSYNVLEW
FLATGGEAAFELETLDLSHNQLLFFPLLPQYSKLRITLLLRDNNMGFYRDLYNTSSPREMV
AQFLLVDGNVTNITTVSLWEEFSSSDLAFLDRFLDMSQNFQYLPDGFRLKMPSLSHLNLH
QNCLMTLHIREHEPPGALTELDLSHNQLSELHLAPGLASCLGSLRLFNLSNQLLGVPFG
LFANARNITTLDMSHNQISLCPLPAASDRVGPSPCVDFRNMASLRSLSLEGCGLGALPDC
PFQGTSLTYLDLSSNWGVNLGSLAPLQDVAPMLQVLSLRNMGLHSSFMALDFSGFGNLRD
LDLSGNCLTTFPRFGGSLALETDLRRNSLTALPQKAVSEQLSRGLRTIYLSQNPYDCCG
VDGWGALQHGQTVADWAMVTCNLSSKIIRVTELPGGVPRDCKWERLDLGLLYLVLIPLSC
LTLVACTVIVLTFKKPLLQVIKSRCHWSSVY

Important features of the protein:**Signal peptide:**

Amino acids 1-18

Transmembrane domain:

Amino acids 651-672

N-glycosylation sites:Amino acids 21-25;74-78;155-159;232-236;292-296;309-313;
312-316;408-414;427-431;500-504;622-626**Glycosaminoglycan attachment site:**

Amino acids 533-537

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 566-570

N-myristoylation sites:Amino acids 24-30;39-45;45-51;141-147;199-205;245-251;
308-314;396-402;416-422;420-426;471-477;
484-490;497-503;522-528;545-551;555-561;610-616**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 657-668

Leucine zipper patterns:

Amino acids 48-70;492-514

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FIGURE 561

TGGCCTACTGGAAAAAAAAAAAAAAAAAAAAAAAAAGTCACCCGGGCCCCGCGGTGGCCACAACAT
GGCTGCGGCGCCGGGGCTGCTCTTCTGGCTGTTTCGTGCTGGGGGCGCTCTGGTGGGTCCCGGG
CCAGTCGGATCTCAGCCACGGACGGCGTTTCTCGGACCTCAAAGTGTGCGGGGACGAAGAGTG
CAGCATGTTAATGTACCGTGGGAAAGCTCTTGAAGACTTCACGGGCCCTGATTGTCGTTTTGT
GAATTTTAAAAAAGGTGACGATGTATATGTCTACTACAACTGGCAGGGGGATCCCTTGAAC
TTGGGCTGGAAGTGTTGAACACAGTTTTGGATATTTTCCAAAAGATTTGATCAAGGTA
TAAATACACGGAAGAAGAGCTACATATTCAGCAGATGAGACAGACTTTGTCTGCTTTGAAG
AGGAAGAGATGATTTTAAATAGTTATAATGTAGAAGAGCTTTTAGGATCTTTGGA
CTCTGTACCTGAAGAGTCGAAGAAAGCTGAAGAAGTTTCTCAGCACAGAGAGAAATCTCCTGA
GGAGTCTCGGGGGCGTGAACCTGACCCTGTGCCTGAGCCCGAGGCATTCAGAGCTGATT
GGATGGAGAAGGTGCTTTCTCAGAGAGCACCGAGGGGCTGCAGGGACAGCCCTCAGCTCAGGA
GAGCCACCCTCACACCAGCGGTCCTGCGGCTAACGCTCAGGGAGTGCAGTCTTCGTTGGACAC
TTTTGAAGAAATTCTGCACGATAAATTGAAAGTGCCGGAAGCGAAAGCAGAACTGGCAATAG
TTCTCCTGCCTCGGTGGAGCGGGAGAAGACAGATGCTTACAAAGTCCTGAAAACAGAAATGAG
TCAGAGAGGAAGTGGACAGTGCCTTATTCATTACAGCAAAGGATTTTCGTTGGCATCAAATCT
AAGTTTGTTTTACAAAGATTGTTTTTTAGTACTAAGCTGCCTTGGCAGTTTGCATTTTTGAGCC
AAACAAAATATATTATTTTCCCTTCTAAGTAAAAAAAAAAAAAAAAAAAAA

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FIGURE 562

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131639
><subunit 1 of 1, 303 aa, 1 stop
><MW: 33900, pI: 4.81, NX(S/T): 2
MAAAPGLLEWLFVLGALWWVPGQSDLSHGRRFSDLKVCGDDECSMLMYRGKALEDFTGPD
CRFVNFKKGDDVYVYYKLAGGSLELWAGSVEHSFGYFPKDLIKVLHKYTEEELHIPADET
DFVCFEGGRDDFNSYNVEELLGSLELEDSVPEESKKAEEVSQHREKSPPEESRGRELDVPV
EPEAFRAEDGEDGAFSESTEGLGQPSAQESHPTSGPAANAQGVQSSLDTFEEILHDK
LKVPGESERTGNSSPASVEREKTDAYKVLKTEMSQRGSGQCVIHYSKGFRWHQNLSLFYK
DCF
```

Important features of the protein:**Signal peptide:**

Amino acids 1-22

N-glycosylation site:

Amino acids 294-298

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 30-34

Tyrosine kinase phosphorylation site:

Amino acids 67-76

N-myristoylation sites:

Amino acids 205-211;225-231;277-283

Amidation site:

Amino acids 28-32

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FIGURE 563

GCCAGCCGTGGGATTAGGCTTCGCCGGCTACGATTGCGGCCCCCATCTTCTGACTTTTCCTCG
TGTGACCCATCTTTTCAAATTCCTTACCTGAGGAAGGAGCCCGATTACAAGGATATTTACCT
GCTCCTACCCCTGATCTAGGGACGAGGATGGGAAGACCGCCTGTGGCCATGAGCCCTCCCCGGT
GCTCCTGGGGCTAAGGCTGGGGCTGCAGCCATGGGGCTGGGTCAGCCCCAGGCCTGGTTGCTG
GGTCTGCCACAGCTGTGGTCTATGGCTCCCTGGCTCTCTTCACCACCATCCTGCACAATGTC
TTCCTGCTCTACTATGTGGACACCTTTGTCTCAGTGTACAAGATCAACAAAATGGCCTTCTGG
GTCGGAGAGACAGTGTTTCTCCTCTGGAACAGCCTCAATGACCCTCTCTTCGGTTGGCTCAGT
GACCGGCAGTTCCTCAGCTCCCAGCCCCGCCTGTGTGGAGAGGAGCTGCTTGTGGGCAGTGAG
GAGGCGGACAGCATCACCTTGGGCCGGTATCTCCGGCAGCTGGCACGCCATCGGAACTTCCTG
TGGTTCGTGAGCATGGACCTGGTGCAGGTGCAGTGGCTCACGCCTGTAATCCCAGCACTTCGG
GACGCCAAGGTGGAAAGACCGCTTGAGCCCAGGAGTTCGAGGCTGCAATTGAGTTATGATTGCA
CCACTGCACTCCAGCCTGGGCGGCAGAGAAAGGCTCCATCTCTAAAAAAGAAGAGCTAAGTG
CTGTACCTAAAACATGCAGTATATAAACTGGCTGAACTTAGAAATAAACTGTTTTCATGTTAT
GAAAA

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FIGURE 564

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131649
><subunit 1 of 1, 153 aa, 1 stop
><MW: 17603, pI: 7.42, NX(S/T): 0
MGLGQPQAWLLGLPTAVVYGSLALFTTILHNVFLYYVDTFVSVYKINKMAFWVGETVFL
LWNSLNDPLFGWLSDRQFLSSQPRLCGEELLVGSEEADSITLGRYLRQLARHRNFLWFVS
MDLVQVQWLTPVIPALRDAKVERPLEPRSSRLQ
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

N-myristoylation sites:

Amino acids 4-10;12-18;93-99

Leucine zipper pattern:

Amino acids 102-124

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FIGURE 565

CGGCACGAGTAAAATGGAGATAATATCACCATGCACTCAGCCCTAGCCACTGCATTGCTGTTA
CTGATACCATTACTGCTGCTACGTCGTTTTTTTGGATGGCTCAGCCCTTAGGGAAGGGGGATCA
AGGGAGAAGCCCGGACCTTCCCGCAGGAGGTGGGCTGGGCACAGCCCTGAACCATGGAGGTCA
CCCACCCTGAGGTCGGGACCTGGGTTCCCTTCCCTATCCACTGGGGGTCCCAGCCTTTGTCTTC
ATCTCTCCAGGTCCCAGCCCTTCACAGTGGGCACTTCCCTGCCTGTGACGGAGGCCCCAGCCA
TCTCC

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FIGURE 566

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131652
><subunit 1 of 1, 89 aa, 1 stop
><MW: 9688, pI: 11.49, NX(S/T): 0
MHSALATALLLLLIPLLLLRFFDGSALREGGSREKPGPSRRRWAGHSPEPWRSP TLRSGP
GFPSYPLGVPAFVFISPGSPSQWALPCL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-18

Glycosaminoglycan attachment site:

Amino acids 58-62

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FIGURE 567

AGTCTAGCAGGAAAGGAGAGGGAGCTTTCCCCGAAGACCCTCCTGGACCAGCCCCAGGCTCCT
GTGCTGGTTGCACGCCAGGGCCTGTACTGACCACCTCCACGTGCCACTGGGGCTGTAAGGAGGA
ATGGCGGCCGTGGGCAGCCTGCTTGGCCTGGCAGCCTCTTCCTGGCTAGGGGGCCAGAACGCC
TCTGACCACAGCCTGTGGCTCCTGAGGAAGCCCCGAGGCTCATCCTGCCCCGGCACGGGTAC
CAGCTCTGCCGGCTGAGGCAGAGCACCGTGAAGGCCACCGGACCTGCACTCCGCCGCTGCAC
ACATCCTCCTGGCGAGCTGACAGCAGCAGGGCCTCACTCACTCGTGTGCACCGCCAGGCTTAT
GCACGACTCTACCCCGTGCTGCTGGTGAAGCAGGATGGCTCCACCATCCACATCCGCTACAGG
GAGCCACGGCGCATGCTGGCGATGCCATAGATCTGGACACCCTGTCTCCTGAGGAGCGCCGG
GCCAGGCTGCGGAAGCGTGAGGCTCAGCTCCAGTCGAGGAAGGAGTACGAGCAGGAGCTCAGT
GATGACTTGATGTGGAGCGCTACCGACAGTTCTGGACCAGGACCAAGAAG**TGA**CCGTGGCTC
CAGCCACCCCGGGACATTGCTAAGATGGGAGGGCTGTTCTTAAATCACTCGTTCTTGAAGCTGC

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FIGURE 568

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131658
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18903, pI: 11.08, NX(S/T): 1
MAAVGSLLGLAASSWLGGQNASDHSLLRKPRGSSCPGTGHQLCRLRQSTVKATGPALR
RLHTSSWRADSSRASLTRVHRQAYARLYPVLLVKQDGSTIHIRYREPRMLAMPIDLDTL
SPEERRARLRKREAQLQSRKEYEQELSDDLHVERYRQFWTRTKK
```

Important features of the protein:**Signal peptide:**

Amino acids 1-18

N-glycosylation site:

Amino acids 20-24

N-myristoylation sites:

Amino acids 5-11;9-15;17-23;18-24

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FIGURE 569

GGTGCCAAGGGTTCGGGGGGGAGCACTGAGGCTTTAGCAGCTCTCCTGTATCCTCATTTGCA
CCTCCTGTAGCAGCTGGAAAATTCAGATTACAGGTGAAATTCCTGGCTGGCAATCTTCTGTA
TATGGACACAGTGATGTGCCAGAAGGGCTTTGCATCCCTGAGACTGAAGGAAGCTCCATTTTT
GGAGCCCTCCCACACCTTGCTCTGTGTGCCTCTCATTCTGATTTGAATTCTTATTTTGCTATA
TGATGAAGCTGTAATCCTAAGTTTAAAAAGGGGAGTAGGTATTGACATCATGGTAGAAATAGG
CTGTCTTATGGAAGTGTAGTTAGGGATCACAGCCTATTGGACCAGCCCCAGCCTTAGCAGCAG
TTCTGTACACTGATTCTTCCAGATTAGTCTACGTTCCCTCGAACAGACCTATGCCATGGGTTA
CAACTACAATTTGTTGTCGATTAGAGTTAACTTACAGACTCTCAAAACCCCATTTCTTTGGGTT
TAGGCAACTTCCAGAAGTAGTCATTTATTTGAATTTTAGTCTAAGATCAACTGAATTAGGGAG
GTTTGAAAGTGTAAGCAAAATCGTACATTTCCAAACACTTTGTAAAGAAGGAATGGGTAGTG
TCAACTAAAGGAAATGGTGTGCATCCCAGCAAAAGAAAGAGACCGAAAGCAAAGTCATAAACC
ATGCCACGAGCTCAGCTGTCTGCTCCGTGTCTCTCCATACCCTTGTTGACTGTGCTCATA
TTAGCCAGAGACCTAAGTGCTCTTGGAGGATGTCCCTGGGGCCCCCTCCCCCTCCGCTGTAC
TGTCTACTTCTGATCCTCTCTTCTGTGCAGGAGAGGTCCAGGCCTTCTATGAGGACCTGAGT
GGCCGGCAGTACGTGAATGAAGTCTTCAACTTCAGCGTGGACAAGCTCTATGACCTCCTCTTC
ACCAACTCGCCCTTCCAGCGGGATTTTCATGGAGCAGCGGCGCTTCTCTGATATCATCTTCCAT
CCATGGAAAAAGGAGGAGAATGGAAACCAGAGCCGAGTGATTCTTTACACCATCACCTTACC
AACCCTCTGGCTCCCAAACTGCCACTGTCAAGGAGACACAGACCATGTACAAGGCGAGCCAG
GAGAGTGAATGTTACGTGATAGATGCCGAAGTCTCACCCACGACGTGCCCTACCACGACTAC
TTCTACACAATCAATCGCTACACGCTCACCCGTGGTGGCTCGGAACAAGAGCCGACTCAGGGTC
TCCACAGAGCTGCGCTATCGAAAACAGCCCTGGGGGTTAGTGAAAACGTTTCATCGAGAAGAAC
TTCTGGAGTGGGCTGGAGGACTACTTCCGCCATTTAGAGAGCGAGCTGGCCAAAACGGAGAGC
ACTTATTTGGCTGAGATGCACAGACAATCTCCAAAGAGAAGGCCAGCAAGACTACAACGGTG
CGGAGGAGGAAGCGTCCCCATGCCACCTGCGAGTCCCTCACCTGGAAGAGGTGATGAGCCCG
GTCACCACGCCCACAGATGAGGATGTGGGCCACAGGATCAAACATGTGGCAGGTTCACACAG
ACGCGGCATATCCCGGAGGACACCCCCAACGGTTTCCACCTGCAGAGCGTGTCCAAGCTGCTG
CTGGTTATCAGCTGTGTTCTGGTGCTGCTGGTCATCCTTAACATGATGCTCTTCTACAAACTC
TGGATGTTGGAATACACCACGCAGACCCCTCACTGCCTGGCAGGGTCTAAGGCTCCAAGAAAG
TTACCCAGTCTCAGACAGAATGGGGCCAGCTCTTAGAGTCCCAACAAAAGTACCACGATACT
GAGCTCCAAAAATGGAGGGAAATCATCAAATCCTCAGTGATGCTCCTTGACCAGATGAAGGAC
TCGCTCATCAACCTTCAGAACGGCATCAGGTCCCGCGACTACACGTCGGAAAGTGAAGAAAAG
AGGAATCGCTATCAT**TGA**CAAGGCAGGAACAGGGTGGCTGCAAGAGGCCTGTGCAATACATGT
ACATAGACCATATAAATATATATATAAATATATATATATACAGAATATAAATATATATATT
ATATACAGATTTTAAAAAGAGATAATGCCTATGTACCAGGGAGAAGGAGCGGGCCCTCCCGC
GCCCTGTGCTGGCCGGAGCAGCGTTTTCTTATGGTGGAGCAGCTGAGGAGGGCAGGAACCGCC
TCTCAGCACCGACCTCCCCTGATCTCCCTCCTCCACCCCTCTGTTCCCCACCCCTTCCCTTGC
TGGCCATCTTTGGCTTTTAGAAGGGAAATGTTGAGCCAAAGTTATGCCTGCGAAGACCTAAG
GTCTCAAAAAGAAGTCTTAAGACGGCATTGCTTAAGGTGCTTCATTCCCTAATCCCTTTTGA
TTTGTTCCTCAAAATAAAAGAGAATCTTTTCTTCCCTAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 570

><subunit 1 of 1, 425 aa, 1 stop
><MW: 49786, pI: 8.84, NX(S/T): 3
MPTSSAVLLRVLSIPLLTVLILARDLSALGGCPWGPLPLRCHCLLPDPLFCAGEVQAFYE
DLSGRQYVNEVFNFSDVKLYDLLFTNSPFQORDFMEQRRFSDIIFHPWKKEENGNSQSRVIL
YTITLTNPLAPKTATVRETQTMKASQSECEYVIDAEVLTHDVPYHDYFYTINRYTLTRV
ARNKSRLRVSTELRYRKQPWGLVKTFFIEKNFWSGLEDFRHLSESELAKTESTYLAEMHRQ
SPKEKASKTTTVRRRKRPHALRVPHLEEVMSPTTPTDEDVGHRIKHVAGSTQTRHIPE
DTPNGFHLQSVSKLLLVISCVLVLLVILNMMLFYKLWMLEYTTQTLTAWQGLRLQERLPQ
SQTEWAQLLESQOKYHDTLQKWREIIKSSVMLLDQMKDSLINLQNGIRSRDYTSESEEEK
RNRYH

Important features of the protein:**Signal peptide:**

Amino acids 1-28

Transmembrane domain:

Amino acids 312-334

N-glycosylation sites:

Amino acids 73-77;114-118;183-187

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 97-101

Tyrosine kinase phosphorylation sites:

Amino acids 144-153;188-196

N-myristoylation sites:

Amino acids 201-207;291-297

Leucine zipper pattern:

325-347

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FIGURE 571

GTAGAGAGTGAAGCAGCAAGACTGCAGAGCCTCATCAAGAAGTGTGGAGTGAAGGGAAGGCTTCAGATGGACAAT
TTGTGTGCTGGGGAAAAAATGGAATGTGCTGCAAATTCCTTGGTCAATCTGTGGTACTCCTCCAGGATGAGGAGGA
TGACCATTTTCAGATTCTGCGGGCCATTGGTAAAGGGAGTTTGGAAAGGTATGCATCGTGAGAAGCGAGACAC
TAAGAAAATGTATGCAATGAAGTACATGAACAAGCAGAAGTGCATCGAGAGGGATGAGGTTCCGAATGTTTTCCG
GGAGCTGCAGATCATGCAAGGGCTGGAGCACCCCTTCTGGTCAATCTGTGGTACTCCTCCAGGATGAGGAGGA
CATGTTTCATGGTGGTGGACCTGCTCCTGGGAGGCGACCTGCGCTACCATCTGCAGCAGAATGTGCATTTACAGA
GGGGACTGTGAAACTCTACATCTGTGAGCTGGCACTGGCCCTGGAGTATCTTCAGAGGTACCACATCATCCACAG
AGACATCAAGCCAGACAATATCCTGCTGGATGAACACGGACATGTTACATTACAGACTTCAACATAGCGACGGT
AGTGAAAGGAGCAGAAAGGGCTTCTCCATGGCTGGCACCAGCCCTACATGGCTCCAGAAGTATTCAGGTGTA
CATGGACAGAGGCCCCGGATACTCGTACCCTGTGCACTGGTGGTCCCTGGGCATCACAGCCTATGAGCTGCTGCG
GGGCTGGAGGCCGTACGAAATCCACTCGGTACGCCCCATCGATGAAATCCTTAACATGTTCAAGGTGGAGCGTGT
CCACTACTCCTCCACGTGGTGCAGGGGATGGTGGCCCTGCTGAGGAAGCTCCTGACCAAGGATCCTGAGAGCCG
CGTGTCCAGCCTTCATGACATACAGAGCGTGCCCTACTTGGCCGACATGAACTGGGACGCGGTGTTCAAGAAGGC
ACTGATGCCCCGCTTTGTGCCAATAAAGGGAGGTTGAACTGCGATCCACATTTGAGCTTGAAGAGATGATTCT
AGAATCCAAGCCACTTCACAAAAGAGAAGCGATTGGCAAAGAACAGATCCAGGGATGGCACAAGGACAGCTG
CCCCTGAATGGACACCTGCAGCACTGTTTGGAGACTGTCCGGGAGGAATTCATCATATTCAACAGAGAGAAGCT
CAGGAGGCAGCAGGGACAGGGCAGCCAGCTCTTGGACACCGACAGCCGAGGGGAGGCCAGGCCCAAAGCAAGCT
CCAGGACGGGTGCAACAACAACCTCCTCACCACACCTGCACCCGTGGCTGCAGCAGCTGAGGCCACACTTGTGTG
CTGCTCAACAGGACTGCACTCGTCTCTGCCCTGCCACCCAGAGCCCTCTTTGTGCCCTGATGGTCCCTGTCTC
ACCCCTGAAAACATCAGATGCAGAAAAAGCCCTGGACTTGGAGCTGGGAAGCCTGGGTTCTGGTCCCATCTCCAT
GACTGATTCACGTGTGACCTCAGACAAGTCACGCCCTCTCTGTGCCCTCCGTTTTCTGCATCTGCCAAAGGGTTA
AACACTTCTGCCCCACTTCAAATTACAAGATTATGGGGAGAACCCTAATTAGGTAGGAAACATGAAAACCTTTGA
TATTTATAAAATCATTTTACGTGCAAAATATAACCTTAATATTTGAAGTGACCCCCATTCCCCAAGCAATCAA
ACCGTCATGACTTTGCAATTTGGCACATCCTAGCTTGTAGAGGGCACTTCCGAAAAACACAGCCCTGACAGCAA
AATAAAGGTCTGATATGTTGGCCCTTCTATGGAACAACGCTGCCAAATCCTGGAGCAAAACCTGAAGTGTCTT
CATGTGCATTCTCTGGCAGGCCACAGTCCTTCTGAGCTTGTAAAGATGGTGCAGCATGCAGACCAGACTTGTCCCC
AAGGTCTCAGCGCTGCGGTCTCACTCCTCCCTCATTTAAGAAGACTATCCTTACCTTTTAGTTTCAGCAGTCCT
CACCACCACCATATCCCCAGTGCTGGGATGGCACACAGGTGTCCATTAGATGAGAGTTGGGTGCTGAGCATTG
GTTACTCCTGCAGAGTGTAAATCAGCACCCCATCCAATGGCCCGAAAGCCAGACCTGCAGCAGAACTCTCCAAC
TCTCTATCAGCTTTTCAGGGTTTCTCTCCTGGGAAGGGTGAAAATCAGCTTGTGAGATTCTTCTTACAGAGAGT
ATCCAATCGGTATTGGTGGAGCGGCTCCCTATTTATACAATAGGAAGCATGGGTGCTTAGAAAGTTTATTTTCAGG
AGGAAAATGGGTTACACAAAAAGCAAACCTACATTCTGATCTGCTCAGGGAGAAGCTTGCCTTTGAACTGGAAGA
TGTTGGGATGAGCAGGGAAGCTTAGACTTTGGAGTCAGGTTTGTGTTTCAAGATCCAGCCCTGCTGGCTACTAAC
TAACTGGGAGACCTTAGGCAAGCATGCAATCGCTCTGAATGGCAGTTTCTCATTTTAAACAGGGATAATAAA
ACTAATATTGCAGGGGAGTTACAGGGTTAAATAAGATCCTGTGTGTAACCCCAAGCATTGGATGACTCATAGAAT
GGCCTTTTTTGTGAGCATAATCGTCATCATTATTTAGATACTTTCTCCTTCACTCACCAGCAGGTGAGTTTTT
TGTGCAAAACAAACCTGTTTAGGATTCTTCCAAATGTTCTTCTGGGGTCTTTGATATTTGTTTGTACATCCTGC
TGAAGTTCGACTGTGTTTTTATTTTTTATCCAACCTCCATTTTTTCACTTTTACATGATTACTCAATCCTTGGG
GCTGTCCATGTCTCTTAGATTTCTTAAAGACATTTTAAATGTATGGTTAGGTTTTATATTTTTATTTTTTAA
AAAAGAAATAGTCAGTGTTTTCTCCTTTCAACCGAGACTATTTCTGATTGTGTGCTCCTCGTCAGTTGACTTGT
TTTGCACACTTTTCTTACTTCATGTCCCCATCAACAACCGTCTGCTCCCCACCTCCCCAGGAAATAAGGGGC
CTGCTCCTCTCCCTACTGTGACCCTGGAGGCTCTTAAGATGATGATGGTTTTTTTTTATTGGGCTGAGTTCACGAA
TTAGGGGCAGGAGCTGGAAGTCGCCCTAGGAACACCAGATTTCTGGTTCTGTTCAAGTTGGCATTCTTGTGTTG
GAATAAACTATTTCTTGG

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FIGURE 572

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA136110
<subunit 1 of 1, 364 aa, 1 stop
<MW: 42195, pI: 7.40, NX(S/T): 1
MKYMNKQKCIERDEVNRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRY
HLQQNVHFTEGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNIATV
VKGAERASSMAGTKPYMAPEVFQVYMDRGP GYSYPVDWWSLGITAYELLRGWRPYEIHVS
TPIDEILNMFKVERVHYSSTWCKGMVALLRKLLTKDPESRVSSLHDIQSVPYLADMNWDA
VFKKALMPGFVPNKGR LNC DPTFELEEMILES KPLHKKKKRLAKNRSRDGTDSCPLNGH
LQHCLETVREEFIIIFNREKLRRQQGQGSQLLDTSRGGGQAQSKLQDGCNNNLLTHTCTR
GCSS
```

Important features of the protein:**N-glycosylation site:**

Amino acids 285-289

N-myristoylation sites:

Amino acids 123-129;290-296;337-343;339-345;348-354

Serine/Threonine protein kinases active-site signature:

Amino acids 92-105

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FIGURE 573

CTCCAGTTCGCCGACTGTAACATGTTTCATCCAGTTCAGTATGTTTTGTATGCAAGTTGGAAATAAATAAACGTC
CTGAACTGGATGAAACATGTTACAGTCGGCCGAAACATGAGAGGCTGTGTGAGAAGCTGCAGCCGCCGCCGAGAGG
AGACCTCAGCATCATCTAGAGCCCAGCGCTGGCCCTGCCTCCGCCTGCGCCGCCGCCGCCGCTCGCCGTTTTCTGTT
CCTGCTACTGTCCCACCTAAACAACCTCCCGTTACACGGACAAGTGAACATCTGTGGCTGTCTCTCTCTTTCTTC
CTCCTCTTCCAACCTCTTCTCTCTCTCCACTTCCAGCCGACGAGAAAGCCCCAACCCAACTGACGCTGGCA
CAACTGCAAACGGTGTCTATCCGCACAACCTTTATCTCGCTCCTCGGGCTCCCTTAAGGCATTGGACCCATCGCCGC
GTCTTTTATTTTTGCAAAGTTGCATCGCTGTACATATTTTTGTCCCCGCCACCTCCCTCTGTCTCTGGAGTGCCC
TACAGCCCCGCAAACCTCTCTGGAGCTGCGCCCTAGTGCCCTGCTGGGCAGTGGCGTTCCCCCCCATCTCTCC
GCGCCAGCCCCCTGCTGCTCTGGGCAGACGATGCTGAAGATGCTCTCCTTTAAGCTGCTGCTGCTGGCCGTGGCT
CTGGGCTTCTTTGAAGGAGATGCTAAGTTTGGGGAAGAAACGAAGGGAGCGGAGCAAGGAGGAGAAGGTGCCTG
AATGGGAACCCCCGAAGCGCTGAAAAGGAGAGACAGGAGGATGATGTCCAGCTGGAGCTGCTGAGTGGGGGA
GAGATGCTGTGCGGTGGCTTCTACCCCTCGGCTGTCCTGCTGCCTGCGGAGTGACAGCCCGGGGCTAGGGCGCCTG
GAGAATAAGATATTTCTGTTACCAACAACACAGAATGTGGGAAGTTACTGGAGGAAATCAAATGTGCACTTTGC
TCTCCACATTCTCAAAGCCTGTTCCACTCACCTGAGAGAGAAGTCTTGAAAGAGACCTAGTACTTCTCTGCTC
TGCAAAGACTATTGCAAAGAATTCTTTTACACTTGCCGAGGCCATATTCCAGGTTTCTTCAAACAACCTGCGGAT
GAGTTTTGCTTTTACTATGCAAGAAAAGATGGTGGGTGTGCTTTCCAGATTTTCCAAGAAAACAGTCAGAGGA
CCAGCATCTAACTACTTGGACCAGATGGAAGAATATGACAAAGTGAAGAGATCAGCAGAAAGCACAAACACAAC
TGCTTCTGTATTTCAGGAGGTTGTGAGTGGGCTGCGGCAGCCCGTTGGTGCCCTGCATAGTGGGGATGGCTCGCAA
CGTCTCTTCACTTCTGGAAGAAAGAGGTTATGTGAAGATACTTACCCCTGAAGGAGAAATTTTCAAGGAGCCTTAT
TTGGACATTACAAACTTGTCAAAGTGAATAAAGGGAGGAGATGAAAGAGGACTGCTAAGCCTCGCATTCAT
CCCAATTACAAGAAAAATGGAAAGTTGTATGTGCTCTATACCACCAACCAAGAACGGTGGGCTATCGGGCCTCAT
GACCACATTCTTAGGGTTGTGGAATACACAGTATCCAGAAAAATCCACACCAAGTTGATTTGAGAACAGCCAGA
GTCTTTCTTGAAGTTGCAGAACTCCACAGAAAGCATCTGGGAGGACAACTGCTCTTTGGCCCTGACGGCTTTTG
TACATCTGTTAGTTGATGGGATGATTACACTGGATGATATGGAAGAAATGGATGGGTAAAGTGATTTTCACAGGC
TCAGTGCTACGGCTGGATGTGGACACAGACATGTGCAACGTGCCTTATTCATACCAAGGAGCAACCCACACTTC
AACAGCACCAACCAGCCCCCGAAGTGTGCTCATGGGCTCCACGATCCAGGCAGATGTGCTGTGGATAGACAT
CCCACTGATATAAACATCAATTTAACGATACTGTGTTTCACTCCAAATGGAAAAACAGATCATCAGCCAGAATT
CTACAGATAATAAAGGGGAAAGATTATGAAAGTGAGCCATCACTTTTAGAATTCAGCCATTGATTAATGGTCTCT
TTGGTTGGTGGATTGTATACCGGGGCTGCCAGTCAGAAAGATTGTATGGAAGCTACGTGTTTGGAGATCGTAAT
GGGAATTTCTTAACCTCTCCAGCAAAGTCTGTGACAAAGCAGTGGCAAGAAAAACCACTCTGTCTCGGCACTAGT
GGGTCTGTAGAGGCTACTTTTCCGGTCACATCTTGGGATTGGGAGAAGATGAAGTGGTGAAGTTTACATTTTA
TCAAGCAGTAAAGTATGACCCAGACTCACAATGGAAAACTCTACAAAATGTAGATCCAAAAGACCTTTAATG
CCTGAGGAATGCAGAGCCACGGTACAACCTGCACAGACACTGACTTCAGAGTGCTCCAGGCTCTGTGCAACGGC
TACTGCACCCCCACGGGAAAGTGCTGCTGCAGTCCAGGCTGGGAGGGGGACTTCTGCAGAACTGCAAAATGTGAG
CCAGCATGTGCTCATGGAGGTGTCTGTGTTAGACCGAACAAGTGCCTCTGTAAAAAAGGATATCTTGGTCTCTAA
TGTGAACAAGTGGACAGAAACATCCGCAGAGTGACAGGGCAGGTATTCTTGATCAGATCATTGACATGACATCT
TACTTGCTGGATCTAACAAGTTACATTGTATAGTTTCTGGGACTGTTTGAATATTCTATTCCAATGGGCATTTAT
TTTTTATCTGTCTATTAAAAAAGACTGTTATCTCTGCTACACACTCCTGTGATTTTATTCTCTTTTATTAA
TTTTAAAAATAATTTCCAGAAATGTGCAGATCCTCTGTGTGTATGTGACATGTTTGTTCACATATGCACATACAC
ATACTCATAACCCCTATATGCGTTGTTGCATAACAGATGATTTTTTAAATATATACTTCCTTATGCAAAGTAAT
TTACACAGAAATTCATTGTAAATTGATAATGGATTTTTTATGTTACTAGAAGAGATTATTTGACTTCCAGGAA
TTTTCTGTCTGTAATCACTAAAGTCACTTTAATAGAGTTTGAACAGTACTGTGCAATCCGATGGATCTAATT
AAAAAAAAGGCAATATTTTTATATTAAGTACTATAGGAGAGAATGTTTCAGAACTCCCTGATGAATTTCTA
AGTGAGCAACTTGATATAAAATTTGTAATCTTCATTTTTGTGCTGATGATCCAGTTACAGAATGCTACACACTTACC
TTTTTATTGGCTGAGAAATCTGGTTATTTTCTTAATCTCAAGATTGTTTTCAAGTGTTTTATAATTAAATCAT
AATAGCATATTTTAAATCAAAA

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FIGURE 574

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA139592
><subunit 1 of 1, 882 aa, 1 stop
><MW: 98428, pI: 8.89, NX(S/T): 5
MKHVTVGRNMRGCVRSCSRRRQRRPQHHLEPSAGPASACAAA VAVSVPATVPPKQLPLHG
QVNICGCPLLFFLLFQLLLLLPLPSRSRKPPTQLTLAQLQTVSSAQLYLAPRAPLRHWH
RRVFYFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCALVPLLGSVPPHPPAPSPCCSG
QTMLKMLSFKLLLLLAVALGFFEGDAKFGERNEGSGARRRRCLNGNPPKRLKRRDRMMSQ
LELLSGGEMLCGGFYPRLSCLLSDSPGLGRLENKIFSVTNNTECGKLLLEEIKCALCSPH
SQSLFHSPEREVLERDLVPLLLCKDYCKEFFYTCRGHIPGFLQTTADEFCFYARKDGGL
CFPDFPRKQVRGPASNYLDQMEEDYKVEEISRKHKHNCFIQEVVSGLRQPVGALHSGDG
SQRLFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLLSLAFHPNYKKNGK
LYVSYTTNQRWAIGPHDHILRVVEYTVSRKNPHQVDLRTARVFLEVAELHRKHLGGQLL
FGPDGFLYIILGDGMITLDDMEEMDGLSDFTGSVLRDLVDVDMCNVPYSIPRSNPHFNST
NQPPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRSSARILQIIKGKDYSEEP
SLLEFKPFSNGPLVGGFVYRGCQSERLYGSYVFGDRNGNFLTQQSPVTKQWQEKPLCLG
TSGSCRGYFSGHILGFGEDDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEECRATV
QPAQTLTSECSRLCRNGYCTPTGKCCSPGWEGDFCRTAKCEPACRHGGVCVRPNKCLCK
KGYLGPPQCEQVDRNIRRVTRAGILDQIIDMTSYLLDLTSYIV
```

Important features of the protein:**Transmembrane domains:**

Amino acids 63-80;186-201

N-glycosylation sites:

Amino acids 152-156;281-285;598-602;629-633;641-645

Glycosaminoglycan attachment site:

Amino acids 417-421

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 856-860

N-myristoylation sites:

Amino acids 12-18;413-419;457-463;698-695;720-726;723-729

EGF-like domain cysteine pattern signatures:

Amino acids 805-817;837-849

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FIGURE 575

CGGCTCGAGAGCGGGGCAAACCTGCTTGGCACCTCTTCAATAGGTGACATTCA**ATG**ATAGATCT
CTGGCTTCCTGCTCTGTTTGTTCTGGTTGCCCTGGAAAGCCTGCTGCTCAGCCCATGCCCCGG
GACTTCCTCCACCCTCACCAGGACATTCTTTCCATCTCTTGCTCCTGTGTGCAAGTCCCTTT
CTCCTGGATTCCATGTCTTGAATGTTTCTTAATTTACTTCCTCATTTTGGCAGAGGATGTCTT
CCAGTTGTTTTCTGGGAATGCTAATATGCAAGTGAACCAG**TGA**CCTGCAGTTCTGCCCACACA
GGGTTAATAACCAATCAGATTCTCTCTTTTCAAGATGGTTAACATAACAGACACCAAGAAAGG
GAAGAGGAGCCGACAGCAGAGGGGGAAGCTGAAAAGACGCACAAAGAATGGCCATAAAAGATA
TGAGCAACCCAGCTTTCCAGACAGTCACTTTTCCCAGTGGTCATACCTGGTCTGGAAGATTC
CCCATCATCTCGAATAAAGCTGTTGTTGCTTTTAACTCCATGGAGAGACCGAATGGAGTGAGC
CCAGCAGGGCATGCTGGGCAAGAGAGGTCCCCGAGTCCCAAATAAGAATTTCAACTAGTATA
AAACGAGGCAGCGAACCCACACGTGGAAGTCTGATACCGCTTGCAAGAGGGAATTGAATAGAT
GTCTCCCTATTGGTAAGGATGTGGTTTTTATTGACTTGAAATAACAAAGCCCGCAAGCAACAAC
TGATCATCCGCGGGATGCTGCCACAAGGAATAATTGAGCACTCATTCAGACACAGGGGAAACC
ACTGCCTCTTTCAGTCTTTCTCCCAGATTCCAACAGTCAGTGTTACAGCATTTTCACCTTGTTT
ACCTCCCTGAGAAGACGTTGCAGCTCACTACCCAGTGGGCACTGGGAGCCTCTGCTCAGGT
GGGAGACAGATGCCCCCACATGCACATCTGGTGTATTATGAAGCAGATACTGGGGCTTCATAA
ACACAGAAGGGGCAGGGAAGTAGCCCCAGGGCATAGTGTGGGGCCTCCTGACTAAAAGTAGCTT
GCAAACCCCTGCCTATAACAGCCACTTCCTGGCAGTCATTGTGCCACTTAGGAGCCCTCCTCA
CCGCTCTTCCCTTTAGTTCCTTCACTCTGTATAGACCCTGCCAGAGCAGCTCAGGGTGGAGCAG
CTGCAGCCATGGGACCTGCTCCAGGCAAGGCCCTATGCTACACAGTCCCTGGGGGTGAGGATT
CCAGAGGAGTCAATTCCCTACCCGCCCTTCCAGGGGATGGCCGAGATGAGCGTTCCACAGGG
AAAGTGAAAGTTGCAAGGCTGTTGCGGAAACACCAGGGGTTCATTTAGGTCTTGCTGCTCAT
CTCACAGAAAGCCAGTCACTGAGACAAGTATTGTGAGGAAGAAGGCTTTATCCAGGTGCTAC
AGACAGGGTGAACAAGAGATCAGTCTCAAATCCATCATCAACTGACTAAAATTAGGGGTT
TATATAGCAGGGAAGAAATGTAACATACATGTGGGAAAACAGGGATTAACGAGGGGCAAGGAAG
AGGAGTTGGCCAACAGGCAGCAGGTGGTCACCTGGGGAATCATGATGGGTGAGGGGTCTGGCT
TCTCACTTTCCAGATGTGGGGATCTGGTAAATTTCACTTTCTTGATACCGTCTGGGAGGATTG
CTGGCTGGTTTCTGAGAAAGGAATTCAGATGACATAAATGTAAATTTCTCCTTGGGGTTCAA
GACTGAGAGGGTCAATTTCTAGGTTTATTCAAGAAAAACCATAAACATCAGTTCTATGGGACA
ATTGGGCCCATTTCAGGCTCTGAGGATAAGGGTTAATGAGGGGACAGAGTCGCTGGAGAAG
TTCAGTGGGGCCTACAAGAACTAGAGAGGCTTCTGGCAAAGCTCTATGCTGTCTATCCTCT
CTTCTCTCCTTGACAGGAAGATTCCAGTATAATAGACCCGAGGTGAAAAGGCTTTTGTTCAATA
AGTAGAAAACCTGAAGGGGGGTGGGAGGCACATGGATTTGAACCAGAGACCGCTTGGCCTGCAG
GCAAATGCTGTACCTTCAGTTGCACCCCTCACTTGTTACAGCTGTTTCTGATAAGCACTTGTTG
CAGCCCCATCAGCACCTCGATTTCTTCTTGGTGAGTCCATGGGAACAGCCCCACTGCAAACAA
CCCATTCTGCTCTCTCTTTCTCTAAACCTCAACCTCCTCCTACCTGGCAGTCCACAGGCC
TACAGCTTCTCCTCAGTGGGAAAGACATCAGCTTGGAACCACTTGGAAGCCAACGTTATC
CTAGAAAAGCTTTTTTAAATGACCCAGCAGGACAAGTCTCCGGATGGCCTTGGCCAACCCGGTG
CTTCCCTCTTTCTTGGTTGTAGTTCTCAGAATAACTAGAGAATGTACTGGGAGTGTTGTCTT
GAGATAAGGAGGAACTGTCCTAAACCTGGACTCTGTTCCCATCACACCTAGAACAGGATGTCC
TGCAACGCTTTAGCCCAATGATCCAAGTTGCCCTTGGGGTATAAACTTGACAGCAGAGGGCG
TTCAGGGTCCCTCAGCTGCAGTGTGAAGTGGGACACACAGGTGAGACTCCATCTGCCCTGGGC
AGGTTCTGAGCCTTGGGGGACCAGTTACCCCTACATCCAGGCTTCTGTTGTCCCTTGCTG
CCTGTAAGGAATAAAGTTGCTTTGCTTA

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FIGURE 576

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA139608
><subunit 1 of 1, 80 aa, 1 stop
><MW: 8927, pI: 3.77, NX(S/T): 0
MIDLWLPALFVLVALESLLLSPCPGTSSTLTRTFFPSLVSCVQVPFSWIPCLECFLIYFL
ILAEDVLQLFSGNANMQVNQ
```

Important features of the protein:**Signal peptide:**

Amino acids 1-29

Transmembrane domain:

Amino acids 47-62

N-myristoylation sites:

Amino acids 25-31

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FIGURE 577

ATCGGTTAGCGCCTTGCCATGATTAATCCAGAGCTGCGGGATGGCAGAGCTGATGGCTTCATA
CATCGGATAGTTCCCAAGTTGATACAAACTGGAAGATTGGCCTTATGTGCTTCCTGAGTATT
ATTATTACTACAGTTTGCATTATTATGATAGCCACATGGTCCAAGCATGCTAAACCTGTGGCA
TGTTCAGGGGACTGGCTTGGAGTGAGAGATAAGTGTTTCTATTTTCTGATGATACCAGAAAT
TGGACAGCCAGTAAAATATTTTGTAGTTTGCAGAAAGCAGAACTTGCTCAGATTGATACACAA
GAAGACATGGAATTTTGAAGAGGTACGCAGGAAGTATGCACTGGATTGGACTAAGCAGG
AAACAAGGAGATTCTTGGAATGGACAAATGGCACCACATTCAATGGTTGGCCATCAAACCTCC
AAATGGTCTTGCAACTGGAGCCTCCGACAATGGCTTCTTCTGCTGGGACCCCTTAGATAGGCC
TCTGAGGGAGCTCTGACTGCCGTTTCCCCAAAACAATGTCCCCTGTCAGCAGGAAGCAGTTAA
ATCAGTCTTCATCCTTATCCTTAATATAACGGCAGTTAGATGTACTTCTTTAGAGGGAGTAAA
TTTATCAATTCAGAGCAATTCATCCTCCTCTTTCCATCTTTGATTACAGTTAATAGGCTATA
AATTTTGATAATGTAGAATAAACTACAGAAAACCTTCTTG

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FIGURE 578

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA143292
><subunit 1 of 1, 160 aa, 1 stop
><MW: 18576, pI: 9.29, NX(S/T): 3
MINPELRDGRADGFIHRIVPKLIQNWKIGLMCFLSIIITTVCIIIMIATWSKHAKPVACSG
DWLGVRDKCFYFSDTRNWTASKIFCSLQKAELAQIDTQEDMEFLKRYAGTDMHWIGLSR
KQGDSWKWTNGTTFNGWPSNSKWSCNWSLRQWLLLLGPLR
```

Important features of the protein:**Signal peptide:**

Amino acids 1-42

N-glycosylation sites:

Amino acids 78-82;130-134;146-150

N-myristoylation site:

Amino acids 131-137

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FIGURE 579

TGAAGGCCTGTGAGTGAGGAATGCCTCTCACCAGCTGTGCCTGAGCTGCAGCACTCCAGCCAC
TGCTGTCTCCTTAGCTGCTCACAT**ATGG**ATACTTTCACAGTTCAGGATTCCTACTGCAATGAGC
TGGTGGAGGAATAATTTCTGGATCATCTTAGCTGTGGCCATCATTGTTGTCTCTGTGGGCCTG
GGCCTCATCCTGTACTGTGTCTGTAAGTGGCAGCTTAGACGAGGCAAGAAATGGGAAATTGCC
AAGCCCCTGAAACACAAGCAAGTAGATGAAGAAAAGATGTATGAGAATGTTCTTAATGAGTCG
CCAGTTCAATTACCGCCTCTGCCACCGAGGAATTGGCCTTCTCTAGAAGACTCTTCCCCACAG
GAAGCCCCAAGTCAGCCGCCCCGCTACATACTCACTGGTAAATAAAGTTAAAAATAAGAAGACT
GTTTCCATCCCAAGCTACATTGAGCCTGAAGATGACTATGACGATGTTGAAATCCCTGCAAAT
ACTGAAAAAGCATCATTTT**TGAA**ACAGCCATTTCTTCTTTTTGGCAAAACTGAAGAGGGTTCAC
ACAACCTATTTTAAAACAATCAAGAATGGTTGAACTTCAGTAGGTCTCTGGGCCCTGAAAGCC
AGTGGTGATTTTATGAAGCTCTATAAGATAAAGCACTTCCCAAACCTTAGATGAAGACACCCC
TGCGATCGGATGACTGCAGCCAGAGGAGACACATGGGTGCTCGGCTCTGAGGACTTAGAGGGG
TCAGCCTTGTGCTGTTGAGGAACTTTCCATGGGAAGGACCACGGGGCTCCATGGCTCCCACC
TGTGGGAACTACTCATTTCTTGGCATTCCTTCCCCCTTCATTCCCTTTGGTTTGCATGGTTC
TGAGTGATATTAAATCTCAGCATTTGGTTGTGCAAAAAAAAAA

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FIGURE 580

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA144844
><subunit 1 of 1, 145 aa, 1 stop
><MW: 16618, pI: 5.26, NX(S/T): 1
MDTFTVQDSTAMSWWRNFWIILAVAIIVSVGLGLILYCVCKWQLRRGKKWEIAKPLKH
KQVDEEKMYENVLNESPVLPLPPRNWPSLEDSSPQEAPSQPPATYSLVNKVKNKKTVS
IPSYIEPEDDYDDVEIPANTEKASF
```

Important features of the protein:**Signal peptide:**

Amino acids 1-35

Tyrosine kinase phosphorylation site:

Amino acids 61-70

Amidation site:

Amino acids 48-52

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FIGURE 581

GGCCGCCTCCGCGGGGCTGTGGGAAGCTTGGGCTGTCCCAGGACCGTCAGTCTCCTCCTCTGA
CCCTCCCTTTCCCCTTGTGTGTAGGGCCGCGTCCCACCCCCACCTCGCCGGAGTCCGGGGCG
GCCCCGGTGTCCCCTCCGAGCCTGCTGCACTCCACGTCCCCCTACCAGGGCTCCAGCCCCAG
GGAAATCTCCGACCAGGCCCGCCAGGAGCCAGATCCAGGCTCCTGGAAGAACCATGTCCGGC
AGCTACTGGTCATGCCAGGCACACACTGCTGCCCAAGAGGAGCTGCTGTTTGAATTATCTGTG
AATGTTGGGAAGAGGAATGCCAGAGCTGCCGGCTGAAAATTACCCAACCAAGAGAAATCTGCAGG
ATGGACTTTCTGGTCCTCTTCTTGTCTACCTGGCTTCGGTGCTGATGGGTCTTGTCTTATC
TGCGTCTGCTCGAAAACCCATAGCTTGAAAGGCCTGGCCAGGGGAGGAGCACAGATATTTTCC
TGTATAATTCCAGAATGTCTTCAGAGAGCCGTGCATGGATTGCTTCATTACCTTTTCCATACG
AGAAACCACACCTTCATTGTCTGCACCTGGTCTTGCAAGGGATGGTTTATACTGAGTACACC
TGGGAAGTATTTGGCTACTGTCAGGAGCTGGAGTTGTCCTTGCAATTACCTTCTTCTGCCCTAT
CTGCTGCTAGGTGTAAACCTGTTTTTTTTTACCCTGACTTGTGGAACCAATCCTGGCATTATA
ACAAAAGCAAATGAATTATTATTTCTTCATGTTTATGAATTTGATGAAGTGATGTTTCCAAAG
AACGTGAGGTGCTCTACTTGTGATTTAAGGAAACCAGCTCGATCCAAGCACTGCAGTGTGTGT
AACTGGTGTGTGCACCGTTTTCGACCATCACTGTGTTTGGGTGAACAACATGCATCGGGGCCTGG
AACATCAGGTACTTCCTCATCTACGTCTTGACCTTGACGGCCTCGGCTGCCACCGTCGCCATT
GTGAGCACCCTTTTCTGGTCCACTTGGTGGTGATGTCAGATTATACCAGGAGACTTACATC
GATGACCTTGGACACCTCCATGTTATGGACACGGTCTTTCTTATTCAGTACCTGTTTCTGACT
TTTCCACGGATTGTCTTCATGCTGGGCTTTGTGCTGGTCTGAGCTTCCTCCTGGGTGGCTAC
CTGTTGTTTGTCTGTATCTGGCGGCCACCAACCAGACTACTAACGAGTGGTACAGAGGTGAC
TGGGCCTGGTGCCAGCGTTGTCCCCTTGTGGCCTGGCCTCCGTCAGCAGAGCCCCAAGTCCAC
CGGAACATTCACTCCCATGGGCTTCGGAGCAACCTTCAAGAGATCTTTCTACCTGCCTTTCCA
TGTCATGAGAGGAAGAAACAAGAA**TGA**CAAGTGTATGACTGCCTTTG

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FIGURE 582

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA144857
><subunit 1 of 1, 344 aa, 1 stop
><MW: 39787, pI: 7.44, NX(S/T): 2
MDFLVLFLEFYLASVLMGLVLICVCSKTHSLKGLARGGAQIFSCIPECLQRAVHGLLHLYL
FHTRNHTFIVLHLVLQGMVYTEYTWEVFGYCOELELSLHYLLLPYLLLGVNLFFFTLTCG
TNPGIITKANELLFLHVYEFDEVMF PKNVRCSTCDLRKPARSKHCSVCNWCVHRFDHHCV
WVNNCIGAWNIRYFLIYVLTLTASAATVAIVSTTFLVHLVMSDLYQETYIDDLGHLHVM
DTVFLIQYLFLETFPRIVFMLGFVVVLSFLLGGYLLFVLYLAATNQTTNEWYRGDWAWCQR
CPLVAWPPSAEPQVHRNIHSHGLRSNLQEIFLPAFPCHERKKQE
```

Important features of the protein:**Signal peptide:**

Amino acids 1-29

Transmembrane domains:

Amino acids 100-116;201-217;256-275

N-glycosylation sites:

Amino acids 65-69;284-290

N-myristoylation sites:

Amino acids 32-38;77-83;120-126;322-328

Cell attachment sequence:

Amino acids 292-298

DHHC zinc finger domain:

Amino acids 140-204

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FIGURE 583

CCGCGGAAC TGGCAGGCGTTTCAGAGCGTCAGAGGCTGCGGATGAGCAGACTTGGAGGACTCCAGGCCAGAGACT
AGGCTGGGCGAAGAGTTCGAGCGTGAAGGGGGCTCCGGGCCAGGGTGACAGGAGGCGTGCTTGAGAGGAAGAAGTT
GACGGGAAGGCCAGTGGCAGCGCAAATCTCGTGAACCTTGGGGGACGAATGCTCAGGATGCGGGTCCCCGCCCTC
CTCGTCTCTCTCTCTGCTTCAGAGGGAGAGCAGGCCCCGTCGCCCCATTTCTGCAACAGCCAGAGGACCTGGTG
GTGCTGCTGGGGGAGGAAGCCCCGCTGCCGTGTGCTCTGGGCGCCTACTGGGGGCTAGTTCACTGGGACTAAGAGTGGG
CTGGCCCTAGGGGGCCAAAGGGACCTACCAGGGTGGTCCCGGTACTGGATATCAGGGAATGCAGCCAATGGCCAG
CATGACCTCCACATTAGGCCCCGTGGAGCTAGAGGATGAAGCATCATATGAATGTGAGGCTACACAAGCAGGCGCTC
CGCTCCAGACCAGCCCAACTGCACGTGCTGGTCCCCCAGAAAGCCCCCAGGTGCTGGGCGGCCCCCTCTGTGTCT
CTGGTTGCTGGAGTTCTTGCAGAACCTGACATGTGCGGAGCCGTGGGGATGCCCGCCCTACCCCTGAATTGCTGTGG
TTCCGAGATGGGGTCTGTTGGATGGAGCCACCTTTTCATCAGACCTGCTGAAGGAAGGGACCCCTGGGTCACTG
GAGAGCACCTTAACCCCTGACCCCTTTTCAGCCATGATGATGGAGCCACCTTTGTCTGCCGGGCCCCGAGCCAGGCC
CTGCCCACAGGAAGAGACACAGCTATCACACTGAGCCTGCAGTACCCCCAGAGGTGACTCTGTCTGCTTCGCCA
CACACTGTGCAGGAGGGAGAGAAGGTCATTTTCTGTGCCAGGCCACAGCCCAGCCTCCTGTACAGGCTACAGG
TGGGCAAAAGGGGGCTCTCCGGTGCTCGGGGCCCGGGGCCAAGGTTAGAGGTCGTGGCAGACGCTCGTTCTCTG
ACTGAGCCCGTGTCTGCGAGGTGAGCAACGCGGTGGGTAGCGCCAACCGCAGTACTGCGCTGGATGTGCTGTTT
GGGCGGATTCTGCAGGCAAAGCCGGAGCCCGTGTCCGTGGACGTGGGGGAAGACGCTTCTTCAGTGCAGCTGG
CGCGGGAACCCGCTTCCACGGTAACCTGGACCCGCCGCGGTGGCGCGCAGGTGCTGGGCTCTGGAGCCACACTG
CGTCTTCCGTGCGTGGGGCCCCGAGGACGAGGCGACTATGTGTGAGAGCTGAGGCTGGGCTATCGGGCTGCGG
GGCGGCGCGCGGAGGCTCGGCTGACTGTGACGCTCCCCCAGTAGTGACCGCCCTGCAGTCTGCGCTGCGCTTC
CTGAGGGGCCCTGCTCGCCTCCAGTGTCTGGTTTTCGCCTCTCCCGCCCCAGATGCCGTGGTCTGGTCTTGGGAT
GAGGGCTTCTTGGAGGCGGGGTGCGAGGGCCGGTTCTGGTGGAGACATTCCCTGCCCCAGAGAGCCGCGGGGA
CTGGGTCCGGGCTGATCTCTGTGCTACACATTTCCGGGACCCAGGAGTCTGACTTTAGCAGGAGCTTTAACTGC
AGTGGCCGGAACCGCTGGGCGAGGGAGGTGCCAGGCCAGCCTGGGCCGTAGAGACTTGCTGCCCAGTGTGCGG
ATAGTGGCCGGAGTGGCCGCTGCCACCACAACCTCTCCTTATGGTCACTACTGGGGTGGCCCTCTGCTGCTGGCGC
CACAGCAAGGCCTCAGCCTCTTCTCCGAGCAAAAGAACCTGATGCGAATCCCTGGCAGCAGCGACGGCTCCAGT
TCACGAGGTCTGAAGAAGAGGAGACAGGCAGCCGCGAGGACCGGGGCCCATTTGTGCACACTGACCACAGTGAT
CTGGTTCTGGAGGAGGAAGGGACTCTGGAGACCAAGGACCCAACCAACGGTTACTACAAGGTCCGAGGAGTCAGT
GTGAGCCTGAGCCTTGGCGAAGCCCTGGAGGAGGTCTCTTCTGCGCACACCTCCCCCTTGGGCCCCCAGG
ACCCCTACCTTCTATGACTTCAACCCACACCTGGGCATGGTCCCCCCTGCAGACTTTACAGAGCCAGGGCAGGC
TATCTCACCACACCCACCCCTCGAGCTTTCACCAGCTACATCAAACCCACATCCTTTGGGCCCCCAGATCTGGCC
CCCCGGAATCCCCCTTCCCATATGCTGCCTTCCCCACACCTAGCCACCCGCTCTCCAGACTCAGTGTGACAT
CTTTCGAATGGAAGAGTCTTGGGATCTCCAACCTTGCCATAATGGATTGTTCTGATTTCTGAGGAGCCAGGACAAG
TTGGCGACCTTACTCTCCAAAACCTGAACACAAGGGGAGGGAAAGATCATTACATTTGTGAGGAGCATTTGTATA
CAGTCAGCTCAGCCAAAGGAGATGCCCCAAGTGGGAGCAACATGGCCACCCAATATGCCACCTATTCCCCGGTG
TAAAAGAGATTCAAGATGGCAGGTAGGCCCTTTGAGGAGAGATGGGGACAGGGCAGTGGGTGTTGGGAGTTTGGG
GCGGGGATGGAAGTTGTTTCTAGCCACTGAAAGAAGATATTTCAAGATGACCATCTGCATTGAGAGGAAAGGTAG
CATAGGATAGATGAAGATGAAGAGCATACCAGGCCCCACCTGGCTCTCCCTGAGGGGAACCTTGCTCGGCCAAT
GGAAATGCAGCCAAGATGGCCATATACTCCCTAGGAACCCAAAATGGCCACCATCTTGATTTTACTTTCTTAAA
GACTCAGAAAGACTTGGACCAAGGAGTGGGGATACAGTGAGAATTACCACTGTTGGGGCAAAATATTGGGATAA
AAATATTTATGTTTAAATAATAAAAAAAGTCAAAGAGAAAAAAA

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FIGURE 584

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA145841
><subunit 1 of 1, 708 aa, 1 stop
><MW: 75093, pI: 6.65, NX(S/T): 3
MLRMRVPALLVLLFCFRGRAGPSPHFLQQPEDLVVLLGEEARLPCALGAYWGLVQWTKSG
IALGGQRDLPGWSRYWISGNAANGQHDHLIRPVELEDEASYECQATQAGLRSRPAQLHVL
VPPEAPQVLGGPSVSLVAGVPANLTCRSRGDARPTPELLWFRDGVLLDGATFHQTLLKEG
TPGSVESTLTLTTPFSHDDGATFVCRARSQALPTGRDTAITLSLQYPPEVTLSPHTVQE
GEKVIFLCQATAQPPVTGYRWAKGGSPVLGARGPRLEVVDASFLTEPVSCVSNVAVGSA
NRSTALDVLFGPILQAKPEPVSVVDGEDASFSCAWRGNPLPRVTWTRRGGAQVLGSGATL
RLPSVGPEDAGDYVCRAEAGLSGLRGGAEARLTVNAPPVVVTAHSAFAFLRGPARLQCL
VFASAPADAVVWSWDEGFLEAGSQGRFLVETFPAPESRGGLGPGGLISVLHISGTQESDFS
RSFNCSARNRLGEGGAQASLGRRDLLPTVRIVAGVAAATTTLLMVITGVALCCWRHASKAS
ASFSEQKNLMRIPGSSDGSSSRGPEEEEETGSREDRGPIVHTDHSDLVLEEEGTLETKDPT
NGYYKVRGVSVSLSLGEAPGGGLFLPPPSPLGPPGTPTFYDFNPHLGMVPPCRLYRARAG
YLTPHPRAFTSYIKPTSFPGPDLAPGTPPPFYAAFPPTSPHRLQTHV
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

Transmembrane domain:

Amino acids 511-531

N-glycosylation sites:

Amino acids 143-147;301-305;484-488

N-myristoylation sites:

Amino acids 48-54;60-66;79-85;139-145;180-186;183-189;355-361;383-389;
387-393;460-466;473-479;494-500;495-501;514-520;528-534;
554-560;592-598;608-614

Amidation site:

Amino acids 500-504

Cell attachment sequence:

Amino acids 149-152

Multicopper oxidases signature 1:

Amino acids 445-466

Immunoglobulin domain:

Amino acids 326-377

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FIGURE 585

GCCCGCCTGAGGAAGCCGTGTGCCTGGGATGCCAAGAGCCAGAGAATGGATCTTCTCCGAGTG
GGGACATTGCTGACAATCCCGGCTTCCCGAGGCGGCTAAGAACAGGCAGTTTGTGTGCGGCTGG
CTGCAGATAACCCAGAGGCACAAAGAGACCGAAGCCACCCGGAGGGACCCACGGACGGACAGAT
GGTAGGCGCGAACCCGAGAGGACCGGCGGAGGCTGAGCACCGAGAGCCGCCAAGGAAGAGAAA
CTAACACAGCCAAGTTACCCCGCGGCTTTCCTTCGCTGCGCTAAGGAATGAAACCCCTTCCA
GCTCGATCTGCTCTTCGTCTGCTTCTTCCTCTTCAGTCAAGAGCTGGGCTCCAGAAGAGAGG
ATGCTGTCTGGTGTGCTGGGCTACATGGCCAAGGACAAGTTTCGGAGAATGAATGAAGGCCAAGT
CTATTCCCTTCAGCCAGCAGCCCCAGGACCAGGTGGTGGTGTGCGGACAGCCAGTGACGCTACT
TTGCGCCATCCCCGAATACGATGGCTTCGTTCTGTGGATCAAGGACGGCTTGGCTCTGGGTGT
GGGCAGGGACCTCTCAAGTTACCCACAGTACCTGGTGGTAGGGAACCACTGTGAGGGGAGCA
CCACCTGAAGATCCTGAGGGCAGAGCTGCAAGACGATGCGGTGTACGAGTGCCAGGCCATCCA
GGCCGCCATCCGCTCCCGCCCCGCACGCCTCACAGTCTGGTGCCGCCTGATGACCCCGTCAT
CCTGGGGGGCCCTGTGATCAGCCTGCGTGCGGGGGACCCCTCTCAACCTCACCTGCCACGCAGA
CAATGCCAAGCCTGCAGCCTCCATCATCTGTTGCGAAAGGGAGAGGTTCATCAATGGGGCCAC
CTACTCCAAGACCCTGCTTCGGGACGGCAAGCGGGAGAGCATCGTCAGCACCCCTCTTCATCTC
CCCTGGTGACGTGGAGAATGGCCAGAGCATCGTGTGTGCTGCCACCAACAAAGCCATCCCGG
AGGAAAGGAGACGTCGGTCACCATTGACATCCAGCACCCCTCCACTGGTCAACCTCTCGGTGGA
GCCACAGCCAGTGCTGGAGGACAACGTCGTCACCTTCCACTGCTCTGCAAAGGCCAACCCAGC
TGTCACCCAGTACAGGTGGGCCAAGCGGGGCCAGATCATCAAGGAGGCATCTGGAGAGGTGTA
CAGGACCACAGTGGACTACACGTACTTCTCAGAGCCCGTCTCCTGTGAGGTGACCAACGCCCTG
GGCAGCACCAACCTCAGCCGCACGGTTGACGTCTACTTTGGGCCCCGGATGACCACAGAACCC
CAATCCTTGCTCGTGGATCTGGGCTCTGATGCCATCTTCAGCTGCGCCTGGACCGGCAACCCA
TCCCTGACCATCGTCTGGATGAAGCGGGGCTCCGGAGTGGTCTGAGCAATGAGAAGACCCTG
ACCCTCAAATCCGTGCGCCAGGAGGACGCGGGCAAGTACGTGTGCCGGGCTGTGGTGCCCCGT
GTGGGAGCCGGGGAGAGAGAGGTGACCCTGACCGTCAATGGACCCCCCATCATCTCCAGCACC
CAGACCCAGCACGCCCTCCACGGCGAGAAGGGCCAGATCAAGTGCTTCATCCGGAGCACGCCG
CCGCCGGACCGCATCGCCTGGTCTGGAAGGAGAACGTTCTGGAGTCGGGCACATCGGGGCGC
TATACGGTGGAGACCATCAGCACCGAGGAGGCGTCATCTCCACCCTGACCATCAGCAACATC
GTGCGGGCCGACTTCCAGACCATCTACAACCTGCACGGCCTGGAACAGCTTCGGCTCCGACACT
GAGATCATCCGGCTCAAGGAGCAAGGTTTCGGAATGAAGTCGGGAGCCGGGCTGGAAGCAGAG
TCTGTGCCGATGGCCGTATCATTTGGGGTGGCCGTAGGAGCTGGTGTGGCCTTCTCGTCCTT
ATGGCAACCATCGTGGCGTTCTGCTGTGCCCGTTCACAGAGAAGTACGGGAGGGAGATCCGGG
ATCTCAGGGAGGGGGACAGAGAAAAGGCCAGGCTTAGGCTGCCCCGGAGAGCAAGTAAGCAG
GAGTGCAATGAACAGGGGTCC**TAA**CAGTGCTGTGAGCTCCTGGGGCAGGGAGTGGGTCTGATG
CATCGGTGTATGTGAGCCTGGGCAACATGGCGCCTGGCAGAGTGGGCGCTAGGCTGAGGTGTA
CCTGGACTAGACTGAACTTCATCTGCAGGGCAGCCAGCATTTTGGATTGAACACATAGCTCTT
TCAGTCAGGAACGTGTACAGAAAGATAGGGGGAAAAGCGGTTTGTGGTTTGATCCTTGCTCTAC
AAGAGCTGTTAGTCTAGAGAGACCCCATCTCTACAACAAAATAAAAATAAAGAGCTGCTAGTC
TCACCAGAAAAGCAGGTCACTCACACAGCTGTGGGGGAGTGGGTGGGGAAGCAATAAAGGAAT
TGCTTTGAGAAAACCTTA

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FIGURE 586

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA148004
><subunit 1 of 1, 600 aa, 1 stop
><MW: 65308, pI: 8.35, NX(S/T): 5
MKPFQLDLLFVCFFLFSQELGLQKRGCCLVGYMAKDKFRRMNEGQVYSFSQQPQDQVVV
SGQPVTLLCAIPEYDGFVLWIKDGLALGVGRDLSSYPQYLVVGNHLSGEHHLKILRAELQ
DDAVYECQAIQAAIRSRPARLTVLVPPDDPVILGGPVISLRAGDPLNLTCHADNAKPAAS
IIWLRKGEVINGATYSKTLLRDGKRESIVSTLFISPGDVENGQSIVCRATNKAIPGGKET
SVTIDIQHPPLVNLSVEPQPVLEDNVVTFHCSAKANPAVTQYRWAKRGQIIKEASGEVYR
TTVDYTYFSEPVSCVTNALGSTNLSRTVDVYFGPRMTTEPQSLLVDLGSDAIFSCAWTG
NPSTLIVWMKRGSGVVLNSNEKTLTLKSVRQEDAGKYVCRAVVPRVGAGEREVTTLTVNGPP
IISSTQTQHALHGEKGQIKCFIRSTPPPDRIAWSWKENVLESSTSGRYTVETISTEEGVI
STLTISNIVRADFQTIYNCTAWNSFGSDTEIIRLKEQGSEMKSGAGLEAESVPMAVIIGV
AVGAGVAFLVLMATIVAFCCARSQRSTGGRSGISGRGTEKKARLRLPRRASKQECNEQGS
```

Important features of the protein:**Signal peptide:**

Amino acids 1-17

Transmembrane domain:

Amino acids 534-555

N-glycosylation sites:

Amino acids 167-171;253-257;324-328;498-502

Glycosaminoglycan attachment sites:

Amino acids 523-527;574-578

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 204-208;370-374;588-592

Tyrosine kinase phosphorylation sites:

Amino acids 40-49;300-308;389-397

N-myristoylation sites:Amino acids 45-51;62-68;84-90;103-109;192-198;236-242;
374-380;436-442;478-484;539-545;543-549;
568-574**Amidation site:**

Amino acids 202-206

Leucine zipper pattern:

Amino acids 8-30

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FIGURE 587

CAAAAAAGGAGCATGTCTTCATCCATGAGAGGCCTCGAAAAATCAATGGTATTTGCATTTCTC
CCAAGAAGGTTGCTTGCCAAAACCTTTGCGCCATTTTCTGCTTTCAGAGTGAGACAAAGTTCA
AAATGACAGTCTGTGAGCTCATTGAAGGCACTAGATACCCTGCCTGCAGGTACCACTATTCCC
CCACAGAGGGGTTTGTCTTGTCACTTGTGATGACTTGAGGCCAGATAGTTTCCTTGGCTATG
TTAAATAACTCAAGATCAGCTACCGAGTCTGAGATCTCTTCTCTCATGGCATTGGAGCTGGCT
GTGCCTGAGGCAGACCTGGACCGTGGACATGGGGCAATGCCTTGAGCGGAAGGGGAAGCCACT
GAATTTTGGGTGTCACCAGGTAAACAGAGCCCTCAGCATCTGAATAGAACTGAACAGGAACA
GAAGAGATTACACTACATCTGAG**ATG**GAGACCTTTCCTCTGCTGCTGCTCAGCCTGGGCCTGG
TTCTTGCAGAAGCATCAGAAAGCACAATGAAGATAATTAAAGAAGAATTTACAGACGAAGAGA
TGCAATATGACATGGCAAAAAGTGGCCAAGAAAAACAGACCATTGAGATATTAATGAACCCGA
TCCTGTTAGTTAAAAATACCAGCCTCAGCATGTCCAAGGATGATATGTCTTCCACATTACTGA
CATTCAGAAGTTTACATTATAATGACCCCAAGGGAAACAGTTCGGGTAATGACAAAGAGTGTT
GCAATGACATGACAGTCTGGAGAAAAGTTTCAGAAGCAAACGGATCGTGCAAGTGGAGCAATA
ACTTCATCCGCAGCTCCACAGAAGTGATGCGCAGGGTCCACAGGGCCCCCAGCTGCAAGTTTGTA
CAGAATCCTGGCATAAGCTGCTGTGAGAGCCTAGAACTGGAAAATACAGTGTGCCAGTTCCT
ACAGGCAAACAATTCCCCAGGTGCCAATACCATAGTGTTACCTCATTAGAGAAGATATTGACA
GTGCTGACAGGTATTCTCTGATGAGCTGGTTAGTTTGTGGCTCTAAGTT**GTA**AATCCACAG
AGCTTTAGGACTAGGGTCTTACTAAAGAAGGACCTCTTCTTGTTCACTTCTGTTTAAACCTTT
CCTTAATATCTACTCTTTAGCACTATAGTGAACCTCTGATTATTTATTCTAACTGGAGGAGTG
AAAAATCCAAAATTGTGGATAATTCAATTAAAAGTTATGACTGATACCG

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FIGURE 588

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA149893
><subunit 1 of 1, 199 aa, 1 stop
><MW: 22427, pI: 6.46, NX(S/T): 3
METFPLLLLSLGLVLAEESESTMKIIKEEFTDEEMQYDMAKSGQEKQTIEILMNPILLVK
NTSLMSKDDMSSTLLTFRSLHYNDPKGNSGNDKECCNDMTVWRKVSEANGSCKWSNNF
IRSSTEVMRRVHRAPSCKFVQNPGISCCESLELENTVCQFTTGKQFPRCQYHSVTSLEKI
LTVLTGHSLSWLVC GSKL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-16

N-glycosylation sites:

Amino acids 61-65;89-93;111-115

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 105-109

N-myristoylation sites:

Amino acids 12-18;88-94;144-150

Microbodies C-terminal targeting signal:

Amino acids 197-201

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FIGURE 589

CAGTCCTGCCGGGACGGTGAGCGCATTACAGCACCTGGACAGCACCGCGGTTGCGCTGCCTCC
AGGGCGGCCCCGGGCTGCTCCTGCTCCGCAGAGCTACGCCCTCCCCCGGGTGCCCCGGACCC
TGCACTTGCCGCCGCTTTCTCTCGCGCTGCTCTGGACCTTGCTAGCCGGCTCTGCACCTCCAG
AAGCCGTGGGCGCGCCGCTCAGCTGCTCCATCGCCTCACTTTCCCAGGCTCGCGCCCGAAGCA
GAGCCATGAGAACCCAGGGTGCCTGGCGAGCCGCTAGCGCC**ATGGG**CCCCGGCGAGGCGCTG
CTGGCGGGTCTCCTGGTGATGGTACTGGCCGTGGCGCTGCTATCCAACGCACTGGTGCTGCTT
TGTTGCGCCTACAGCGCTGAGCTCCGCACTCGAGCCTCAGGCGTCCTCCTGGTGAATCTGTCT
CTGGGCCACCTGCTGCTGGCGGCGCTGGACATGCCCTTCACGCTGCTCGGTGTGATGCGCGGG
CGGACACCGTCGGCGCCCCGGCGCATGCCAAGTCATTGGCTTCCTGGACACCTTCCTGGCGTCC
AACGCGGCGCTGAGCGTGGCGGCGCTGAGCGCAGACCAGTGGCTGGCAGTGGGCTTCCCACTG
CGCTACGCCGGACGCCTGCGACCGCGCTATGCCGGCCTGCTGCTGGGCTGTGCCTGGGGACAG
TCGCTGGCCTTCTCAGGCGCTGCACTTGGCTGCTCGTGGCTTGGCTACAGCAGCGCCTTCGCG
TCCTGTTTCGCTGCGCCTGCCGCCGAGCCTGAGCGTCCGCGCTTCGCAGCCTTCACCGCCACG
CTCCATGCCGTGGGCTTCGTGCTGCCGCTGGCGGTGCTCTGCCCTCACCTCGCTCCAGGTGCAC
CGGGTGGCACGCAGACACTGCCAGCGCATGGACACCGTCACCATGAAGGCGCTCGCGCTGCTC
GCCGACCTGCACCCCAGTGTGCGGCAGCGCTGCCTCATCCAGCAGAAGCGGCGCCGCCACCGC
GCCACCAGGAAGATTGGCATTGCTATTGCGACCTTCCTCATCTGCTTTGCCCCGTATGTCATG
ACCAGGCTGGCGGAGCTCGTGCCCTTCGTCACCGTGAACGCCAGTGGGGCATCCTCAGCAAG
TGCTGACCTACAGCAAGGCGGTGGCCGACCCGTTACGTA CTCTCTGCTCCGCCGGCCGTTTC
CGCCAAGTCCTGGCCGGCATGGTGCACCGGCTGCTGAAGAGAACCCCGCGCCAGCATCCACC
CATGACAGCTCTCTGGATGTGGCCGGCATGGTGCACCAGCTGCTGAAGAGAACCCCGCGCCCA
GCGTCCACCCACAACGGCTCTGTGGACACAGAGAATGATTCTGCTGCAGCAGACACACT**TGA**
GGGCCTGGCAGGGCTCATCGCCCCACCTTCTAAGAAGCCCTGTGGAAAGGGCACTGGCCCTG
CCACAGAGATGCCACTGGGGACCCCGAGACACCAGTGGCTTGACTTTGAGCTAAGGCTGAG

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FIGURE 590

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA149930
><subunit 1 of 1, 363 aa, 1 stop
><MW: 39332, pI: 10.42, NX(S/T): 3
MGPGEALLAGLLVMVLAVALLSNALVLLCCAYSaelRTRASGVLLVNLSLGHLLLAALDM
PFTLLGVMRGRTPSAPGACQVIGFLDTFLASNAALSVAALSADQWLAVGFPLRYAGRRLRP
RYAGLLLGCAWGQSLAFSGAALGCSWLGYSSAFASCSLRLPPEPERPRFAAFTATLHAVG
FVLPLAVLCLTSLQVHRVARRHCQRMDTVMTKALALLADLHPSVRQRCLIQKRRRRHRAT
RKIGIAIATFLICFAPYVMTRLAELVPFVTVNAQWGILSKCLTYSKAVADPFTYSLLRRP
FRQVLAGMVHRLKRTPRPASTHDSSLDVAGMVHQLLKRTPRPASTHNGSVDTENDSCLQ
QTH
```

Important features of the protein:**Signal peptide:**

Amino acids 1-24

Transmembrane domains:

Amino acids 46-60;85-103;130-150;175-192;246-264

N-glycosylation sites:

Amino acids 47-51;348-352;355-359

Tyrosine kinase phosphorylation site:

Amino acids 286-295

N-myristoylation sites:Amino acids 66-72;124-130;128-134;132-138;139-145;244-250;
349-355**G-protein coupled receptor proteins:**

Amino acids 72-112

7 transmembrane receptor (rhodopsin family):

Amino acids 22-294

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FIGURE 591

AAC**ATG**GCTGCGGCGCCTGGGCTGCTCGTCTGGCTGCTCGTGCTCCGGCTGCCCTGGCGGGTG
CCGGGCCAGCTGGACCCCAGCACTGGCCGGCGGTTCTCGGAGCACAACTCTGCGCGGACGAC
GAATGCAGCATGATGTACCGCGGTGAGGCTCTTGAAGATTTACAGGCCCGGATTGTCGTTTT
GTGAATTTTAAAAAGGTGATCCTGTATATGTTTACTATAAACTGGCAAGAGGATGGCCTGAA
GTTTGGGCTGGAAGTGTTGGACGCACTTTTGGATATTTTCCAAAAGATTTAATCCAGGTAGTT
CATGAATATACCAAAGAAGAGCTACAAGTTCCAACAGATGAGACGGATTTTGTGTTGTTTGTAT
GGAGGAAGAGATGATTTTCATAATTATAATGTAGAAGAACTTTTAGGGTTTTTGGAACTGTAC
AATTCTGCAGCTACAGATTCTGAGAAAGCTGTAGAAAAAACTTTACAGGATATGGAAAAAAC
CCTGAATTATCTAAGGAAAGGGAACCTGAACCTGAACCAGTAGAAGCCAACTCAGAGGAAAGT
GATAGTGTATTCTCAGAAAACACTGAGGATCTTCAGGAACAGTTTACAACCTCAGAAGCACCAC
TCCCATGCAAACAGCCAAGCAAATCATGCTCAGGGAGAGCAGGCTTCATTTGAATCTTTTGAA
GAAATGCTGCAAGATAAACTAAAAGTGCCAGAAAGTGAAAACAACAAAACCAGCAATAGTTCT
CAGGTCTCAAATGAACAGGATAAGATTGATGCCTATAAACTTTTGAAAAAGAAATGACTCTA
GACTTGAAAACCAAATTTGGCTCAACAGCTGATGCACCTTGATCTGATGATGAGACAACCAGA
CTCGTTACTTCATTAGAAGATGATTTTGATGAGGAATTGGATACTGAGTATTATGCAGTTGGA
AAGGAAGATGAGGAGAACCAAGAAGACTTTGATGAGTTGCCATTACTTACCTTTACAGATGGG
GAAGATATGAAAACCTCAGCAAAGTCTGGCGTTGAGAAATATCCAACAGATAAAGAGCAGAAT
TCAAATGAAGAGGACAAGGTTCACTAACTGTGCCCCCTGGCATCAAAAATGATGATAAAAAT
ATACTAACACCTGGGGGGACACTATCTTCTCTATTGTACAGGAGGTGAAGAAACAAGAGAT
ACGATGGATTTAGAGAGCTCTAGTTCAGAGGAAGAAAAAGAAGATGATGATGATGCATTAGTC
CCAGATAGCAAACAGGGGAAACCACAGTCAGCAACAGATTATAGTGACCCTGACAATGTAGAT
GATGGTCTTTTTATTGTAGACATTCCTAAAACAAATAATGACAAAAGAAGTAAACGCAGAACAT
CACATTAAAGGAAAAGGGAGGGGAGTTCAAGGAATCCAAGAGGGGCCTGGTACAAGATGAGACA
GAATTAGAGGATGAAAATCAAGAAGGCTTTAAAACAGAGCCATAAACTAT**TGA**CCTCTGAGG
TTTCATTGGAAAGAAAGTGACTGTGCATTATCCATTACAGTAAAGGATTTCAATTGGCTTCAA
AATCCAAAAGTTTATTTTAAAAGGTTTGTGTTAGAACTAAGCTGCCTTGGCAGTGTGCATTT
TTGAGCCAAACAATTCAAAAATGTCATTTCTTCCCTAAATAAAAATCACCTTTTAAGCTAGAG
CGTCCTTACAACCTTTGAAATGTGCAATAAAGAATACCTGTGTTTTAGCTAATGTAGCATATGT
AATTGCAAAATGATTTAGAATGTCATGAAAAATATGAACATTTCTGTGGAAATGCTTTAAGA
ACATGTATTTCCATTATCCTATTTTGTAGTGTACACCAGCTGAATACGGAGCAATGGTGTATTAT
AAGCGTTTTTTTAACTATCTGGTCACAAAGACTGTTACGCTAAAAATGTTTACTAAAAGATC
ACTAACTATCTCCCCTCTTGCTGAAGTTCTTTGTAGTAATAGCTCATAAAAATTTGTTTATT
AATATTTAAAAA

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FIGURE 592

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA150157
><subunit 1 of 1, 499 aa, 1 stop
><MW: 56471, pI: 4.31, NX(S/T): 2
MAAAPGLLVWLLVLRLEPWRVPGQLDPSTGRRFSEHKLCADDECSMMYRGEALEDFTGPDC
RFVNFKKGDPVYVYYKLARGWPEVWAGSVGRTFGYFPKDLIQVVHEYTKHEELQVPTDET
FVCFDGGRRDDFHNYNVEELLGFLELYNSAATDSEKAVEKTLQDMEKNPELSKEREPEPEP
VEANSEESDSVFSENTEDLQEQFTTQKHSHANSQANHAQGEQASFESEEMLQDKLKVP
ESENKTSNSSQVSNEQDKIDAYKLLKKEMTLDLKTKFGSTADALVSDDETTRLVTSLED
DFDEELDTYYAVGKEDEENQEDFDELPLLTFTDGEDMKTPAKSGVEKYPTDKEQNSNEE
DKVQLTVPPGIKNDDKNILTTWGDITFSIVTGGEETRDMDLESSSSEEEKEDDDALVP
DSKQKGKQSATDYSDDPNVDDGLFIVDIPKTNNKVEVNAEHHIKGKGRGVQESKRGLVQD
ETELEDENQEGFKTEPIKL
```

Important features of the protein:**Signal peptide:**

Amino acids 1-22

N-glycosylation sites:

Amino acids 245-249;249-253

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 30-34

Tyrosine kinase phosphorylation site:

Amino acids 66-72

N-myristoylation sites:

Amino acids 392-398;469-475

Amidation site:

Amino acids 28-32

Aminoacyl-transfer RNA synthetases class-II signature 1:

Amino acids 47-70

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FIGURE 593

GGGCCAGTAGAGTGTGTCTGGGTCAGCTGAGTGA CTACATCAAAGCTCCCAGCCTTGAAAAAC
ACATGCTGTTCCCAGGCCTCAAGATATTGAAACATTAATTAGATAATTTAAAGTAGCGTTTTTC
TTCTACA**ATGT**CTGAAGAAGTGACCTACGCGACACTCACATTT CAGGATTCTGCTGGAGCAAG
GAATAACCGAGATGGAAATAACCTAAGAAAAAGAGGGGCATCCAGCTCCATCTCCCATTTGGCG
TCATGCTGCTCTGGGTCTGGTA ACTCTTTGCCTGATGTTGCTGATTGGGCTGGTGACGTTGGG
GATGATGTTTTTGCAGATATCTAATGACATTA ACTCAGATTCAGAGAAATTGAGTCAACTTCA
GAAAACCATCCAACAGCAGCAGGATAACTTATCCCAGCAACTGGGCAACTCCAACA ACTTGTC
CATGGAGGAGGAATTTCTCAAGTCACAGATCTCCAGTCTACTGAAGAGGCAGGAACAAATGGC
CATCAA ACTGTGCCAAGAGCTAATCATT CATACTTCAGACCACAGATGTAATCCATGTCCTAA
GATGTGGCAATGGTACC AAAATAGTTGCTACTATTTTACAACAAATGAGGAGAAAACCTGGGC
TAACAGTAGAAAAGGACTGCATAGACAAGA ACTCCACCCTAGTGAAGATAGACAGTTTGGAAGA
AAAGGATTTTCTTATGTCACAGCCATTACTCATGTTTTTCGTTCTTTTGGCTGGGATTATCATG
GGACTCCTCTGGCAGAAAGTTGGTTCTGGGAAGATGGCTCTGTTCCCTCTCCATCCTTG TACGT
CTCTAACTAT**TGA**GGGTAAACACAAGCTTTCCATGGAATCCTGGGAAAATTAATAATGATTGT
GAGAATTATAAATACAGACATAAAAAGAGGAGTACAACATACTGAGAAAAGAGCTCCAGTAAC
AAATATTGAAAGGAGATTTAGTACTAAAGAACTTGACCAGATCAATGGATCCAAGGATGTGC
TTATTTTCAAAAAGGAAATATTTATATTTCTCGCTGTAGTGCTGAAATTTTTTGGATT TGCGA
GAAGACAGCTGCCCCAGTGAAGACTGAGGATTTGGATTAGTATGCTTCTTCCAATTCTCCAA
GAAGTAAGAGACTTGTGAGTAAGCTCATATGAGGAAAGAGGAAACTACGGTACCAGAGCAAGG
CCGAATTCTGCA

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FIGURE 594

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA150163
><subunit 1 of 1, 232 aa, 1 stop
><MW: 26754, pI: 5.80; NX(S/T): 3
MSEEVTYATLTFQDSAGARNNRDGNLRLKRGHPAPSPIWRHAALGLVTLCLMLLIGLVTL
GMMFLQISNDINSDEKLSQLQKTIQQQQDNLSQLGNSNNLSMEEEFLLKSQISSLLKRQ
EQMAIKLCQELIIHTSDHRCNCPKMWQWYQNSCYFTTNEEKTWANSRKDCIDKNSTLV
KIDSLEEKDFLMSQPLLMFSFFWLGLSWDSSGRSWFWEDGSVPSPSLYVSNY
```

Important features of the protein:**Transmembrane domain:**

Amino acids 42-62

N-glycosylation sites:

Amino acids 91-95;101-105;176-180

N-myristoylation sites:

Amino acids 17-23;97-103

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FIGURE 595

CGGACGCGTGGGGAAGAGGAGGAGGAGGAAGAAGACGTGGACAAGGACCCCCATCCTACCCAG
AACACCTGCCTGCGCTGCCGCCACTTCTCTTTAAGGGAGAGGAAAAGAGAGCCTAGGAGAACC
ATGGGGGGCTGCGAAGTCCGGGAATTTCTTTTGCAATTTGGTTTCTTCTTGCCCTATGCTGACA
GCGTGGCCAGGCGACTGCAGTCACGTCTCCAACAACCAAGTTGTGTTGCTTGATACAACAAC
GTACTGGGAGAGCTAGGATGGAAAACATATCCATTAAATGGGTGGGATGCCATCACTGAAATG
GATGAACATAATAGGCCCATTCACACATACCAGGTATGTAATGTAATGGAACCAAACCAAAAC
AACTGGCTTCGTACAAACTGGATCTCCCGTGATGCAGCTCAGAAAATTTATGTGGAAATGAAA
TTCACACTAAGGGATTGTAACAGCATCCCATGGGTCTTGGGGACTTGCAAAGAAACATTTAAT
CTGTTTTATATGGAATCAGATGAGTCCCACGGAATTAAATTCAAGCCAAACCAGTATACAAAG
ATCGACACAATTGCTGCTGATGAGAGTTTTACCCAGATGGATTTGGGTGATCGCATCCTCAAA
CTCAACACTGAAATTCGTGAGGTGGGGCCTATAGAAAGGAAAGGATTTTATCTGGCTTTTCAA
GACATTGGGGCGTGCAATTGCCCTGGTTTCAGTCCGTGTTTTCTACAAGAAATGCCCTTCACT
GTTTCGTAACCTGGCCATGTTTCCTGATACCATTCCAAGGGTTGATTCCCTCCTCTTTGGTTGAA
GTACGGGGTTCTTGTGTGAAGAGTGCTGAAGAGCGTGACACTCCTAACTGTATTGTGGAGCT
GATGGAGATTGGCTGGTTCCTCTTGGAAGGTGCATCTGCAGTACAGGATATGAAGAAATTGAG
GGTTCTTGCCATGGAGCCTCCAAAGGCCGCTGCTTCT**TAG**TTGGCCATCTTGGCCCCACCCGA
AACAGTAACCTTTGAAGAATAAAAAGAAAAAGCAAAAGAGTAGCATTACTAAAATATTAAACGG
TTACATTTACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 596

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA153579
><subunit 1 of 1, 285 aa, 1 stop
><MW: 32368, pI: 5.32, NX(S/T): 0
MGGCEVREFLLQFGFFLPMLTAWPGDCSHVSNNQVLLDTTTVLGELGWKTYPLNGWDAI
TEMDEHNRPIHTYQVCNVMEPNQNNWLRTNWI SRDAAQKIYVEMKFTLRDCNSIPWVLGT
CKETFNLFYMESDESHGIKFKPNQYTKIDTIAADESFTQMDLGDRILKLNTEIREVGPIE
RKGFYLAFAQDIGACIALVSVRVFYKKCPFTVRNLAMFPDTIPRVDSSSLVEVRGSCVKSA
EERDTPKLYCGADGDWLVPLGRCICSTGYEEIEGSCHGASKGRCF
```

Important features of the protein:**Signal peptide:**

Amino acids 1-22

N-myristoylation sites:

Amino acids 192-198;274-280;278-284

Receptor tyrosine kinase class V signature 1:

Amino acids 192-209

Ephrin receptor ligand binding domain:

Amino acids 34-207

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FIGURE 597

ACACTGGCCAAACAAAAACGAAAGCACTCCGTGCTGGAAGTAGGAGGAGAGTCAGGACTCCCA
GGACAGAGAGTGCACAAACTACCCAGCACAGCCCCCTCCGCCCCCTCTGGAGGCTGAAGAGGG
ATTCCAGCCCCTGCCACCCACAGACACGGGCTGACTGGGGTGTCTGCCCCCCTTGGGGGGGG
CAGCACAGGGCCTCAGGCCTGGGTGCCACCTGGCACCTAGAAG**ATG**CCTGTGCCCTGGTTCTT
GCTGTCCTTGGCACTGGGCCGAAGCCCAGTGGTCCTTTCTCTGGAGAGGCTTGTGGGGCCTCA
GGACGCTACCCACTGCTCTCCGGGCCTCTCCTGCCGCCTCTGGGACAGTGACATACTCTGCCT
GCCTGGGGACATCGTGCCTGCTCCGGGGCCCCGTGCTGGCGCCTACGCACCTGCAGACAGAGCT
GGTGCTGAGGTGCCAGAAGGAGACCGACTGTGACCTCTGTCTGCGTGTGGCTGTCCACTTGGC
CGTGCAATGGGCACTGGGAAGAGCCTGAAGATGAGGAAAAGTTTGGAGGAGCAGCTGACTCAGG
GGTGGAGGAGCCTAGGAATGCCTCTCTCCAGGCCCAAGTCGTGCTCTCCTTCCAGGCCTACCC
TACTGCCCGCTGCGTCTGCTGGAGGTGCAAGTGCCTGCTGCCCTTGTGCAGTTTGGTCAGTC
TGTGGGCTCTGTGGTATATGACTGCTTCGAGGCTGCCCTAGGGAGTGAGGTACGAATCTGGTC
CTATACTCAGCCCAGGTACGAGAAGGAACTCAACCACACACAGCAGCTGCCTGCCCTGCCCTG
GCTCAACGTGTGACGAGATGGTGACAACGTGCATCTGGTTCTGAATGTCTCTGAGGAGCAGCA
CTTCGGCCTCTCCCTGTACTGGAATCAGGTCCAGGGCCCCCCTAAAACCCCGGTGGCACAAAA
CCTGACTGGACCGCAGATCATTACCTTGAACCACACAGACCTGGTTCCCTGCCTCTGTATTCA
GGTGTGGCCTCTGGAACCTGACTCCGTTAGGACGAACATCTGCCCTTCAGGGAGGACCCCCG
CGCACACCAGAACCTCTGGCAAGCCGCCGACTGCGACTGCTGACCCTGCAGAGCTGGCTGCT
GGACGCACCGTGCTCGCTGCCCGCAGAAGCGGCACTGTGCTGGCGGGCTCCGGGTGGGGACCC
CTGCCAGCCACTGGTCCCACCGCTTTCTGAGGAGAACGTCAGTGTGGACAAGGTTCTCGAGTT
CCCATTGCTGAAAGGCCACCCTAACCTCTGTGTTTCAAGTGAACAGCTCGGAGAAGCTGCAGCT
GCAGGAGTGCTTGTGGGCTGACTCCCTGGGGCCTCTCAAAGACGATGTGCTACTGTTGGAGAC
ACGAGGCCCCCAGGACAACAGATCCCTCTGTGCCTTGGAAACCCAGTGGCTGTACTTCACTACC
CAGCAAAGCCTCCACGAGGGCAGCTCGCCTTGGAGAGTACTTACTACAAGACCTGCAGTCAGG
CCAGTGTCTGCAGCTATGGGACGATGACTTGGGAGCGCTATGGGCCTGCCCCATGGACAAATA
CATCCACAAGCGCTGGGCCCTCGTGTGGCTGGCCTGCCTACTCTTTGCCGCTGCGCTTTCCCT
CATCCTCCTTCTCAAAAAGGATCACGCGAAAGGGTGGCTGAGGCTCTTGAAACAGGACGTCCG
CTCGGGGGCGGCCGCCAGGGGCCGCGCGGCTCTGCTCCTCTACTCAGCCGATGACTCGGGTTT
CGAGCGCCTGGTGGGCGCCCTGGCGTCCGGCCCTGTGCCAGCTGCCGCTGCGCGTGGCCGTAGA
CCTGTGGAGCCGTCGTGAAGTGAAGCGCGCAGGGGGCCGTTGGCTTGGTTTACGCGCAGCGGCG
CCAGACCTTGCAGGAGGGCGGCGTGGTGGTCTTGCTCTTCTCTCCGGTGCGGTGGCGCTGTG
CAGCGAGTGGCTACAGGATGGGGTGTCCGGGGCCCGGGCGCACGGCCCGCACGACGCCTTCCG
CGCCTCGCTCAGCTGCGTGTGCCCCGACTTCTTGCAAGGGCCGGCGCCCGGAGCTACGTGGG
GGCCTGCTTCGACAGGCTGCTCCACCCGACGCGGTACCCGCCCTTTTCCGCACCGTGCCCGT
CTTCACACTGCCCTCCCAACTGCCAGACTTCTGGGGGCCCTGCAGCAGCCTCGCGCCCCGCG
TTCCGGGGCGGCTCCAAGAGAGAGCGGAGCAAGTGTCCCGGGCCCTTCAGCCAGCCCTGGATAG
CTACTTCCATCCCCCGGGACTCCCGCGCCGGGACGCGGGGTGGGACCAGGGGCGGGACCTGG
GGCGGGGGACGGGACT**TAA**ATAAAGGCAGACGCTGTTTTTCTAAAAAA

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FIGURE 598

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA164625
><subunit 1 of 1, 705 aa, 1 stop
/><MW: 76970, pI: 6.00, NX(S/T): 9
MPVPWFLLSLALGRSPVVLSTLERLVGPQDATHCSPGLSCRLWDSILCLPGDIVPAPGP
VLAPTHLQTELVLRCQKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRN
ASLQAQVVLSTFQAYPTARCVLLEVQVPAALVQFGQSVGSVVYDCFEAALGSEVRIWSYT
QPRYEKELNHTQQLPALPWLNVSADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWH
KNLTGPGQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLT
LQSWLLDAPCSLPAEAALCWRAPGGDPCQPLVPPLSWENVTVDKVLEFPLLKGHPNLCV
QVNSSEKLQEQELWADSLGPLKDDVLLLETRGPDNRSLCALEPSGCTSLPSKASTRA
ARLGEYLLQDLQSGQCLQLWDDDLGALWACPMCKYIHKRWALVWLACLLFAAALSILL
LKKDHAKGWLRLLLKQDVRSAAAARGRAALLYSADDSGFERLVGALASALCQLPLRVAV
DLWSRRELSAQGPVAVFHAQRRQTLQEGGVVLLFSPGAVALCSEWLQDGVSGPGAHGP
HDAFRASLSCVLPDFLQGRAPGSYVGACFDRLPHPDVAVPALFRTVPVFTLPSQLPDFLG
ALQQPRAPRSGRLQERAEQVSRLQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

Transmembrane domain:

Amino acids 453-473

N-glycosylation sites:Amino acids 118-122;186-190;198-202;211-215;238-242;
248-252;334-338;357-360;391-395;**Glycosaminoglycan attachment site:**

Amino acids 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 552-556

N-myristoylation sites:Amino acids 107-113;152-158;319-325;438-444;516-522;612-618;
692-698;696-702;700-706

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FIGURE 599

GGTCCTTA**ATG**GCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTGC
TGTCGGGCTGGTCCCGGGCTGGGCGAGCCGACCCTCACTCTCTTTGCTATGACATCACCGTCA
TCCCTAAGTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGACTT
TTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCCTGGGGAAGAACTAA
ATGTCACAACGGCCTGGAAAGCACAGAACCCAGTACTGAGAGAGGTGGTGGACATACTTACAG
AGCAACTGCGTGACATTAGCTGGAGAATTACACACCCAAGGAACCCCTCACCTGCAGGCCAA
GGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGTTTCGATG
GGCAGATCTTCCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCCTGGAGCCA
GAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATTACTTCTCAA
TGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACCCCTGGAGCCAA
GTGCAGGAGCACCACTCGCCATGTCCTCAGGCACAACCCAACCTCAGGGCCACAGCCACCACCC
TCATCCTTTGCTGCCTCCTCATCATCCTCCCCTGCTTCATCCTCCCTGGCATCT**GA**GGAGAGT
CCTTTAGAGTGACAGGTTAAAGCTGATACCAAAGGCTCCTGTGAGCACGGTCTTGATCAAAC
TCGCCCTTCTGTCTGGCCAGCTGCCCACGACCTACGGTGTATGTCCAGTGGCCTCCAGCAGAT
CATGATGACATCATGGACCCAATAGCTCATTCAGTGCCTTGATTCCTTTTGCCAACAATTTTA
CCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACCTGATGGAATTCCTGCA
CTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTCTCTTTTGTGGAAAA
TCAAGTACTTCTTTGAATGATGATCTCTTTCTTGCAAATGATATTGTCAGTAAAATAATCACG
TTAGACTTCAGACCTCTGGGGATTCTTTCCGTGTCCTGAAAGAGAATTTTAAATTATTTAAT
AAGAAAAAATTTATATTAATGATTGTTTCCTTTAGTAATTTATTGTTCTGTACTGATATTTAA
ATAAAGAGTTCTATTTCCCAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 600

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTFLH
YDCGNKTVTPVSPPLGKKLNVTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQARMS
CEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFSMGD
CIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

Important features:

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

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FIGURE 601

GCAGTCAGAGACTTCCCCTGCCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCTT
GCTTCCTGAAGTAGCTCACAGTAGCCCGCGGCCAGGGCAATCCGACCACATTTCACTCTCA
CCGCTGTAGGAATCCAG**ATG**CAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATGATG
GGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCCCGGC
GCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCTGCTGACTTTGT
GCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTTCAGTACTACCAGCTCT
CCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGATTAGGAAATACGTCCCAAGAGT
TGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAAAC
TCTGTCTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAGAACAATGGA
AATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAGGACTGTAAAT
ATTTCTGCCTTAGTGAAAACCTACCATGCTGAAGATAAACAACAAGAAGACCTGGAATTTG
CCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTTTGCGCCCTGACA
GTGGCAAGGCCTGGCTGTGGATGGATGGAACCCCTTTCACTTCTGAACTGTTCCATATTATAA
TAGATGTCACCAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGGGATGATCTTCTCAA
AGGACTGCAAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAATGGTGAAGCCAGAGA
GCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACT**TGA**TTCGCCCTCTGCAACTACAAAT
AGCAGAGTGAGCCAGGCGGTGCCAAGCAAGGGCTAGTTGAGACATTGGGAAATGGAACATAA
TCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTTCCTCGTGTTTCCTGTTTCAGGATCAC
CAGCATTTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCACAAGAAGTCTTATTTACATGC
CACCAACCAACCTCAGAAACCCATAATGTCATCTGCCTTCTTGGCTTAGAGATAACTTTTAGC
TCTCTTTCTTCTCAATGTCTAATATCACCTCCCTGTTTTTCATGTCTTCCTTACACTTGGTGGA
ATAAGAAACTTTTTGAAGTAGAGGAAATACATTGAGGTAACATCCTTTTCTCTGACAGTCAAG
TAGTCCATCAGAAATTGGCAGTCACTTCCCAGATTGTACCAGCAAATACACAAGGAATTCTTT
TTGTTTGTTCAGTTCATACTAGTCCCTTCCCAATCCATCAGTAAAGACCCCATCTGCCTTGT
CCATGCCGTTTCCCAACAGGGATGTCACCTTGATATGAGAATCTCAAATCTCAATGCCTTATAA
GCATTCCTTCCTGTGTCCATTAAAGACTCTGATAATTGTCTCCCCTCCATAGGAATTTCTCCCA
GGAAAGAAATATATCCCATCTCCGTTTCATATCAGAACTACCGTCCCCGATATTCCCTTCAG
AGAGATTAAAGACCAGAAAAAAGTGAGCCTCTTCATCTGCACCTGTAATAGTTTCAGTTCCTA
TTTTCTTCATTGACCCATATTTATACCTTTCAGGTACTGAAGATTTAATAATAATAAATGTA
AATACTGTGAAAAA

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FIGURE 602

MQAKYSSTRDMLDDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCLVLLI
GLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRELY
NKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAASQSY
SEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSPRSRDCVAILNGMIFSKDCKEL
KRCVCERRAGMVKPESLHVPPETLGEGD

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FIGURE 603

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTCC
CAGCAAT**ATG**CATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCCCT
GTCTGGATGGGCGGCCAGCGATGACCCCAATTGAGAAGGTCATTGAAGGGATCAACCGAGGGCT
GAGCAATGCAGAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGAATCACGCATGC
CGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGCAAGGA
GTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGATCAACCA
TGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACGCTGCTGG
ACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCACCAGGCTGG
GAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGGAAAGGAAGT
GGAGAAGCTTGGCCAAGGTGCCCAACCATGCTGCTGGCCAGGCCGGAAGGAGCTGCAGAATGC
TCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGCAACCATCAAAG
CGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGGGGCCTCAGTCAA
CACGCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCATGCCCT**TAA**ACTGG
CATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTCACATCAGCTGACATGACCTGGAGGGG
TTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTAAGGGGATTTGTGAATAAA
CTTGATACACCA

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FIGURE 604

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675
><subunit 1 of 1, 247 aa, 1 stop
><MW: 25335, pI: 7.00, NX(S/T): 0
MHLARLVGSCSLLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVKGALDGINSGITHAGR
EVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAGQA
GKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQNAHN
GVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP
```

Important features of the protein:**Signal peptide:**

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

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FIGURE 605

GCGACGCGCGGCGGGGCGGCGAGAGGAAACGCGGCGCCGGGCGGGCCCGGCCCTGGAG**ATGG**
TCCCCGGCGCCGCGGGGCTGGTGTTGTCTCGTGCTCTGGCTCCCCGCGTGCCTCGCGGCCACG
GCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCCTGGGGACATTCGATACATCT
TCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTACACAAGGTATGAGCAGATTACACC
TTGTCCCCGCTGAACCTCCAGAGGCCTGCGGGGAACCTCAGCAACGGTTTCTTCATCCAGGACC
AGATTGCTCTGGTGGAGAGGGGGGGCTGCTCCTTCCTCTCCAAGACTCGGGTGGTCCAGGAGC
ACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTACGTGGAGA
TGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCCTGCTCGGCCGAGACG
GCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTTCCATCCCAG
TCAATGTCACCAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTCTGG**TAGA**AAGA
GTTTGTCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCCAGGAATTTTGC
TACTTGGAATTTGGAGATAGCATCTGGGGACAAGTGGAGCCAGGTAGAGGAAAAGGGTTTGGG
CGTTGCTAGGCTGAAAGGGAAGCCACCACTGGCCTTCCCTTCCCCAGGGCCCCCAAGGGTG
TCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTAGAACCCGAAACAAA
AGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACTCACCTGGCTCCAGCC
TCCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGGAGTGGTTTAAAGAGCT
GGTGTTTGGGGACTCAATAAACCTCACTGACTTTTGTAGCAATAAAGCTTCTCATCAGGGTTG
CAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 606

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532
><subunit 1 of 1, 188 aa, 1 stop
><MW: 21042, pI: 5.36, NX(S/T): 2
MVPGAAGWCCLVLWLPACVAAHGFRIDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQI
HLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDनावDNDsfyv
EMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW
```

Signal peptide:
amino acids 1-20

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FIGURE 607

GCATTTGCCACTGGTTGCAGATCAGGCGGACGAGGAGCCGGGAAGGCAGAGCC**ATGT**GGCTGC
CCCCTGCTCTGCTCCTTCTCAGCCTCTCAGGCTGTTTCTCCATCCAAGGCCAGAGTCTGTGA
GAGCCCCAGAGCAGGGGTCCCTGACGGTTCAATGCCACTATAAGCAAGGATGGGAGACCTACA
TTAAGTGGTGGTGGCGAGGGGTGCGCTGGGATACATGCAAGATCCTCATTGAAACCAGAGGGT
CGGAGCAAGGAGAGAAGAGTGACCGTGTGTCCATCAAGGACAATCAGAAAGACCGCACGTTCA
CTGTGACCATGGAGGGGCTCAGGCGAGATGACGCAGATGTTTACTGGTGTGGGATTGAAAGAA
GAGGACCTGACCTTGGGACTCAAGTGAAAGTGATCGTTGACCCAGAGGGAGCGGCTTCCACAA
CAGCAAGCTCACCTACCAACAGCAATATGGCAGTGTTTCATCGGCTCCCACAAGAGGAACCACT
ACATGCTCCTGGTATTTGTGAAGGTGCCATCTTGCTCATCTTGGTCACTGCCATCCTCTGGT
TGAAGGGGTCTCAGAGGGTCCCTGAGGAGCCAGGGGAACAGCCTATCTACATGAACTTCTCCG
AACCTCTGACTAAAGACATGGCCACT**TAG**AGAGATGGATCTGCAGAGCCTTCCCTGCCCTGGCC
ACGTTTCCAGAAGAGACTCGGGCTGTGGAAGGAACATCTACGAGTCTCGGGATGCAGTGACT
GAGATAGGGGCCCTGGGCCCTCCGCCCTGGCCTTGGAGCTGGTGGGCACCTCCCTGTTCTGCAC
AGCTCAGGGACTTAGCCAGGTCTCTCCTGAGCCACCATCACCTCCTGGGGTGCCAGCACCTG
TTCTCTTGGTCAGGAGCTGTAGAGATGGAGCTCAAGCACTGGACGACTCTGTCCCCACTGCTG
GAATAACTCGGGCACAGAGCATGGGACCAAAGTACAGAAAGAGGTTGGGGGAGACCCCCCAG
CCCTAGACTTCCATCATTCCGGAGACCAACTCAACACCGTCTTGCCTGAGAACCTGATATATCC
GTGTTTTTAAATTTTTTTTTTTCTAGCAAAGTTGGGTTTTAATGACTTATGTTTCATAGGAAAC
CTCTCTGATCCCACACACAAGGAGGGTGATTCTGGGATGAGTTCCTGGTTCTAGGGCATGAGG
GGCTGGATGGACCCTGTCCCCAGGGAGGACATGGCTCTGAGTCCACAGGGCTGAGGAGGCAAT
GGGAACCTCCCTGGCCCCGGCCCGGTGCTTGCTCCTCCCCCTCCACCTCTTCTCCTCCTAGCT
CCCCAAGCTCCCTGCCTATTCCCCCACCTCCGAGGGGCTGCAGCTTGGGAGCCTCCTCAGCAT
GACAGCTTGGGTCTCCTCCCCAAAAGAGCCTGTCAGGCCTCAAGAACCACCTCCAGGTGGGGA
GGGCAGTAACGAAAACCATCGCAGGAAATGGCACCCCTCCCTTTTCGGTGATGTTGAAATCATG
TTACTAATGAAAACGTCTCCTAGGGAAGTGGTCTGTCTCCTCACAGGCTTCACCCACGGCGAT
GAGGCCCTTGAATGTGGTCACTTTGTGCTGTATGGTTGAGGGACCCTCACACCAAAGGGACCT
TCCCATGTGAGATGTGCTCCCGCCCCACCTGCCCACAAGCAAACACACCACACATGTTCCGGC
ATGTTGCCCTTTGAACACCCATGAGGACGCCTCCAACCTGCTCTTGGTTCTAATAGGGAGTAC
TGACTGTCAGCAGTGGATAAAGGAGAGGGGACCCTCTGGTCCCTAGCATGGCACCCAGAGCCT
CCCCTCTTCTTGCTCCTTCAGCCAAAGAGAACTTTCTCTGACTTTGAACTGAATTTAGGTCTC
TGGCCAATGATGGGCCTGAAAATTCATAATGGCCAGAGAGGAGAGTTTCGAGCCCCGGCTAAGA
TCCCCTGAGTCATTCTGTGAGGGACCAAGACCCACAGTCCACCAGCCCCAGGGCCCTACCTCC
TGGAATGCTTTCCTGGATCCAGCTTCCCGAAGATCCGACCAGACCCAGGGAGGACGGCACCGC
TCCGCGGGAGGGAAAGCCAAAGCATGGTGCTTCACCAGCTGGACTCAGGGGCGAGGGGACATG
GGCGCTTGTCAACGTGATGTCATTCTTTTCCACCGTTTCTTCTGTTGATATTCAATGAATC
CGTCAATCTCTCTGGGAAA

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FIGURE 608

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA105849
><subunit 1 of 1, 201 aa, 1 stop
><MW: 22689, pI: 7.41, NX(S/T): 1
MWLPPALLLLSLSGCFSTIQGPESVRAPEQGSITVQCHYKQGWETIYIKWWCRGVRWDTCKI
LIETRGSEQGEKSDRVSIKDNQKDRTFTVTMEGLRRDDADVWCGIERRGPDLTQVKVI
VDPEGAASTTASSPTNSNMAVFIGSHKRNHYMLLVFVKVPILLILVTAILWLKGSQRVPE
EPGEQPIYMNFSEPLTKDMAT
```

Important features of the protein:**Signal peptide:**

Amino acids 1-17

Transmembrane domain:

Amino acids 151-170

N-glycosylation site:

Amino acids 190-194

Tyrosine kinase phosphorylation site:

Amino acids 95-103

N-myristoylation sites:

Amino acids 66-72;125-131

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 5-16

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FIGURE 609

GATGGCGCAGCCACAGCTTCTGTGAGATTTCGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGGG
GACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCAAA
ACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTT
CCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACG
ACCTGTGCCACCAACTCGCACTCAGACTCTGAACTCAGACCTGAAATCTTCTCTTCACGGGAG
GCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTAGGCCTAAGATGAAAGCCTCTAGT
CTTGCCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAG
ACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCT
GAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACT
GAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTC
TATCTGGACAGGGTATTTAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGC
AGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCATGCCACATGACA
TGCCATTGTGGGGAGGAAGCAATGAAGAAATAAGCCAGATTCTGAGTCACTTTGAAAAGCTG
GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAAGTAGACATTCTTCTGCAATGGATGGAG
GAGACAGAAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTTCGAGGTCAAGAGCTCCAGTCT
TCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACTGTACTAGTCTTGTGCT
GGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCATGATTGTCTTTATGCATCCCC
AATCTTAATTGAGACCATACTTGTATAAGATTTTTGTAATATCTTTCTGCTATTGGATATATT
TATTAGTTAATATATTTATTTATTTTTTGCTATTTAATGTATTTATTTTTTTTACTTGACATG
AACTTTAAAAAATTACAGATTATATTTATAACCTGACTAGAGCAGGTGATGTATTTTTAT
ACAGTAAAAAAAAAAACCTTGTAATTCTAGAAGAGTGGCTAGGGGGGTTATTCAATTTGTAT
TCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGATATTTGAAATTGAACCAATGAC
TACTTAGGATGGGTGTGGAATAAGTTTTGATGTGGAATTGCACATCTACCTTACAATTACTG
ACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTATCTTCCAGCCAGGAATCCTACACGG
CCAGCATGTATTTCTACAAATAAAGTTTTCTTGCATACCAAAAAAAAAAAAAAAAAAAAA

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FIGURE 610

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNKGATTCATNSHSDSEL
RPEIFSSREAWQFFLLLWSPDFRPKMKASSLAFLLSAAFYLLWTPSTGLKTLNLGSCVI
ATNLQEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVF
KNYQTPDHYTLRKISSLANSEFLTIKKDLRLSHAMTCHCGEAMKKYSQILSHFEKLEPQ
AAVVKALGELDILLQWMEETE
```

Important features of the protein:**Signal peptide:**

Amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 192-196;225-229

N-myristoylation sites:

Amino acids 42-48;46-52;136-142